U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

SEARCH REQUEST FORM

5-54

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:
Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 5-7-98
Searcher: MARK
Terminal time: 6
Elapsed time: prep 10
CPU time: _____
Total time: 16
Number of Searches: 1
Number of Databases: 11

Search Site
_____ STIC
/ CM-1
_____ Pre-S

Type of Search
/ N.A. Sequence
/ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors
/ ~~IG~~ MPSRCH
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other

PTO-1590 (9-90)

(TM)

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:18:28 1998; MasPar time 3.90 Seconds
375.094 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150
Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 29.680; Variance 124.309; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	56.4	455	7	US-08-321-	Sequence 2, Applicatio	1.28e-100
2	1124	56.4	455	7	US-08-050-	Sequence 25, Applicati	1.28e-100
3	1115	55.9	199	7	US-08-050-	Sequence 48, Applicati	1.05e-99
4	996	49.9	167	7	US-08-050-	Sequence 2, Applicatio	1.15e-87
5	996	49.9	167	7	US-08-050-	Sequence 57, Applicati	1.15e-87
6	981	49.2	124	7	US-08-050-	Sequence 4, Applicatio	3.78e-86
7	800	40.1	157	7	US-08-050-	Sequence 50, Applicati	6.45e-68
8	666	33.4	158	7	US-08-050-	Sequence 54, Applicati	1.67e-54
9	477	23.9	153	7	US-08-050-	Sequence 52, Applicati	8.82e-36
10	339	17.0	41	7	US-08-050-	Sequence 36, Applicati	2.30e-22
11	324	16.2	40	7	US-08-050-	Sequence 26, Applicati	6.30e-21
12	318	15.9	43	7	US-08-050-	Sequence 31, Applicati	2.36e-20
13	225	11.3	325	5	US-08-292-	Sequence 2, Applicatio	1.31e-11
14	225	11.3	325	10	PCT-US91-0	Sequence 2, Applicatio	1.31e-11
15	221	11.1	326	5	US-08-292-	Sequence 4, Applicatio	3.06e-11
16	221	11.1	326	10	PCT-US91-0	Sequence 4, Applicatio	3.06e-11
17	212	10.6	474	1	5395760-4	Patent No. 5395760.	2.05e-10
18	210	10.5	355	5	US-08-292-	Sequence 6, Applicatio	3.12e-10
19	183	9.2	283	15	PCT-US96-1	Sequence 2, Applicatio	8.68e-08
20	183	9.2	595	5	US-08-225-	Sequence 2, Applicatio	8.68e-08
21	183	9.2	595	7	US-08-570-	Sequence 2, Applicatio	8.68e-08
22	181	9.1	228	12	PCT-US93-0	Sequence 8, Applicatio	1.31e-07
23	181	9.1	228	13	PCT-US94-0	Sequence 4, Applicatio	1.31e-07
24	181	9.1	228	14	PCT-US95-0	Sequence 4, Applicatio	1.31e-07
25	181	9.1	228	7	US-08-188-	Sequence 4, Applicatio	1.31e-07
26	181	9.1	228	7	US-08-453-	Sequence 8, Applicatio	1.31e-07
27	180	9.0	461	7	US-08-385-	Sequence 2, Applicatio	1.61e-07
28	180	9.0	461	1	5395760-2	Patent No. 5395760.	1.61e-07
29	180	9.0	486	7	US-08-243-	Sequence 1, Applicatio	1.61e-07
30	180	9.0	518	7	US-08-385-	Sequence 4, Applicatio	1.61e-07
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33	169	8.5	399	7	US-08-453-	Sequence 10, Applicati	1.53e-06
34	169	8.5	399	12	PCT-US93-0	Sequence 10, Applicati	1.53e-06
35	167	8.4	70	4	US-07-920-	Sequence 24, Applicati	2.30e-06
36	167	8.4	71	6	US-08-314-	Sequence 24, Applicati	2.30e-06
37	167	8.4	93	7	US-08-445-	Sequence 2, Applicatio	2.30e-06
38	167	8.4	93	7	US-08-343-	Sequence 4, Applicatio	2.30e-06
39	165	8.3	186	4	US-08-069-	Sequence 6, Applicatio	3.46e-06
40	160	8.0	177	6	US-08-187-	Sequence 6, Applicatio	9.51e-06
41	160	8.0	198	6	US-08-187-	Sequence 5, Applicatio	9.51e-06
42	160	8.0	217	6	US-08-187-	Sequence 4, Applicatio	9.51e-06
43	156	7.8	206	5	US-08-097-	Sequence 7, Applicatio	2.13e-05
44	156	7.8	438	5	US-08-097-	Sequence 11, Applicati	2.13e-05
45	139	7.0	335	14	PCT-US95-1	Sequence 2, Applicatio	6.25e-04

ALIGNMENTS

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08321668.
XX
CC    Sequence 2, Application US/08321668
CC    Patent No. 5665859
CC     GENERAL INFORMATION:
CC       APPLICANT:  WALLACH, David
CC       APPLICANT:  BRAKEBUSCH, Cord
CC       APPLICANT:  VARFOLOMEEV, Eugene
CC       APPLICANT:  BATKIN, Michael
CC       TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC       TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC       NUMBER OF SEQUENCES:  42
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  BROWDY AND NEIMARK
CC         STREET:  419 Seventh Street, N.W., Suite 300
CC         CITY:  Washington
CC         STATE:  D.C.
CC         COUNTRY:  USA
CC         ZIP:  20004
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/321,668
CC         FILING DATE:  12-OCT-1994
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  IL 107268
CC         FILING DATE:  12-OCT-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  BROWDY, Roger L.
CC         REGISTRATION NUMBER:  25,618
CC         REFERENCE/DOCKET NUMBER:  WALLACH-13
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-628-5197
CC         TELEFAX:  202-737-3528
CC         TELEX:  248633
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CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50494 MW; 1048031 CN;

  Query Match           56.4%;  Score 1124;  DB 7;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.28e-100;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
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Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


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ID   US-08-050-319B-25     STANDARD;     PRT;   455 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 25, Application US/08050319B.
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CC    Sequence 25, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  25:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50579 MW; 1048388 CN;

  Query Match           56.4%;  Score 1124;  DB 7;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.28e-100;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
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Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


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ID   US-08-050-319B-48     STANDARD;     PRT;   199 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 48, Application US/08050319B.
XX
CC    Sequence 48, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  48:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  199 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   199 AA; 22186 MW; 195553 CN;

  Query Match           55.9%;  Score 1115;  DB 7;  Length 199;
  Best Local Similarity  98.6%;  Pred. No. 1.05e-99;
  Matches   141;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
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Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


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ID   US-08-050-319B-2     STANDARD;     PRT;   167 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08050319B.
XX
CC    Sequence 2, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC      INFORMATION FOR SEQ ID NO:  2:
CC        SEQUENCE CHARACTERISTICS:
CC          LENGTH:  167 amino acids
CC          TYPE:  amino acid
CC          TOPOLOGY:  linear
CC        MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           49.9%;  Score 996;  DB 7;  Length 167;
  Best Local Similarity 100.0%;  Pred. No. 1.15e-87;
  Matches   127;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
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Qy    143 KQNTVCT 149


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XX
DT   01-JAN-1900
XX
DE   Sequence 57, Application US/08050319B.
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CC    Sequence 57, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC      INFORMATION FOR SEQ ID NO:  57:
CC        SEQUENCE CHARACTERISTICS:
CC          LENGTH:  167 amino acids
CC          TYPE:  amino acid
CC          TOPOLOGY:  linear
CC        MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           49.9%;  Score 996;  DB 7;  Length 167;
  Best Local Similarity 100.0%;  Pred. No. 1.15e-87;
  Matches   127;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
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Qy    143 KQNTVCT 149


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ID   US-08-050-319B-4     STANDARD;     PRT;   124 AA.
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 4, Application US/08050319B.
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CC    Sequence 4, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  124 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   124 AA; 14047 MW; 75840 CN;

  Query Match           49.2%;  Score 981;  DB 7;  Length 124;
  Best Local Similarity 100.0%;  Pred. No. 3.78e-86;
  Matches   124;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db      61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
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Qy      85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db     121 NTVC 124
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Qy     145 NTVC 148


RESULT    7
ID   US-08-050-319B-50     STANDARD;     PRT;   157 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 50, Application US/08050319B.
XX
CC    Sequence 50, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  50:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  157 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   157 AA; 17570 MW; 122247 CN;

  Query Match           40.1%;  Score 800;  DB 7;  Length 157;
  Best Local Similarity 96.2%;  Pred. No. 6.45e-68;
  Matches   102;  Conservative    2;  Mismatches   2;  Indels   0;  Gaps   0;

Db      36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 95
           | : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119

Db      96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCS 141
           ||||||||||||||||||||||||||||||||||||||||||||||:
Qy     120 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165


RESULT    8
ID   US-08-050-319B-54     STANDARD;     PRT;   158 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 54, Application US/08050319B.
XX
CC    Sequence 54, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
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CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  54:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  158 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   158 AA; 17375 MW; 124033 CN;

  Query Match           33.4%;  Score 666;  DB 7;  Length 158;
  Best Local Similarity  97.7%;  Pred. No. 1.67e-54;
  Matches    86;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCTCH 128
           |||||||||||||||||||||||||| |:
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCR 110


RESULT    9
ID   US-08-050-319B-52     STANDARD;     PRT;   153 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 52, Application US/08050319B.
XX
CC    Sequence 52, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  52:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  153 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   153 AA; 17148 MW; 116104 CN;

  Query Match           23.9%;  Score 477;  DB 7;  Length 153;
  Best Local Similarity  66.0%;  Pred. No. 8.82e-36;
  Matches    66;  Conservative    9;  Mismatches  19;  Indels   6;  Gaps   4;

Db     44 CPQGKYIHPQNN-SIC--CTKCHK--GTYLYNDCPGPGQDT-DCRKNQYRHYWSENLFQC 97
          |  | :  ::|:   |  |:||:|  |    : |    :    ||||||||||||||||
Qy     66 CESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC 125

Db     98 FNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCS 137
          ||||||||||||||||||||||||||||||||||||||||:
Qy    126 FNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165


RESULT   10
ID   US-08-050-319B-36     STANDARD;     PRT;   41 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 36, Application US/08050319B.
XX
CC    Sequence 36, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  36:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  41 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
SQ   SEQUENCE   41 AA; 4856 MW; 8601 CN;

  Query Match           17.0%;  Score 339;  DB 7;  Length 41;
  Best Local Similarity 100.0%;  Pred. No. 2.30e-22;
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  Matches   41;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 GCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVC 41
          |||||||||||||||||||||||||||||||||||||||||
Qy    108 GCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVC 148


RESULT   11
ID   US-08-050-319B-26     STANDARD;     PRT;   40 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 26, Application US/08050319B.
XX
CC    Sequence 26, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  26:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  40 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   40 AA; 4459 MW; 7536 CN;

  Query Match           16.2%;  Score 324;  DB 7;  Length 40;
  Best Local Similarity 100.0%;  Pred. No. 6.30e-21;
  Matches   40;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCR 40
          ||||||||||||||||||||||||||||||||||||||||
Qy     25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCR 64


RESULT   12
ID   US-08-050-319B-31     STANDARD;     PRT;   43 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 31, Application US/08050319B.
XX
CC    Sequence 31, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  31:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  43 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   43 AA; 4767 MW; 9758 CN;

  Query Match           15.9%;  Score 318;  DB 7;  Length 43;
  Best Local Similarity 100.0%;  Pred. No. 2.36e-20;
  Matches   43;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 43
          |||||||||||||||||||||||||||||||||||||||||||
Qy     65 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 107


RESULT   13
ID   US-08-292-549-2     STANDARD;     PRT;   325 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08292549.
XX
CC    Sequence 2, Application US/08292549
CC    Patent No. 5464938
CC     GENERAL INFORMATION:
CC       APPLICANT:  Smith, Craig A.
CC       APPLICANT:  Goodwin, Raymond G.
CC       TITLE OF INVENTION:  Isolated Viral Protein TNF Antagonists
CC       NUMBER OF SEQUENCES:  10
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  Washington
CC         COUNTRY:  USA
CC         ZIP:  98101
```

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CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/292,549
CC         FILING DATE:
CC         CLASSIFICATION:  530
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  07/963,330
CC         FILING DATE:  10/19/92
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2602-A
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (206) 587-0430
CC         TELEFAX:  (206) 233-0644
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  325 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   325 AA; 35132 MW; 591446 CN;

  Query Match           11.3%;  Score 225;  DB 5;  Length 325;
  Best Local Similarity  34.8%;  Pred. No. 1.31e-11;
  Matches    39;  Conservative   21;  Mismatches  45;  Indels   7;  Gaps   6;

Db       4 LIAL-LVCVVYVYGDDVPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC 61
           |:|: |:|:  :          |||   |  :::::||: || | |    | ||| :| |
Qy       6 LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC 63

Db      62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY 111
             || |:|||| ||   |:|| : |   ::: :  :|   :| || |    |
Qy      64 RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY 114


RESULT   14
ID   PCT-US91-02207-2     STANDARD;     PRT;   325 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application PC/TUS9102207.
XX
CC    Sequence 2, Application PC/TUS9102207
CC     GENERAL INFORMATION:
CC       APPLICANT:  Smith, Craig A.
CC       APPLICANT:  Goodwin, Raymond G.
CC       TITLE OF INVENTION:  Isolated Viral Protein Cytokine Antagonists
CC       NUMBER OF SEQUENCES:  4
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  Washington
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.24
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  PCT/US91/02207
CC         FILING DATE:  19910329
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Wight, Christopher L.
CC         REGISTRATION NUMBER:  31,680
CC         REFERENCE/DOCKET NUMBER:  2602
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (206) 587-0430
CC         TELEFAX:  (206) 587-0606
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  325 amino acids
CC         TYPE:  AMINO ACID
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   325 AA; 35132 MW; 591446 CN;

  Query Match           11.3%;  Score 225;  DB 10;  Length 325;
  Best Local Similarity  34.8%;  Pred. No. 1.31e-11;
  Matches    39;  Conservative   21;  Mismatches  45;  Indels   7;  Gaps   6;

Db       4 LIAL-LVCVVYVYGDDVPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC 61
           |:|: |:|:  :          |||   |  :::::||: || | |    | ||| :| |
Qy       6 LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC 63

Db      62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY 111
             || |:|||| ||   |:|| : |   ::: :  :|   :| || |    |
Qy      64 RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY 114


RESULT   15
ID   US-08-292-549-4     STANDARD;     PRT;   326 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 4, Application US/08292549.
XX
CC    Sequence 4, Application US/08292549
CC    Patent No. 5464938
CC     GENERAL INFORMATION:
CC       APPLICANT:  Smith, Craig A.
CC       APPLICANT:  Goodwin, Raymond G.
CC       TITLE OF INVENTION:  Isolated Viral Protein TNF Antagonists
CC       NUMBER OF SEQUENCES:  10
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  Washington
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/292,549
CC         FILING DATE:
CC         CLASSIFICATION:  530
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  07/963,330
CC         FILING DATE:  10/19/92
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2602-A
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (206) 587-0430
CC         TELEFAX:  (206) 233-0644
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  326 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
```

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CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   326 AA; 35208 MW; 586550 CN;

  Query Match           11.1%;  Score 221;  DB 5;  Length 326;
  Best Local Similarity  39.5%;  Pred. No. 3.06e-11;
  Matches    32;  Conservative   15;  Mismatches  30;  Indels   4;  Gaps   3;

Db      34 EKDGLCCTSCPPGSYASRLC-GPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSE 92
           :::::||| |  |:|    | ||| || |  | : :|||| ||   |:|| ::|   :::
Qy      35 QNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC-SKCRKEMGQ 93

Db      93 SQ--SCDKTRDRVCDCSAGNY 111
            :  ||   || || |    |
Qy      94 VEISSCTVDRDTVCGCRKNQY 114


Search completed: Wed May  6 08:18:46 1998
Job time : 18 secs.
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MPSRCH (TM)

****

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 10:00:45 1998; MasPar time 59.61 Seconds
927.602 Million cell updates/sec
Tabular output not generated.

Title: >US-08-804-166-1
Description: (1-1049) from US08804166.seq
Perfect Score: 1049
N.A. Sequence: 1 TCCACATGGCTACAGGTAAG.....TTATTATCACAAATCTTAAG 1049
Comp: AGGTGTACCGATGTCCATTC.....AATAATAGTGTTTAGAATTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.672; Variance 4.371; scale 1.984

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	424	40.4	2062	7	US-08-050-	Sequence 24, Applicati	0.00e+00
2	424	40.4	2175	7	US-08-321-	Sequence 1, Applicatio	0.00e+00
3	424	40.4	6889	6	US-08-286-	Sequence 2, Applicatio	0.00e+00
4	424	40.4	6889	14	PCT-US95-0	Sequence 2, Applicatio	0.00e+00
5	420	40.0	600	7	US-08-050-	Sequence 47, Applicati	0.00e+00
6	381	36.3	504	7	US-08-050-	Sequence 56, Applicati	1.31e-290
7	379	36.1	501	7	US-08-050-	Sequence 1, Applicatio	6.34e-289
8	370	35.3	372	7	US-08-050-	Sequence 3, Applicatio	2.44e-281
9	302	28.8	474	7	US-08-050-	Sequence 49, Applicati	3.55e-224
10	300	28.6	2771	7	US-08-273-	Sequence 5, Applicatio	1.69e-222
11	298	28.4	4283	7	US-08-343-	Sequence 3, Applicatio	8.01e-221
12	298	28.4	4283	7	US-08-445-	Sequence 1, Applicatio	8.01e-221
13	255	24.3	477	7	US-08-050-	Sequence 53, Applicati	7.22e-185
14	169	16.1	462	7	US-08-050-	Sequence 51, Applicati	1.18e-113
15	69	6.6	534	6	US-08-187-	Sequence 3, Applicatio	9.14e-34
16	69	6.6	654	6	US-08-187-	Sequence 1, Applicatio	9.14e-34
17	59	5.6	321	4	US-07-920-	Sequence 23, Applicati	3.06e-26
18	59	5.6	321	6	US-08-314-	Sequence 23, Applicati	3.06e-26
19	59	5.6	597	6	US-08-187-	Sequence 2, Applicatio	3.06e-26
20	57	5.4	7218	7	US-08-232-	Sequence 14, Applicati	9.29e-25
21	52	5.0	2248	7	US-08-475-	Sequence 1, Applicatio	4.33e-21
22	52	5.0	2248	7	US-08-780-	Sequence 1, Applicatio	4.33e-21
23	52	5.0	2248	7	US-08-636-	Sequence 1, Applicatio	4.33e-21
24	52	5.0	2248	6	US-08-369-	Sequence 1, Applicatio	4.33e-21
25	38	3.6	633	7	US-08-388-	Sequence 1, Applicatio	3.33e-11
26	36	3.4	4810	13	PCT-US94-0	Sequence 3, Applicatio	7.43e-10
27	36	3.4	4810	7	US-08-453-	Sequence 7, Applicatio	7.43e-10
28	36	3.4	4810	7	US-08-188-	Sequence 3, Applicatio	7.43e-10
29	36	3.4	4810	14	PCT-US95-0	Sequence 3, Applicatio	7.43e-10
30	36	3.4	4810	12	PCT-US93-0	Sequence 7, Applicatio	7.43e-10
31	36	3.4	5125	12	PCT-US93-0	Sequence 11, Applicati	7.43e-10
32	36	3.4	5125	7	US-08-453-	Sequence 11, Applicati	7.43e-10
33	36	3.4	5323	12	PCT-US93-0	Sequence 9, Applicatio	7.43e-10
34	36	3.4	5323	7	US-08-453-	Sequence 9, Applicatio	7.43e-10
c 35	34	3.2	215	6	US-08-238-	Sequence 5, Applicatio	1.58e-08
c 36	33	3.1	7218	7	US-08-232-	Sequence 14, Applicati	7.16e-08
37	30	2.9	33	7	US-08-050-	Sequence 14, Applicati	6.07e-06
38	29	2.8	215	6	US-08-238-	Sequence 5, Applicatio	2.58e-05
39	26	2.5	74	14	PCT-US95-1	Sequence 94, Applicati	1.76e-03
40	26	2.5	81	14	PCT-US95-1	Sequence 92, Applicati	1.76e-03
c 41	25	2.4	81	14	PCT-US95-1	Sequence 98, Applicati	6.91e-03
42	25	2.4	82	14	PCT-US95-1	Sequence 97, Applicati	6.91e-03
43	24	2.3	69	7	US-08-471-	Sequence 142, Applicat	2.64e-02
c 44	24	2.3	74	14	PCT-US95-1	Sequence 100, Applicat	2.64e-02
c 45	24	2.3	82	14	PCT-US95-1	Sequence 97, Applicati	2.64e-02

ALIGNMENTS

RESULT 1
ID US-08-050-319B-24 STANDARD; DNA; UNC; 2062 BP.

XX
AC xxxxxx
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DT 01-JAN-1900
XX
DE Sequence 24, Application US/08050319B.
XX
CC Sequence 24, Application US/08050319B
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:

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CC        LENGTH:  2062 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  155..1519
SQ   Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

  Query Match           40.4%;  Score 424;  DB 7;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGT 700
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Qy    764 TCCTGT 769


RESULT    2
ID   US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08321668.
XX
CC   Sequence 1, Application US/08321668
CC   Patent No. 5665859
CC    GENERAL INFORMATION:
CC      APPLICANT:  WALLACH, David
CC      APPLICANT:  BRAKEBUSCH, Cord
CC      APPLICANT:  VARFOLOMEEV, Eugene
CC      APPLICANT:  BATKIN, Michael
CC      TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC      TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC      NUMBER OF SEQUENCES:  42
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  BROWDY AND NEIMARK
CC        STREET:  419 Seventh Street, N.W., Suite 300
CC        CITY:  Washington
CC        STATE:  D.C.
CC        COUNTRY:  USA
CC        ZIP:  20004
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/321,668
CC        FILING DATE:  12-OCT-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  IL 107268
CC        FILING DATE:  12-OCT-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  BROWDY, Roger L.
CC        REGISTRATION NUMBER:  25,618
CC        REFERENCE/DOCKET NUMBER:  WALLACH=13
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  202-628-5197
CC        TELEFAX:  202-737-3528
CC        TELEX:  248633
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2175 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  256..1620
SQ   Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

  Query Match           40.4%;  Score 424;  DB 7;  Length 2175;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
        ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 TCCTGT 801
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Qy    764 TCCTGT 769


RESULT    3
ID   US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08286740.
XX
CC   Sequence 2, Application US/08286740
CC   Patent No. 5561053
CC    GENERAL INFORMATION:
CC      APPLICANT:  Crowley, Craig W.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/286,740
CC        FILING DATE:  05-AUG-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:
CC        REFERENCE/DOCKET NUMBER:  798
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC     INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           40.4%;  Score 424;  DB 6;  Length 6889;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db   2145 TCCTGT 2150
           ||||||
Qy    764 TCCTGT 769


RESULT    4
ID   PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application PC/TUS9509576.
XX
CC   Sequence 2, Application PC/TUS9509576
CC    GENERAL INFORMATION:
CC      APPLICANT:  GENENTECH, INC.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/09576
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/286740
CC        FILING DATE:  05-AUG-1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:  00,000
CC        REFERENCE/DOCKET NUMBER:  798PCT
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC     INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           40.4%;  Score 424;  DB 14;  Length 6889;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    2145 TCCTGT 2150
          ||||||
Qy     764 TCCTGT 769


RESULT    5
ID   US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 47, Application US/08050319B.
XX
CC   Sequence 47, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  47:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  600 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..597
SQ   Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

  Query Match           40.0%;  Score 420;  DB 7;  Length 600;
  Best Local Similarity  99.3%;  Pred. No. 0.00e+00;
  Matches   423;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db     121 GATAGTGTGTGTCCCACAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
           ||||||||||||||  ||||||||||||||||||||||||||||| ||||||||||||
Qy     344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db     181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db     241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db     301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db     361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db     421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db     481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db     541 TCCTGT 546
           ||||||
Qy     764 TCCTGT 769


RESULT    6
ID   US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 56, Application US/08050319B.
XX
CC   Sequence 56, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
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CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  56:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  504 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

  Query Match           36.3%;  Score 381;  DB 7;  Length 504;
  Best Local Similarity  99.7%;  Pred. No. 1.31e-290;
  Matches   382;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
        ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    481 AAACAGAACACCGTGTGCACCTG 503
        |||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTG 726


RESULT    7
ID   US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08050319B.
XX
CC   Sequence 1, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  501 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

  Query Match           36.1%;  Score 379;  DB 7;  Length 501;
  Best Local Similarity  99.7%;  Pred. No. 6.34e-289;
  Matches   380;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
        ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    481 AAACAGAACACCGTGTGCACC 501
        |||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACC 724


RESULT    8
ID   US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.
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XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08050319B.
XX
CC   Sequence 3, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  372 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..372
SQ   Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

  Query Match           35.3%;  Score 370;  DB 7;  Length 372;
  Best Local Similarity  99.7%;  Pred. No. 2.44e-281;
  Matches   371;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy     350 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACCAAGTGC 409

Db      61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     410 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 469

Db     121 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     470 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 529

Db     181 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     530 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 589

Db     241 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy     590 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 649

Db     301 TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     650 TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAG 709

Db     361 AACACCGTGTGC 372
          ||||||||||||
Qy     710 AACACCGTGTGC 721


RESULT    9
ID   US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 49, Application US/08050319B.
XX
CC   Sequence 49, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  49:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  474 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..471
SQ   Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;

  Query Match           28.8%;  Score 302;  DB 7;  Length 474;
  Best Local Similarity  97.8%;  Pred. No. 3.55e-224;
  Matches   309;  Conservative    0;  Mismatches   7;  Indels   0;  Gaps   0;

Db     105 GGACAGGGAGAAGAGAGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 164
          ||| | |||    || ||||||||||||||||||||||||||||||||||||||||||||
Qy     454 GGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 513

Db     165 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 224
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    514 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 573

Db    225 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG 284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    574 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG 633

Db    285 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    634 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 693

Db    345 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    694 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 753

Db    405 CGAGTGTGTCTCCTGT 420
          ||||||||||||||||
Qy    754 CGAGTGTGTCTCCTGT 769


RESULT   10
ID   US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 5, Application US/08273411.
XX
CC   Sequence 5, Application US/08273411
CC   Patent No. 5625124
CC    GENERAL INFORMATION:
CC      APPLICANT:  Falk, Per
CC      APPLICANT:  Gordon, Jeffrey I.
CC      TITLE OF INVENTION:  Animal Model for Gastro-Intestinal
CC      TITLE OF INVENTION:  Disease
CC      NUMBER OF SEQUENCES:  10
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Patrea L. Pabst
CC        STREET:  1100 Peachtree Street, Suite 2800
CC        CITY:  Atlanta
CC        STATE:  Georgia
CC        COUNTRY:  USA
CC        ZIP:  30309-4530
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/273,411
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Pabst, Patrea L.
CC        REGISTRATION NUMBER:  31,284
CC        REFERENCE/DOCKET NUMBER:  WU106
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (404) 815-6508
CC        TELEFAX:  (404) 815-6555
CC    INFORMATION FOR SEQ ID NO:  5:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2771 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  Genes & Dev.
CC        VOLUME:  2
CC        PAGES:  1318-1332
CC        DATE:  1988
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 561 TO 629
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Seeburg, et al.
CC        JOURNAL:  DNA
CC        VOLUME:  1
CC        PAGES:  239-249
CC        DATE:  1982
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 620 TO 2771
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  J. Biol. Chem.
CC        VOLUME:  261
CC        PAGES:  5553-5561
CC        DATE:  1986
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 1 TO 617
SQ   Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;

  Query Match           28.6%;  Score 300;  DB 7;  Length 2771;
  Best Local Similarity  97.3%;  Pred. No. 1.69e-222;
  Matches   329;  Conservative    0;  Mismatches   5;  Indels   4;  Gaps   2;

Db    680 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db    740 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTGAATG--AG 797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||   |
Qy     66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db    798 TATCGCCATGTAAGCCCAGTAT--GGCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 855
          ||||||||||||||||||||||  ||||||||||||||||||||  ||||||||||||
Qy    126 TATCGCCATGTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTCCTCCCTGGAGGGAT 185

Db    856 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    186 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 245

Db    916 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    246 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 305

Db    976 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1013
          |||||||||||||||||||||||||||||||||||||
Qy    306 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343


RESULT   11
ID   US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08343401A.
XX
CC   Sequence 3, Application US/08343401A
CC   Patent No. 5661132
CC    GENERAL INFORMATION:
CC      APPLICANT:  Swain, William F
CC      APPLICANT:  Macklin, Michael D
CC      APPLICANT:  Eriksson, Elof
CC      APPLICANT:  Andree, Christophe
CC      TITLE OF INVENTION:  Improved Wound Healing
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  PO Box 2113
CC        CITY:  Madison
CC        STATE:  WI
```

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CC         COUNTRY:  USA
CC         ZIP:  53701-2113
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/343,401A
CC         FILING DATE:  22-NOV-1994
CC         CLASSIFICATION:  514
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Seay, Nicholas J
CC         REGISTRATION NUMBER:  27,386
CC         REFERENCE/DOCKET NUMBER:  11-229-9103-9
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  608-251-5000
CC         TELEFAX:  608-251-9166
CC     INFORMATION FOR SEQ ID NO:  3:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  4283 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  double
CC         TOPOLOGY:  circular
CC       MOLECULE TYPE:  DNA (genomic)
CC       IMMEDIATE SOURCE:
CC         CLONE:  pWRG1630
CC       FEATURE:
CC         NAME/KEY:  exon
CC         LOCATION:  713..721
CC       FEATURE:
CC         NAME/KEY:  exon
CC         LOCATION:  981..1253
CC       FEATURE:
CC         NAME/KEY:  CDS
CC         LOCATION:  join(713..721, 981..1253)
CC       FEATURE:
CC         NAME/KEY:  sig_peptide
CC         LOCATION:  713..1049
SQ    Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           28.4%;  Score 298;  DB 7;  Length 4283;
  Best Local Similarity  96.2%;  Pred. No. 8.01e-221;
  Matches   326;  Conservative    0;  Mismatches  10;  Indels   3;  Gaps   3;

Db     713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy       6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db     772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
           |||||||||||||||||||||||||||||||||||| || ||| |||| ||| | |
Qy      66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db     832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGG-A 890
           |||||||| |||||||||||||||||||||||||||||  |||||||||| |
Qy     126 TATCGCCATGTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTC-CTCCCTGGAGGGA 184

Db     891 TGGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGG 950
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy     185 TGGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGG 244

Db     951 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTT 1010
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Qy     245 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTT 304

Db    1011 GGCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
           |||||||||||||||||||||||||||||||||||||||
Qy     305 GGCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343


RESULT   12
ID   US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.
XX
AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08445265A.
XX
CC   Sequence 1, Application US/08445265A
CC   Patent No. 5697901
CC    GENERAL INFORMATION:
CC      APPLICANT:  Eriksson, Elof
CC      TITLE OF INVENTION:  GENE DELIVERY BY MICRONEEDLE INJECTION
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  1 South Pinckney Street
CC        CITY:  Madison
CC        STATE:  WI
CC        COUNTRY:  US
CC        ZIP:  53703
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/445,265A
CC        FILING DATE:
CC        CLASSIFICATION:  604
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Seay, Nicholas J
CC        REGISTRATION NUMBER:  27386
CC        REFERENCE/DOCKET NUMBER:  110229.91080
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  608-251-5000
CC        TELEFAX:  608-251-9166
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  4283 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  circular
CC      MOLECULE TYPE:  other nucleic acid
CC        DESCRIPTION:  /desc = "Plasmid DNA"
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  join(713..721, 981..1250)
SQ    Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           28.4%;  Score 298;  DB 7;  Length 4283;
  Best Local Similarity  96.2%;  Pred. No. 8.01e-221;
  Matches   326;  Conservative    0;  Mismatches  10;  Indels   3;  Gaps   3;

Db     713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy       6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db     772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
           |||||||||||||||||||||||||||||||||||| || ||| |||| ||| | |
Qy      66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db     832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGG-A 890
           |||||||| |||||||||||||||||||||||||||||  |||||||||| |
Qy     126 TATCGCCATGTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTC-CTCCCTGGAGGGA 184

Db     891 TGGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGG 950
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy     185 TGGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGG 244

Db     951 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTT 1010
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     245 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTT 304
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Db   1011 GGCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
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Qy    305 GGCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343


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ID   US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 53, Application US/08050319B.
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CC   Sequence 53, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  53:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  477 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..474
SQ   Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

  Query Match           24.3%;  Score 255;  DB 7;  Length 477;
  Best Local Similarity  98.9%;  Pred. No. 7.22e-185;
  Matches   258;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523
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Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTACCTGC 381
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DT   01-JAN-1900
XX
DE   Sequence 51, Application US/08050319B.
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CC   Sequence 51, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  51:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  462 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..459
SQ   Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

  Query Match           16.1%;  Score 169;  DB 7;  Length 462;
  Best Local Similarity 100.0%;  Pred. No. 1.18e-113;
  Matches   169;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    240 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
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Qy    601 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 660

Db    300 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 359
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Qy    661 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 720

Db    360 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGT 408
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ID   US-08-187-756C-3 STANDARD; DNA; UNC; 534 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08187756C.
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CC   Sequence 3, Application US/08187756C
CC   Patent No. 5597709
CC    GENERAL INFORMATION:
CC      APPLICANT:  ROSEN, ET AL.
CC      TITLE OF INVENTION:  Human Growth Hormone
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
CC        ADDRESSEE:  CECCHI, STEWART & OLSTEIN
CC        STREET:  6 BECKER FARM ROAD
CC        CITY:  ROSELAND
CC        STATE:  NEW JERSEY
CC        COUNTRY:  USA
CC        ZIP:  07068
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5 INCH DISKETTE
CC        COMPUTER:  IBM PS/2
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WORD PERFECT 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/187,756C
CC        FILING DATE:  January 27, 1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  FERRARO, GREGORY D.
CC        REGISTRATION NUMBER:  36,134
CC        REFERENCE/DOCKET NUMBER:  325800-55
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  201-994-1700
CC        TELEFAX:  201-994-1744
CC     INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  534 BASE PAIRS
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  SINGLE
CC        TOPOLOGY:  LINEAR
CC      MOLECULE TYPE:  cDNA
SQ   Sequence 534 BP; 108 A; 166 C; 143 G; 117 T; 0 other;

  Query Match            6.6%;  Score 69;  DB 6;  Length 534;
  Best Local Similarity  98.6%;  Pred. No. 9.14e-34;
  Matches    70;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      8 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAG 67
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Qy    273 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAG 332

Db     68 AGGGCAGTGCC 78
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Qy    333 AGGGCAGTGCC 343


Search completed: Wed May  6 10:02:47 1998

Job time : 122 secs.
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****

MPSRCH (TM)

****

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:27:00 1998; MasPar time 4.88 Seconds
394.142 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-8
Description: (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 30.838; Variance 140.153; scale 0.220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
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2	1322	52.0	455	7	US-08-050-	Sequence 25, Applicati	1.11e-110
3	1243	48.9	199	7	US-08-050-	Sequence 48, Applicati	2.75e-103
4	1025	40.3	145	6	US-08-425-	Sequence 2, Applicatio	6.14e-83
5	1025	40.3	145	6	US-08-425-	Sequence 1, Applicatio	6.14e-83
6	1020	40.1	145	7	US-08-298-	Sequence 1, Applicatio	1.79e-82
7	995	39.2	145	6	US-08-425-	Sequence 10, Applicati	3.81e-80
8	996	39.2	167	7	US-08-050-	Sequence 57, Applicati	3.07e-80
9	996	39.2	167	7	US-08-050-	Sequence 2, Applicatio	3.07e-80
10	981	38.6	124	7	US-08-050-	Sequence 4, Applicatio	7.64e-79
11	928	36.5	157	7	US-08-050-	Sequence 50, Applicati	6.44e-74
12	740	29.1	114	6	US-08-425-	Sequence 9, Applicatio	1.61e-56
13	734	28.9	114	6	US-08-425-	Sequence 7, Applicatio	5.77e-56
14	714	28.1	117	6	US-08-425-	Sequence 11, Applicati	4.01e-54
15	684	26.9	114	6	US-08-425-	Sequence 8, Applicatio	2.31e-51
16	666	26.2	158	7	US-08-050-	Sequence 54, Applicati	1.04e-49
17	651	25.6	117	6	US-08-425-	Sequence 12, Applicati	2.47e-48
18	613	24.1	149	6	US-08-425-	Sequence 5, Applicatio	7.49e-45
19	605	23.8	153	7	US-08-050-	Sequence 52, Applicati	4.04e-44
20	339	13.3	41	7	US-08-050-	Sequence 36, Applicati	3.84e-20
21	324	12.8	40	7	US-08-050-	Sequence 26, Applicati	8.05e-19
22	318	12.5	43	7	US-08-050-	Sequence 31, Applicati	2.71e-18
23	298	11.7	39	7	US-08-050-	Sequence 40, Applicati	1.53e-16
24	296	11.6	45	1	5451527-1	Patent No. 5451527.	2.28e-16
25	287	11.3	111	6	US-08-425-	Sequence 4, Applicatio	1.39e-15
26	287	11.3	111	6	US-08-425-	Sequence 3, Applicatio	1.39e-15
27	282	11.1	112	6	US-08-425-	Sequence 6, Applicatio	3.77e-15
28	268	10.5	46	5	US-08-086-	Sequence 14, Applicati	6.14e-14
29	261	10.3	46	5	US-08-086-	Sequence 12, Applicati	2.47e-13
30	260	10.2	131	1	5177193-3	Patent No. 5177193.	3.01e-13
31	249	9.8	46	5	US-08-086-	Sequence 11, Applicati	2.65e-12
32	249	9.8	46	5	US-08-086-	Sequence 13, Applicati	2.65e-12
33	230	9.1	41	5	US-08-086-	Sequence 17, Applicati	1.10e-10
34	227	8.9	34	1	5451527-4	Patent No. 5451527.	1.98e-10
35	227	8.9	39	1	5451527-8	Patent No. 5451527.	1.98e-10
36	227	8.9	39	1	5451527-12	Patent No. 5451527.	1.98e-10
37	227	8.9	39	13	PCT-US94-0	Sequence 29, Applicati	1.98e-10
38	225	8.9	325	5	US-08-292-	Sequence 2, Applicatio	2.93e-10
39	225	8.9	325	10	PCT-US91-0	Sequence 2, Applicatio	2.93e-10
40	221	8.7	326	5	US-08-292-	Sequence 4, Applicatio	6.38e-10
41	221	8.7	326	10	PCT-US91-0	Sequence 4, Applicatio	6.38e-10
42	212	8.3	41	5	US-08-086-	Sequence 15, Applicati	3.65e-09
43	210	8.3	355	5	US-08-292-	Sequence 6, Applicatio	5.38e-09
44	212	8.3	474	1	5395760-4	Patent No. 5395760.	3.65e-09
45	209	8.2	36	1	5451527-5	Patent No. 5451527.	6.52e-09

ALIGNMENTS

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DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08321668.
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CC    Sequence 2, Application US/08321668
CC    Patent No. 5665859
CC     GENERAL INFORMATION:
CC       APPLICANT:  WALLACH, David
CC       APPLICANT:  BRAKEBUSCH, Cord
CC       APPLICANT:  VARFOLOMEEV, Eugene
CC       APPLICANT:  BATKIN, Michael
CC       TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC       TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC       NUMBER OF SEQUENCES:  42
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  BROWDY AND NEIMARK
CC         STREET:  419 Seventh Street, N.W., Suite 300
CC         CITY:  Washington
CC         STATE:  D.C.
CC         COUNTRY:  USA
CC         ZIP:  20004
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/321,668
CC         FILING DATE:  12-OCT-1994
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  IL 107268
CC         FILING DATE:  12-OCT-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  BROWDY, Roger L.
CC         REGISTRATION NUMBER:  25,618
CC         REFERENCE/DOCKET NUMBER:  WALLACH=13
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-628-5197
CC         TELEFAX:  202-737-3528
CC         TELEX:  248633
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CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50494 MW; 1048031 CN;

  Query Match           52.0%;  Score 1322;  DB 7;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 1.11e-110;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    2
ID   US-08-050-319B-25     STANDARD;     PRT;   455 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 25, Application US/08050319B.
XX
CC    Sequence 25, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  25:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50579 MW; 1048388 CN;

  Query Match           52.0%;  Score 1322;  DB 7;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 1.11e-110;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    3
ID   US-08-050-319B-48     STANDARD;     PRT;   199 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 48, Application US/08050319B.
XX
CC    Sequence 48, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  48:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  199 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   199 AA; 22186 MW; 195553 CN;

  Query Match           48.9%;  Score 1243;  DB 7;  Length 199;
  Best Local Similarity 99.4%;  Pred. No. 2.75e-103;
  Matches   158;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQI 199
          |||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQI 181


RESULT    4
ID   US-08-425-673-2     STANDARD;     PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08425673.
XX
CC    Sequence 2, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   145 AA; 15544 MW; 114662 CN;

  Query Match           40.3%;  Score 1025;  DB 6;  Length 145;
  Best Local Similarity  99.3%;  Pred. No. 6.14e-83;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    127 SLPSPSRLPGPSDTPILPQ 145
          |||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT    5
ID   US-08-425-673-1     STANDARD;     PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08425673.
XX
CC    Sequence 1, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  1:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   145 AA; 15544 MW; 114662 CN;

  Query Match           40.3%;  Score 1025;  DB 6;  Length 145;
  Best Local Similarity  99.3%;  Pred. No. 6.14e-83;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317
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Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT    6
ID   US-08-298-189B-1     STANDARD;     PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08298189B.
XX
CC    Sequence 1, Application US/08298189B
CC    Patent No. 5674727
CC     GENERAL INFORMATION:
CC       APPLICANT:  Dr. Laurence A. Cole and Dr. Andrew Kardana
CC       TITLE OF INVENTION:  No. 5674727el Methods for Detecting Reproductive
CC       TITLE OF INVENTION:  Cancers or Tumors and Assay Products
CC       TITLE OF INVENTION:  Therefor
CC       NUMBER OF SEQUENCES:  1
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Dr. Laurence A. Cole , c/o Dept. of Obstetrics and
CC         STREET:  333 Cedar Street
CC         CITY:  New Haven
CC         STATE:  Connecticut
CC         COUNTRY:  USA
CC         ZIP:  06510
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  3.5" diskette
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  Windows 95
CC         SOFTWARE:  Microsoft Word 7.0
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/298,189B
CC         FILING DATE:  08/31/94
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Brian D. Voyce
CC         REGISTRATION NUMBER:  28,917
CC         REFERENCE/DOCKET NUMBER:  DSI1
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  919-638-3939 or 803-272-1471
CC         TELEFAX:  919-638-3939 or 803-272-1471
CC     INFORMATION FOR SEQ ID NO:  1:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  No. 5674727 applicable
CC         TOPOLOGY:  Unknown
CC       MOLECULE TYPE:  subunit of hormone, specifically the
CC       MOLECULE TYPE:  beta\subunit of hCG
CC       ORIGINAL SOURCE:  human urine
CC       FEATURE:
CC         NAME/KEY:  beta subunit of hCG that is nicked by GBNE
CC         LOCATION:  hCG
CC         IDENTIFICATION METHOD:  N-terminal sequence analysis
CC       PUBLICATION INFORMATION:
CC         AUTHORS:  Keutmann et alia
CC         TITLE:  "A Receptor-binding Region in Human        Choriogonadotrophin/Lutopr
CC         JOURNAL:  Proc Nat'l Acad Sci USA
CC         VOLUME:  84
CC         ISSUE:  No. 5674727 applicable
CC         PAGES:  2038-2042
CC         DATE:  1987
SQ   SEQUENCE   145 AA; 15476 MW; 116769 CN;

  Query Match           40.1%;  Score 1020;  DB 7;  Length 145;
  Best Local Similarity  98.6%;  Pred. No. 1.79e-82;
  Matches   137;  Conservative    2;  Mismatches   0;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCKKSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||::||||||||||||||||||||||||||||||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT    7
ID   US-08-425-673-10     STANDARD;     PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 10, Application US/08425673.
XX
CC    Sequence 10, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  10:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   145 AA; 15448 MW; 114931 CN;

  Query Match           39.2%;  Score 995;  DB 6;  Length 145;
  Best Local Similarity  96.4%;  Pred. No. 3.81e-80;
  Matches   134;  Conservative    1;  Mismatches   4;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
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Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||  :||||||||||||||||||||||||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT    8
ID   US-08-050-319B-57     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 57, Application US/08050319B.
XX
CC    Sequence 57, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  57:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           39.2%;  Score 996;  DB 7;  Length 167;
  Best Local Similarity 100.0%;  Pred. No. 3.07e-80;
  Matches   127;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
          |||||||
Qy    143 KQNTVCT 149


RESULT    9
ID   US-08-050-319B-2     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08050319B.
XX
CC    Sequence 2, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           39.2%;  Score 996;  DB 7;  Length 167;
  Best Local Similarity 100.0%;  Pred. No. 3.07e-80;
  Matches   127;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
          |||||||
Qy    143 KQNTVCT 149


RESULT   10
ID   US-08-050-319B-4     STANDARD;     PRT;   124 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
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XX
DE   Sequence 4, Application US/08050319B.
XX
CC    Sequence 4, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  124 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   124 AA; 14047 MW; 75840 CN;

  Query Match           38.6%;  Score 981;  DB 7;  Length 124;
  Best Local Similarity 100.0%;  Pred. No. 7.64e-79;
  Matches   124;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db     61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db    121 NTVC 124
          ||||
Qy    145 NTVC 148


RESULT   11
ID   US-08-050-319B-50     STANDARD;     PRT;   157 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 50, Application US/08050319B.
XX
CC    Sequence 50, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  50:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  157 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   157 AA; 17570 MW; 122247 CN;

  Query Match           36.5%;  Score 928;  DB 7;  Length 157;
  Best Local Similarity 97.5%;  Pred. No. 6.44e-74;
  Matches   119;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db     36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 95
          | : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119

Db     96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    120 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 179

Db    156 QI 157
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Qy    180 QI 181


RESULT   12
ID   US-08-425-673-9     STANDARD;     PRT;   114 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 9, Application US/08425673.
XX
CC    Sequence 9, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
```

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CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  9:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  114 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   114 AA; 12250 MW; 68564 CN;

  Query Match           29.1%;  Score 740;  DB 6;  Length 114;
  Best Local Similarity  93.3%;  Pred. No. 1.61e-56;
  Matches    97;  Conservative    1;  Mismatches   6;  Indels   0;  Gaps   0;

Db       7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDCGGPKDHPSYC 110
           |||||||||||||||||||||||||||   :||||||||||  |
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC 301


RESULT   13
ID   US-08-425-673-7     STANDARD;     PRT;   114 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 7, Application US/08425673.
XX
CC    Sequence 7, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  114 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   114 AA; 12401 MW; 67071 CN;

  Query Match           28.9%;  Score 734;  DB 6;  Length 114;
  Best Local Similarity  91.7%;  Pred. No. 5.77e-56;
  Matches    99;  Conservative    0;  Mismatches   9;  Indels   0;  Gaps   0;

Db       7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCTVRGLGPSYCDDPR 114
           |||||||||||||||||||||||||||||||||||  |  |||||
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 305


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ID   US-08-425-673-11     STANDARD;     PRT;   117 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 11, Application US/08425673.
XX
CC    Sequence 11, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
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CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  11:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  117 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   117 AA; 12890 MW; 72412 CN;

  Query Match           28.1%;  Score 714;  DB 6;  Length 117;
  Best Local Similarity  98.9%;  Pred. No. 4.01e-54;
  Matches    93;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 100
          |||||||||||||||||||||||||||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291


RESULT   15
ID   US-08-425-673-8     STANDARD;     PRT;   114 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 8, Application US/08425673.
XX
CC    Sequence 8, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  8:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  114 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   114 AA; 12242 MW; 69571 CN;

  Query Match           26.9%;  Score 684;  DB 6;  Length 114;
  Best Local Similarity  94.7%;  Pred. No. 2.31e-51;
  Matches    89;  Conservative    1;  Mismatches   4;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDC 100
          |||||||||||||||||||||||||||   :|||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291


Search completed: Wed May  6 08:27:26 1998
Job time : 26 secs.
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     | |\ \/ /| |  | |_____   | |___   | |_____   | |___   | |__| |
     | | \__/ | |  |_____  |  |___  |  |_____  |  |___  |  |  __  |
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     |_|      |_|  |_____|_|  |_____|  |_____|_|  |_____|  |_|  |_|  (TM)
*****************************************************************************

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               Distribution rights by Oxford Molecular Ltd

MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:          Wed May  6 11:17:48 1998;  MasPar time 73.35 Seconds
                                            934.882 Million cell updates/sec
Tabular output not generated.

Title:           >US-08-804-166-7
Description:     (1-1301) from US08804166.seq
Perfect Score:   1301
N.A. Sequence:         1 CTCGAGATGGCTACAGGTAA.........CACAATAAGGATCCCTCGAG 1301
     Comp:               GAGCTCTACCGATGTCCATT.........GTGTTATTCCTAGGGAGCTC

Scoring table:   TABLE default
                 Gap 6

Nmatch   STD :   Dbase 0;  Query 0

Searched:        102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        n-issued
                   1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                   10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics:      Mean 8.845;  Variance 4.678;  scale 1.891

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

                    %
Result              Query
  No.   Score       Match  Length DB  ID          Description            Pred. No.
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    1     514        39.5    2062  7  US-08-050-  Sequence 24, Applicati  0.00e+00
    2     514        39.5    2175  7  US-08-321-  Sequence 1, Applicatio  0.00e+00
    3     514        39.5    6889  6  US-08-286-  Sequence 2, Applicatio  0.00e+00
    4     514        39.5    6889 14  PCT-US95-0  Sequence 2, Applicatio  0.00e+00
    5     474        36.4     600  7  US-08-050-  Sequence 47, Applicati  0.00e+00
    6     383        29.4     504  7  US-08-050-  Sequence 56, Applicati  6.44e-278
    7     381        29.3     501  7  US-08-050-  Sequence 1, Applicatio  2.60e-276
    8     372        28.6     372  7  US-08-050-  Sequence 3, Applicatio  4.39e-269
    9     354        27.2     474  7  US-08-050-  Sequence 49, Applicati  1.22e-254
   10     304        23.4    2771  7  US-08-273-  Sequence 5, Applicatio  1.27e-214
   11     303        23.3    4283  7  US-08-343-  Sequence 3, Applicatio  7.97e-214
   12     303        23.3    4283  7  US-08-445-  Sequence 1, Applicatio  7.97e-214
   13     257        19.8     477  7  US-08-050-  Sequence 53, Applicati  3.56e-177
   14     221        17.0     462  7  US-08-050-  Sequence 51, Applicati  1.21e-148
   15     103         7.9     138  5  US-08-086-  Sequence 2, Applicatio  6.08e-57
   16      99         7.6     138  5  US-08-086-  Sequence 1, Applicatio  6.30e-54
   17      84         6.5    7218  7  US-08-232-  Sequence 14, Applicati  1.00e-42
   18      69         5.3     534  6  US-08-187-  Sequence 3, Applicatio  9.66e-32
   19      69         5.3     654  6  US-08-187-  Sequence 1, Applicatio  9.66e-32
   20      59         4.5     321  4  US-07-920-  Sequence 23, Applicati  1.37e-24
   21      59         4.5     321  6  US-08-314-  Sequence 23, Applicati  1.37e-24
   22      59         4.5     597  6  US-08-187-  Sequence 2, Applicatio  1.37e-24
   23      52         4.0    2248  7  US-08-636-  Sequence 1, Applicatio  1.08e-19
   24      52         4.0    2248  7  US-08-780-  Sequence 1, Applicatio  1.08e-19
   25      52         4.0    2248  6  US-08-369-  Sequence 1, Applicatio  1.08e-19
   26      52         4.0    2248  7  US-08-475-  Sequence 1, Applicatio  1.08e-19
c  27      42         3.2     215  6  US-08-238-  Sequence 5, Applicatio  6.38e-13
c  28      41         3.2    7218  7  US-08-232-  Sequence 14, Applicati  2.91e-12
   29      38         2.9     633  7  US-08-388-  Sequence 1, Applicatio  2.61e-10
   30      36         2.8    4810  7  US-08-453-  Sequence 7, Applicatio  4.97e-09
   31      36         2.8    4810 13  PCT-US94-0  Sequence 3, Applicatio  4.97e-09
   32      36         2.8    4810 12  PCT-US93-0  Sequence 7, Applicatio  4.97e-09
   33      36         2.8    4810 14  PCT-US95-0  Sequence 3, Applicatio  4.97e-09
   34      36         2.8    4810  7  US-08-188-  Sequence 3, Applicatio  4.97e-09
   35      36         2.8    5125 12  PCT-US93-0  Sequence 11, Applicati  4.97e-09
   36      36         2.8    5125  7  US-08-453-  Sequence 11, Applicati  4.97e-09
   37      36         2.8    5323  7  US-08-453-  Sequence 9, Applicatio  4.97e-09
   38      36         2.8    5323 12  PCT-US93-0  Sequence 9, Applicatio  4.97e-09
   39      32         2.5     196  1  5177193-2   Patent No. 5177193.     1.56e-06
   40      32         2.5     215  6  US-08-238-  Sequence 5, Applicatio  1.56e-06
   41      32         2.5    1006  6  US-08-239-  Sequence 1, Applicatio  1.56e-06
   42      30         2.3      33  7  US-08-050-  Sequence 14, Applicati  2.53e-05
   43      26         2.0      74 14  PCT-US95-1  Sequence 94, Applicati  5.44e-03
c  44      26         2.0     105  5  US-07-865-  Sequence 13, Applicati  5.44e-03
c  45      26         2.0     242  7  US-08-273-  Sequence 1, Applicatio  5.44e-03

                              ALIGNMENTS

RESULT    1
ID   US-08-050-319B-24 STANDARD; DNA; UNC; 2062 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 24, Application US/08050319B.
XX
CC   Sequence 24, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  24:
CC      SEQUENCE CHARACTERISTICS:
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CC        LENGTH:  2062 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  155..1519
SQ   Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

  Query Match           39.5%;  Score 514;  DB 7;  Length 2062;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 788
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    2
ID   US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 1, Application US/08321668.
XX
CC   Sequence 1, Application US/08321668
CC   Patent No. 5665859
CC    GENERAL INFORMATION:
CC      APPLICANT:  WALLACH, David
CC      APPLICANT:  BRAKEBUSCH, Cord
CC      APPLICANT:  VARFOLOMEEV, Eugene
CC      APPLICANT:  BATKIN, Michael
CC      TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC      TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC      NUMBER OF SEQUENCES:  42
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  BROWDY AND NEIMARK
CC        STREET:  419 Seventh Street, N.W., Suite 300
CC        CITY:  Washington
CC        STATE:  D.C.
CC        COUNTRY:  USA
CC        ZIP:  20004
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/321,668
CC        FILING DATE:  12-OCT-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  IL 107268
CC        FILING DATE:  12-OCT-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  BROWDY, Roger L.
CC        REGISTRATION NUMBER:  25,618
CC        REFERENCE/DOCKET NUMBER:  WALLACH-13
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  202-628-5197
CC        TELEFAX:  202-737-3528
CC        TELEX:  248633
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2175 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  256..1620
SQ   Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

  Query Match           39.5%;  Score 514;  DB 7;  Length 2175;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824
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Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 889
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    3
ID   US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.

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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08286740.
XX
CC   Sequence 2, Application US/08286740
CC   Patent No. 5561053
CC    GENERAL INFORMATION:
CC      APPLICANT:  Crowley, Craig W.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/286,740
CC        FILING DATE:  05-AUG-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:
CC        REFERENCE/DOCKET NUMBER:  798
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC     INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           39.5%;  Score 514;  DB 6;  Length 6889;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 2204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db   2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    4
ID   PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
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DE   Sequence 2, Application PC/TUS9509576.
XX
CC   Sequence 2, Application PC/TUS9509576
CC    GENERAL INFORMATION:
CC      APPLICANT:  GENENTECH, INC.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/09576
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/286740
CC        FILING DATE:  05-AUG-1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:  00,000
CC        REFERENCE/DOCKET NUMBER:  798PCT
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC     INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
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CC       TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           39.5%;  Score 514;  DB 14;  Length 6889;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 2204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db   2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
           |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    5
ID   US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 47, Application US/08050319B.
XX
CC   Sequence 47, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  47:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  600 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..597
SQ   Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

  Query Match           36.4%;  Score 474;  DB 7;  Length 600;
  Best Local Similarity 99.4%;  Pred. No. 0.00e+00;
  Matches   477;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCACAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
           ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTTAG 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824


RESULT    6
ID   US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 56, Application US/08050319B.
XX
CC   Sequence 56, Application US/08050319B
CC   Patent No. 5633145
```

```
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  56:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  504 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

  Query Match           29.4%;  Score 383;  DB 7;  Length 504;
  Best Local Similarity 100.0%;  Pred. No. 6.44e-278;
  Matches   383;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACCTG 503
          |||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTG 727
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RESULT    7
ID   US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08050319B.
XX
CC   Sequence 1, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  501 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

  Query Match           29.3%;  Score 381;  DB 7;  Length 501;
  Best Local Similarity 100.0%;  Pred. No. 2.60e-276;
  Matches   381;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584
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Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACC 501
          |||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACC 725


RESULT    8
ID   US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08050319B.
XX
CC   Sequence 3, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  372 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..372
SQ   Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

  Query Match           28.6%;  Score 372;  DB 7;  Length 372;
  Best Local Similarity 100.0%;  Pred. No. 4.39e-269;
  Matches   372;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    351 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 410

Db     61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    411 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 470

Db    121 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    471 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 530

Db    181 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    531 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 590

Db    241 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    591 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 650

Db    301 TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    651 TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAG 710

Db    361 AACACCGTGTGC 372
          ||||||||||||
Qy    711 AACACCGTGTGC 722


RESULT    9
ID   US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 49, Application US/08050319B.
XX
CC   Sequence 49, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  49:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  474 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
```

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CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..471
SQ   Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;

  Query Match           27.2%;  Score 354;  DB 7;  Length 474;
  Best Local Similarity  97.8%;  Pred. No. 1.22e-254;
  Matches   362;  Conservative    0;  Mismatches   8;  Indels   0;  Gaps   0;

Db    105 GGACAGGGAGAAGAGAGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 164
          ||| | |||    || ||||||||||||||||||||||||||||||||||||||||||||
Qy    455 GGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 514

Db    165 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 224
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    515 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 574

Db    225 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG 284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    575 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG 634

Db    285 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    635 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 694

Db    345 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    695 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 754

Db    405 CGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACC 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    755 CGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACC 814

Db    465 CCAGATTTAG 474
          ||||||| ||
Qy    815 CCAGATTGAG 824


RESULT   10
ID   US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 5, Application US/08273411.
XX
CC   Sequence 5, Application US/08273411
CC   Patent No. 5625124
CC    GENERAL INFORMATION:
CC      APPLICANT:  Falk, Per
CC      APPLICANT:  Gordon, Jeffrey I.
CC      TITLE OF INVENTION:  Animal Model for Gastro-Intestinal
CC      TITLE OF INVENTION:  Disease
CC      NUMBER OF SEQUENCES:  10
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Patrea L. Pabst
CC        STREET:  1100 Peachtree Street, Suite 2800
CC        CITY:  Atlanta
CC        STATE:  Georgia
CC        COUNTRY:  USA
CC        ZIP:  30309-4530
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/273,411
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Pabst, Patrea L.
CC        REGISTRATION NUMBER:  31,284
CC        REFERENCE/DOCKET NUMBER:  WU106
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (404) 815-6508
CC        TELEFAX:  (404) 815-6555
CC    INFORMATION FOR SEQ ID NO:  5:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2771 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  Genes & Dev.
CC        VOLUME:  2
CC        PAGES:  1318-1332
CC        DATE:  1988
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 561 TO 629
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Seeburg, et al.
CC        JOURNAL:  DNA
CC        VOLUME:  1
CC        PAGES:  239-249
CC        DATE:  1982
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 620 TO 2771
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  J. Biol. Chem.
CC        VOLUME:  261
CC        PAGES:  5553-5561
CC        DATE:  1986
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 1 TO 617
SQ   Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;

  Query Match           23.4%;  Score 304;  DB 7;  Length 2771;
  Best Local Similarity  97.9%;  Pred. No. 1.27e-214;
  Matches   331;  Conservative    0;  Mismatches   3;  Indels   4;  Gaps   2;

Db    680 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      7 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Db    740 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTGAATG--AG 797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Qy     67 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTGAATGTGAG 126

Db    798 TATCGCCATGTAAGCCCAGTAT--GGCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 855
          |||||||||||||||||||||  |||||| ||||||||||||||||||||||||||||||
Qy    127 TATCGCCATGTAAGCCCAGTATTTGGCCAATGTCAGAAAGCTCCTGGTCCCTGGAGGGAT 186

Db    856 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 915
          |||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Qy    187 GGAGAGAGAAAAACAAACACCTCCTGGAGCAGGGAGAGTGCTGCCCTCTTGCTCTCCGGC 246

Db    916 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 975
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    247 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306

Db    976 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1013
          |||||||||||||||||||||||||||||||||||||||
Qy    307 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 344


RESULT   11
ID   US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.

XX
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08343401A.
XX
CC   Sequence 3, Application US/08343401A
CC   Patent No. 5661132
CC    GENERAL INFORMATION:
CC      APPLICANT:  Swain, William F
CC      APPLICANT:  Macklin, Michael D
CC      APPLICANT:  Eriksson, Elof
CC      APPLICANT:  Andree, Christophe
CC      TITLE OF INVENTION:  Improved Wound Healing
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  PO Box 2113
CC        CITY:  Madison
CC        STATE:  WI
CC        COUNTRY:  USA
CC        ZIP:  53701-2113
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/343,401A
CC        FILING DATE:  22-NOV-1994
CC        CLASSIFICATION:  514
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Seay, Nicholas J
CC        REGISTRATION NUMBER:  27,386
CC        REFERENCE/DOCKET NUMBER:  11-229-9103-9
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  608-251-5000
CC        TELEFAX:  608-251-9166
CC     INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  4283 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  circular
CC      MOLECULE TYPE:  DNA (genomic)
CC      IMMEDIATE SOURCE:
CC        CLONE:  pWRG1630
CC      FEATURE:
CC        NAME/KEY:  exon
CC        LOCATION:  713..721
CC      FEATURE:
CC        NAME/KEY:  exon
CC        LOCATION:  981..1253
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  join(713..721, 981..1253)
CC      FEATURE:
CC        NAME/KEY:  sig_peptide
CC        LOCATION:  713..1049
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           23.3%;  Score 303;  DB 7;  Length 4283;
  Best Local Similarity  95.6%;  Pred. No. 7.97e-214;
  Matches   323;  Conservative    0;  Mismatches  14;  Indels   1;  Gaps   1;

Db    713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy      7 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Db    772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          |||||||||||||||||||||||||||||||||||| || ||| ||||||||||||
Qy     67 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTGAATGTGAG 126

Db    832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
          ||||||||| |||||||||||||||||||| |||||||||||||||  ||  |  ||||
Qy    127 TATCGCCATGTAAGCCCAGTATTTGGCCAATGTCAGAAAGCTCCTGGTCCCTGGAGGGAT 186

Db    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
          |||||||||||||||||| |||||||||||||||||| || ||||||||||||||||
Qy    187 GGAGAGAGAAAAACAAACACCTCCTGGAGCAGGGAGAGTGCTGCCCTCTTGCTCTCCGGC 246

Db    952 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    247 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306

Db   1012 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
          |||||||||||||||||||||||||||||||||||||
Qy    307 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 344


RESULT   12
ID   US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08445265A.
XX
CC   Sequence 1, Application US/08445265A
CC   Patent No. 5697901
CC    GENERAL INFORMATION:
CC      APPLICANT:  Eriksson, Elof
CC      TITLE OF INVENTION:  GENE DELIVERY BY MICRONEEDLE INJECTION
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  1 South Pinckney Street
CC        CITY:  Madison
CC        STATE:  WI
CC        COUNTRY:  US
CC        ZIP:  53703
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/445,265A
CC        FILING DATE:
CC        CLASSIFICATION:  604
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Seay, Nicholas J
CC        REGISTRATION NUMBER:  27386
CC        REFERENCE/DOCKET NUMBER:  110229.91080
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  608-251-5000
CC        TELEFAX:  608-251-9166
CC     INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  4283 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  circular
CC      MOLECULE TYPE:  other nucleic acid
CC        DESCRIPTION:  /desc = "Plasmid DNA"
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  join(713..721, 981..1250)
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           23.3%;  Score 303;  DB 7;  Length 4283;
  Best Local Similarity  95.6%;  Pred. No. 7.97e-214;
  Matches   323;  Conservative    0;  Mismatches  14;  Indels   1;  Gaps   1;
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Db    713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy      7 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Db    772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          |||||||||||||||||||||||||||||||||||| || ||| ||||||||||||||
Qy     67 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTGAATGTGAG 126

Db    832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
          |||||||| |||||||||||||||||||| |||||||||||||||  ||  |  ||||
Qy    127 TATCGCCATGTAAGCCCAGTATTTGGCCAATGTCAGAAAGCTCCTGGTCCCTGGAGGGAT 186

Db    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
          |||||||||||||||||| |||||||||||||||||| || ||||||||||||||||
Qy    187 GGAGAGAGAAAAACAAACACCTCCTGGAGCAGGGAGAGTGCTGCCCTCTTGCTCTCCGGC 246

Db    952 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    247 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306

Db   1012 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
          |||||||||||||||||||||||||||||||||||||
Qy    307 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 344


RESULT   13
ID   US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 53, Application US/08050319B.
XX
CC   Sequence 53, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  53:
CC       SEQUENCE CHARACTERISTICS:
CC        LENGTH:  477 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC       MOLECULE TYPE:  cDNA to mRNA
CC       FEATURE:
CC         NAME/KEY:  CDS
CC         LOCATION:  1..474
SQ   Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

  Query Match           19.8%;  Score 257;  DB 7;  Length 477;
  Best Local Similarity  99.2%;  Pred. No. 3.56e-177;
  Matches   259;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTACCTGC 381
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Qy    585 CGGGACACCGTGTGTGGCTGC 605


RESULT   14
ID   US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 51, Application US/08050319B.
XX
CC   Sequence 51, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  51:
CC       SEQUENCE CHARACTERISTICS:
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CC        LENGTH:  462 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..459
SQ   Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

  Query Match           17.0%;  Score 221;  DB 7;  Length 462;
  Best Local Similarity  99.6%;  Pred. No. 1.21e-148;
  Matches   222;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    240 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    602 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 661

Db    300 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 359
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Qy    662 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 721

Db    360 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAA 419
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    722 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAA 781

Db    420 GAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTTAG 462
        |||||||||||||||||||||||||||||||||||||| ||
Qy    782 GAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824


RESULT   15
ID   US-08-086-915-2 STANDARD; DNA; UNC; 138 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08086915.
XX
CC   Sequence 2, Application US/08086915
CC   Patent No. 5444167
CC    GENERAL INFORMATION:
CC      APPLICANT:  Pettersson, Kim SI
CC      TITLE OF INVENTION:  Variant Luteinizing Hormone Encoding DNA
CC      NUMBER OF SEQUENCES:  17
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Adduci, Mastriani, Schaumberg & Schill
CC        STREET:  1140 Connecticut Avenue, N.W., Suite 250
CC        CITY:  Washington
CC        STATE:  D.C.
CC        COUNTRY:  U.S.A.
CC        ZIP:  20036
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/086,915
CC        FILING DATE:  07-JUL-1993
CC        CLASSIFICATION:  536
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Kubovcik, Ronald J.
CC        REGISTRATION NUMBER:  25,401
CC        REFERENCE/DOCKET NUMBER:  15873005
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  202-467-6300
CC        TELEFAX:  202-466-2006
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  138 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      ORIGINAL SOURCE:
CC        ORGANISM:  Homo sapiens
CC        DEVELOPMENTAL STAGE:  Adult
SQ   Sequence 138 BP; 24 A; 51 C; 42 G; 21 T; 0 other;

  Query Match            7.9%;  Score 103;  DB 5;  Length 138;
  Best Local Similarity  99.0%;  Pred. No. 6.08e-57;
  Matches   104;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     34 CCACGGTGCCACCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 93
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Qy    870 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 929

Db     94 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATG 138
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Qy    930 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATG 974


Search completed: Wed May  6 11:19:13 1998
Job time : 85 secs.
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:23:57 1998; MasPar time 4.43 Seconds
368.292 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6
Description: (1-285) from US08804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 30.064; Variance 126.027; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1306	59.8	455	7	US-08-321-	Sequence 2, Applicatio	7.75e-119
2	1306	59.8	455	7	US-08-050-	Sequence 25, Applicati	7.75e-119
3	1227	56.2	199	7	US-08-050-	Sequence 48, Applicati	8.08e-111
4	994	45.5	167	7	US-08-050-	Sequence 2, Applicatio	3.05e-87
5	994	45.5	167	7	US-08-050-	Sequence 57, Applicati	3.05e-87
6	979	44.8	124	7	US-08-050-	Sequence 4, Applicatio	9.96e-86
7	912	41.8	157	7	US-08-050-	Sequence 50, Applicati	5.63e-79
8	666	30.5	158	7	US-08-050-	Sequence 54, Applicati	2.50e-54
9	589	27.0	153	7	US-08-050-	Sequence 52, Applicati	1.12e-46
10	337	15.4	41	7	US-08-050-	Sequence 36, Applicati	4.74e-22
11	324	14.8	40	7	US-08-050-	Sequence 26, Applicati	8.28e-21
12	318	14.6	43	7	US-08-050-	Sequence 31, Applicati	3.09e-20
13	284	13.0	39	7	US-08-050-	Sequence 40, Applicati	5.18e-17
14	225	10.3	325	5	US-08-292-	Sequence 2, Applicatio	1.64e-11
15	225	10.3	325	10	PCT-US91-0	Sequence 2, Applicatio	1.64e-11
16	221	10.1	326	5	US-08-292-	Sequence 4, Applicatio	3.81e-11
17	221	10.1	326	10	PCT-US91-0	Sequence 4, Applicatio	3.81e-11
18	212	9.7	474	1	5395760-4	Patent No. 5395760.	2.54e-10
19	210	9.6	355	5	US-08-292-	Sequence 6, Applicatio	3.86e-10
20	183	8.4	283	15	PCT-US96-1	Sequence 2, Applicatio	1.06e-07
21	183	8.4	595	7	US-08-570-	Sequence 2, Applicatio	1.06e-07
22	183	8.4	595	5	US-08-225-	Sequence 2, Applicatio	1.06e-07
23	181	8.3	228	12	PCT-US93-0	Sequence 8, Applicatio	1.59e-07
24	181	8.3	228	7	US-08-188-	Sequence 4, Applicatio	1.59e-07
25	181	8.3	228	7	US-08-453-	Sequence 8, Applicatio	1.59e-07
26	181	8.3	228	13	PCT-US94-0	Sequence 4, Applicatio	1.59e-07
27	181	8.3	228	14	PCT-US95-0	Sequence 4, Applicatio	1.59e-07
28	180	8.2	461	7	US-08-385-	Sequence 2, Applicatio	1.96e-07
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30	180	8.2	486	7	US-08-243-	Sequence 1, Applicatio	1.96e-07
31	180	8.2	518	7	US-08-385-	Sequence 4, Applicatio	1.96e-07
32	167	7.7	70	4	US-07-920-	Sequence 24, Applicati	2.77e-06
33	167	7.7	71	6	US-08-314-	Sequence 24, Applicati	2.77e-06
34	167	7.7	93	7	US-08-445-	Sequence 2, Applicatio	2.77e-06
35	167	7.7	93	7	US-08-343-	Sequence 4, Applicatio	2.77e-06
36	169	7.7	333	7	US-08-453-	Sequence 12, Applicati	1.85e-06
37	169	7.7	333	12	PCT-US93-0	Sequence 12, Applicati	1.85e-06
38	169	7.7	399	7	US-08-453-	Sequence 10, Applicati	1.85e-06
39	169	7.7	399	12	PCT-US93-0	Sequence 10, Applicati	1.85e-06
40	165	7.6	186	4	US-08-089-	Sequence 6, Applicatio	4.16e-06
41	160	7.3	177	6	US-08-187-	Sequence 6, Applicatio	1.14e-05
42	160	7.3	198	6	US-08-187-	Sequence 5, Applicatio	1.14e-05
43	160	7.3	217	6	US-08-187-	Sequence 4, Applicatio	1.14e-05
44	155	7.1	206	5	US-08-097-	Sequence 7, Applicatio	3.10e-05
45	155	7.1	438	5	US-08-097-	Sequence 11, Applicati	3.10e-05

ALIGNMENTS

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RESULT    1
ID   US-08-321-668-2     STANDARD;     PRT;   455 AA.
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 2, Application US/08321668.
XX
CC    Sequence 2, Application US/08321668
CC    Patent No. 5665859
CC     GENERAL INFORMATION:
CC       APPLICANT:  WALLACH, David
CC       APPLICANT:  BRAKEBUSCH, Cord
CC       APPLICANT:  VARFOLOMEEV, Eugene
CC       APPLICANT:  BATKIN, Michael
CC       TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC       TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC       NUMBER OF SEQUENCES:  42
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  BROWDY AND NEIMARK
CC         STREET:  419 Seventh Street, N.W., Suite 300
CC         CITY:  Washington
CC         STATE:  D.C.
CC         COUNTRY:  USA
CC         ZIP:  20004
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/321,668
CC         FILING DATE:  12-OCT-1994
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  IL 107268
CC         FILING DATE:  12-OCT-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  BROWDY, Roger L.
CC         REGISTRATION NUMBER:  25,618
CC         REFERENCE/DOCKET NUMBER:  WALLACH=13
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-628-5197
CC         TELEFAX:  202-737-3528
CC         TELEX:  248633
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CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50494 MW; 1048031 CN;

  Query Match           59.8%;  Score 1306;  DB 7;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 7.75e-119;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
           |||||||||||||||||||||||||||||| ||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    2
ID   US-08-050-319B-25     STANDARD;     PRT;   455 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 25, Application US/08050319B.
XX
CC    Sequence 25, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  25:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50579 MW; 1048388 CN;

  Query Match           59.8%;  Score 1306;  DB 7;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 7.75e-119;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
           |||||||||||||||||||||||||||||| ||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    3
ID   US-08-050-319B-48     STANDARD;     PRT;   199 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 48, Application US/08050319B.
XX
CC    Sequence 48, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  48:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  199 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   199 AA; 22186 MW; 195553 CN;

  Query Match           56.2%;  Score 1227;  DB 7;  Length 199;
  Best Local Similarity  98.1%;  Pred. No. 8.08e-111;
  Matches   156;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db     41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
```

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Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQI 199
          |||||||||||||||||||||||||||||| ||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQI 181


RESULT    4
ID   US-08-050-319B-2     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08050319B.
XX
CC    Sequence 2, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           45.5%;  Score 994;  DB 7;  Length 167;
  Best Local Similarity  99.2%;  Pred. No. 3.05e-87;
  Matches   126;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
          |||||||
Qy    143 KQNTVCT 149


RESULT    5
ID   US-08-050-319B-57     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 57, Application US/08050319B.
XX
CC    Sequence 57, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  57:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           45.5%;  Score 994;  DB 7;  Length 167;
  Best Local Similarity  99.2%;  Pred. No. 3.05e-87;
  Matches   126;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
          |||||||
Qy    143 KQNTVCT 149


RESULT    6
ID   US-08-050-319B-4     STANDARD;     PRT;   124 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
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```
DE   Sequence 4, Application US/08050319B.
XX
CC    Sequence 4, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  124 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   124 AA; 14047 MW; 75840 CN;

  Query Match           44.8%;  Score 979;  DB 7;  Length 124;
  Best Local Similarity  99.2%;  Pred. No. 9.96e-86;
  Matches   123;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db      61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Qy      85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQ 144

Db     121 NTVC 124
           ||||
Qy     145 NTVC 148


RESULT    7
ID   US-08-050-319B-50     STANDARD;     PRT;   157 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 50, Application US/08050319B.
XX
CC    Sequence 50, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  50:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  157 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   157 AA; 17570 MW; 122247 CN;

  Query Match           41.8%;  Score 912;  DB 7;  Length 157;
  Best Local Similarity  95.9%;  Pred. No. 5.63e-79;
  Matches   117;  Conservative    2;  Mismatches   3;  Indels   0;  Gaps   0;

Db      36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 95
           | : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119

Db      96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 155
           |||||||||:||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy     120 ENLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLP 179

Db     156 QI 157
           ||
Qy     180 QI 181


RESULT    8
ID   US-08-050-319B-54     STANDARD;     PRT;   158 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 54, Application US/08050319B.
XX
CC    Sequence 54, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
```

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CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  54:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  158 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   158 AA; 17375 MW; 124033 CN;

  Query Match           30.5%;  Score 666;  DB 7;  Length 158;
  Best Local Similarity  97.7%;  Pred. No. 2.50e-54;
  Matches    86;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCTCH 128
          |||||||||||||||||||||||||| |:
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCR 110


RESULT    9
ID   US-08-050-319B-52     STANDARD;     PRT;   153 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 52, Application US/08050319B.
XX
CC    Sequence 52, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  52:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  153 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   153 AA; 17148 MW; 116104 CN;

  Query Match           27.0%;  Score 589;  DB 7;  Length 153;
  Best Local Similarity  69.8%;  Pred. No. 1.12e-46;
  Matches    81;  Conservative    9;  Mismatches  20;  Indels   6;  Gaps   4;

Db     44 CPQGKYIHPQNN-SIC--CTKCHK--GTYLYNDCPGPGQDT-DCRKNQYRHYWSENLFQC 97
          |  | :  ::|:   |  |:||:|  |    : |    :    ||||||||||||||||
Qy     66 CESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC 125

Db     98 FNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQI 153
          |||:|||||||||||||||||||||||||||||||||||||||||||||||| ||||
Qy    126 FNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQI 181


RESULT   10
ID   US-08-050-319B-36     STANDARD;     PRT;   41 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 36, Application US/08050319B.
XX
CC    Sequence 36, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  36:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  41 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
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SQ   SEQUENCE   41 AA; 4856 MW; 8601 CN;

  Query Match           15.4%;  Score 337;  DB 7;  Length 41;
  Best Local Similarity  97.6%;  Pred. No. 4.74e-22;
  Matches    40;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 GCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVC 41
           |||||||||||||||||||||:||||||||||||||||||||
Qy     108 GCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQNTVC 148


RESULT   11
ID   US-08-050-319B-26     STANDARD;     PRT;   40 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 26, Application US/08050319B.
XX
CC    Sequence 26, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  26:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  40 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   40 AA; 4459 MW; 7536 CN;

  Query Match           14.8%;  Score 324;  DB 7;  Length 40;
  Best Local Similarity 100.0%;  Pred. No. 8.28e-21;
  Matches    40;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCR 40
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Qy      25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCR 64


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ID   US-08-050-319B-31     STANDARD;     PRT;   43 AA.
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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 31, Application US/08050319B.
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CC    Sequence 31, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  31:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  43 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   43 AA; 4767 MW; 9758 CN;

  Query Match           14.6%;  Score 318;  DB 7;  Length 43;
  Best Local Similarity 100.0%;  Pred. No. 3.09e-20;
  Matches    43;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 43
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Qy      65 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 107


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AC   xxxxxx
XX
DT   01-JAN-1900
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DE   Sequence 40, Application US/08050319B.
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CC    Sequence 40, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
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CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  40:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  39 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   39 AA; 4335 MW; 8059 CN;

  Query Match           13.0%;  Score 284;  DB 7;  Length 39;
  Best Local Similarity  97.4%;  Pred. No. 5.18e-17;
  Matches    38;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 TCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGT 39
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Qy     149 TCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGT 187


RESULT   14
ID   US-08-292-549-2     STANDARD;     PRT;   325 AA.
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 2, Application US/08292549.
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CC    Sequence 2, Application US/08292549
CC    Patent No. 5464938
CC     GENERAL INFORMATION:
CC       APPLICANT:  Smith, Craig A.
CC       APPLICANT:  Goodwin, Raymond G.
CC       TITLE OF INVENTION:  Isolated Viral Protein TNF Antagonists
CC       NUMBER OF SEQUENCES:  10
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  Washington
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/292,549
CC         FILING DATE:
CC         CLASSIFICATION:  530
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  07/963,330
CC         FILING DATE:  10/19/92
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2602-A
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (206) 587-0430
CC         TELEFAX:  (206) 233-0644
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  325 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   325 AA; 35132 MW; 591446 CN;

  Query Match           10.3%;  Score 225;  DB 5;  Length 325;
  Best Local Similarity  34.8%;  Pred. No. 1.64e-11;
  Matches    39;  Conservative   21;  Mismatches  45;  Indels   7;  Gaps   6;

Db       4 LIAL-LVCVVYVYGDDVPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC 61
             |:|: |:|:  :           |||   |  :::::||: || | |    | ||| :| |
Qy       6 LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC 63

Db      62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY 111
             || |:|||| ||   |:|| : |   ::: :  :|   :| || |     |
Qy      64 RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY 114


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AC   xxxxxx
XX
DT   01-JAN-1900
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DE   Sequence 2, Application PC/TUS9102207.
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CC    Sequence 2, Application PC/TUS9102207
CC     GENERAL INFORMATION:
CC       APPLICANT:  Smith, Craig A.
CC       APPLICANT:  Goodwin, Raymond G.
CC       TITLE OF INVENTION:  Isolated Viral Protein Cytokine Antagonists
CC       NUMBER OF SEQUENCES:  4
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  Washington
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.24
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  PCT/US91/02207
CC         FILING DATE:  19910329
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Wight, Christopher L.
CC         REGISTRATION NUMBER:  31,680
CC         REFERENCE/DOCKET NUMBER:  2602
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (206) 587-0430
CC         TELEFAX:  (206) 587-0606
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  325 amino acids
CC         TYPE:  AMINO ACID
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
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SQ   SEQUENCE   325 AA; 35132 MW; 591446 CN;

  Query Match           10.3%;  Score 225;  DB 10;  Length 325;
  Best Local Similarity  34.8%;  Pred. No. 1.64e-11;
  Matches    39;  Conservative   21;  Mismatches  45;  Indels   7;  Gaps   6;

Db       4 LIAL-LVCVVYVYGDDVPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC 61
           |:|: |:|:  :          |||   |  :::::||: || | |    | ||| :| |
Qy       6 LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC 63

Db      62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY 111
             || |:|||| ||   |:|| : |   ::: :  :|   :| || |    |
Qy      64 RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY 114


Search completed: Wed May  6 08:24:12 1998
Job time : 15 secs.
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 10:56:07 1998; MasPar time 65.66 Seconds
920.693 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-5
Description: (1-1147) from US08804166.seq
Perfect Score: 1147
N.A. Sequence: 1 TCGAGATGGCTACAGGTAAG.....AATCTTAAGGATCCCTCGAG 1147
Comp: AGCTCTACCGATGTCCATTC.....TTAGAATTCCTAGGGAGCTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.727; Variance 4.288; scale 2.035

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	506	44.1	2062	7	US-08-050-	Sequence 24, Applicati	0.00e+00
	2	506	44.1	2175	7	US-08-321-	Sequence 1, Applicatio	0.00e+00
	3	504	43.9	6889	14	PCT-US95-0	Sequence 2, Applicatio	0.00e+00
	4	504	43.9	6889	6	US-08-286-	Sequence 2, Applicatio	0.00e+00
	5	464	40.5	600	7	US-08-050-	Sequence 47, Applicati	0.00e+00
	6	375	32.7	504	7	US-08-050-	Sequence 56, Applicati	8.54e-293
	7	373	32.5	501	7	US-08-050-	Sequence 1, Applicatio	4.58e-291
	8	364	31.7	372	7	US-08-050-	Sequence 3, Applicatio	2.74e-283
	9	345	30.1	474	7	US-08-050-	Sequence 49, Applicati	6.94e-267
	10	288	25.1	2771	7	US-08-273-	Sequence 5, Applicatio	8.12e-218
	11	287	25.0	4283	7	US-08-343-	Sequence 3, Applicatio	5.86e-217
	12	287	25.0	4283	7	US-08-445-	Sequence 1, Applicatio	5.86e-217
	13	255	22.2	477	7	US-08-050-	Sequence 53, Applicati	1.56e-189
	14	213	18.6	462	7	US-08-050-	Sequence 51, Applicati	1.02e-153
	15	67	5.8	534	6	US-08-187-	Sequence 3, Applicatio	4.70e-33
	16	67	5.8	654	6	US-08-187-	Sequence 1, Applicatio	4.70e-33
	17	58	5.1	321	6	US-08-314-	Sequence 23, Applicati	3.86e-26
	18	58	5.1	321	4	US-07-920-	Sequence 23, Applicati	3.86e-26
	19	57	5.0	597	6	US-08-187-	Sequence 2, Applicatio	2.21e-25
	20	50	4.4	2248	7	US-08-475-	Sequence 1, Applicatio	3.87e-20
	21	50	4.4	2248	7	US-08-780-	Sequence 1, Applicatio	3.87e-20
	22	50	4.4	2248	7	US-08-636-	Sequence 1, Applicatio	3.87e-20
	23	50	4.4	2248	6	US-08-369-	Sequence 1, Applicatio	3.87e-20
	24	51	4.4	7218	7	US-08-232-	Sequence 14, Applicati	7.03e-21
	25	38	3.3	633	7	US-08-388-	Sequence 1, Applicatio	1.67e-11
c	26	38	3.3	7218	7	US-08-232-	Sequence 14, Applicati	1.67e-11
c	27	34	3.0	215	6	US-08-238-	Sequence 5, Applicatio	9.19e-09
	28	34	3.0	4810	12	PCT-US93-0	Sequence 7, Applicatio	9.19e-09
	29	34	3.0	4810	7	US-08-453-	Sequence 7, Applicatio	9.19e-09
	30	34	3.0	4810	13	PCT-US94-0	Sequence 3, Applicatio	9.19e-09
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	33	34	3.0	5125	7	US-08-453-	Sequence 11, Applicati	9.19e-09
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	43	25	2.2	82	14	PCT-US95-1	Sequence 97, Applicati	5.37e-03
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ALIGNMENTS

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DT 01-JAN-1900
XX
DE Sequence 24, Application US/08050319B.
XX
CC Sequence 24, Application US/08050319B
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:

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CC        LENGTH:  2062 base pairs
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CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  155..1519
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  Query Match           44.1%;  Score 506;  DB 7;  Length 2062;
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  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

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Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


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CC   Patent No. 5665859
CC    GENERAL INFORMATION:
CC      APPLICANT:  WALLACH, David
CC      APPLICANT:  BRAKEBUSCH, Cord
CC      APPLICANT:  VARFOLOMEEV, Eugene
CC      APPLICANT:  BATKIN, Michael
CC      TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC      TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC      NUMBER OF SEQUENCES:  42
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  BROWDY AND NEIMARK
CC        STREET:  419 Seventh Street, N.W., Suite 300
CC        CITY:  Washington
CC        STATE:  D.C.
CC        COUNTRY:  USA
CC        ZIP:  20004
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/321,668
CC        FILING DATE:  12-OCT-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  IL 107268
CC        FILING DATE:  12-OCT-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  BROWDY, Roger L.
CC        REGISTRATION NUMBER:  25,618
CC        REFERENCE/DOCKET NUMBER:  WALLACH=13
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  202-628-5197
CC        TELEFAX:  202-737-3528
CC        TELEX:  248633
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2175 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  256..1620
SQ   Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

  Query Match           44.1%;  Score 506;  DB 7;  Length 2175;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
        |||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
        |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855
        |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823
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Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT 905
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    3
ID   PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.

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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 2, Application PC/TUS9509576.
XX
CC   Sequence 2, Application PC/TUS9509576
CC    GENERAL INFORMATION:
CC      APPLICANT:  GENENTECH, INC.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/09576
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/286740
CC        FILING DATE:  05-AUG-1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:  00,000
CC        REFERENCE/DOCKET NUMBER:  798PCT
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC     INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           43.9%;  Score 504;  DB 14;  Length 6889;
  Best Local Similarity  99.0%;  Pred. No. 0.00e+00;
  Matches   509;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
          |||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db   2145 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 2204
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db   2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
          |||||||||||||||||||||||||||||||||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 857


RESULT    4
ID   US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.

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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08286740.
XX
CC   Sequence 2, Application US/08286740
CC   Patent No. 5561053
CC    GENERAL INFORMATION:
CC      APPLICANT:  Crowley, Craig W.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/286,740
CC        FILING DATE:  05-AUG-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:
CC        REFERENCE/DOCKET NUMBER:  798
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC     INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
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CC        TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           43.9%;  Score 504;  DB 6;  Length 6889;
  Best Local Similarity  99.0%;  Pred. No. 0.00e+00;
  Matches   509;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
           |||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db   2145 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 2204
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db   2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
           |||||||||||||||||||||||||||||||||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 857


RESULT    5
ID   US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 47, Application US/08050319B.
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CC   Sequence 47, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  47:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  600 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..597
SQ   Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

  Query Match           40.5%;  Score 464;  DB 7;  Length 600;
  Best Local Similarity  98.3%;  Pred. No. 0.00e+00;
  Matches   472;  Conservative    0;  Mismatches   8;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCACAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
           ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
           |||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTTAG 600
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823


RESULT    6
ID   US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 56, Application US/08050319B.
XX
CC   Sequence 56, Application US/08050319B
CC   Patent No. 5633145
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CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  56:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  504 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

  Query Match           32.7%;  Score 375;  DB 7;  Length 504;
  Best Local Similarity  99.0%;  Pred. No. 8.54e-293;
  Matches   379;  Conservative    0;  Mismatches   4;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
        |||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    481 AAACAGAACACCGTGTGCACCTG 503
        ||||||||||||||| ||||||||
Qy    704 AAACAGAACACCGTCTGCACCTG 726
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RESULT    7
ID   US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08050319B.
XX
CC   Sequence 1, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  501 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

  Query Match           32.5%;  Score 373;  DB 7;  Length 501;
  Best Local Similarity  99.0%;  Pred. No. 4.58e-291;
  Matches   377;  Conservative    0;  Mismatches   4;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
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Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
          |||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    481 AAACAGAACACCGTGTGCACC 501
          ||||||||||||||| ||||||
Qy    704 AAACAGAACACCGTCTGCACC 724


RESULT    8
ID   US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08050319B.
XX
CC   Sequence 3, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  372 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..372
SQ   Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

  Query Match           31.7%;  Score 364;  DB 7;  Length 372;
  Best Local Similarity  98.9%;  Pred. No. 2.74e-283;
  Matches   368;  Conservative    0;  Mismatches   4;  Indels   0;  Gaps   0;

Db      1 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    350 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 409

Db     61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy    410 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGACTGCAGG 469

Db    121 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    470 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 529

Db    181 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    530 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 589

Db    241 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    590 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 649

Db    301 TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAG 360
          |||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Qy    650 TGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAGAAACAG 709

Db    361 AACACCGTGTGC 372
          |||||||| |||
Qy    710 AACACCGTCTGC 721


RESULT    9
ID   US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 49, Application US/08050319B.
XX
CC   Sequence 49, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  49:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  474 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
```

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CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..471
SQ   Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;

  Query Match           30.1%;  Score 345;  DB 7;  Length 474;
  Best Local Similarity  98.3%;  Pred. No. 6.94e-267;
  Matches   351;  Conservative    0;  Mismatches   6;  Indels   0;  Gaps   0;

Db    118 AGAGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGC 177
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    467 AGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGC 526

Db    178 TGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGG 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    527 TGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGG 586

Db    238 GACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTC 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    587 GACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTC 646

Db    298 CAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAA 357
          |||||||||||||||| |||||||||||||||||||||||||||||||| |||||||||
Qy    647 CAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAGAAA 706

Db    358 CAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCC 417
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Qy    707 CAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCC 766

Db    418 TGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTTAG 474
          |||||||||||||||||||||||||||||||||||| |||||||||||| ||
Qy    767 TGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823


RESULT   10
ID   US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 5, Application US/08273411.
XX
CC   Sequence 5, Application US/08273411
CC   Patent No. 5625124
CC    GENERAL INFORMATION:
CC      APPLICANT:  Falk, Per
CC      APPLICANT:  Gordon, Jeffrey I.
CC      TITLE OF INVENTION:  Animal Model for Gastro-Intestinal
CC      TITLE OF INVENTION:  Disease
CC      NUMBER OF SEQUENCES:  10
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Patrea L. Pabst
CC        STREET:  1100 Peachtree Street, Suite 2800
CC        CITY:  Atlanta
CC        STATE:  Georgia
CC        COUNTRY:  USA
CC        ZIP:  30309-4530
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/273,411
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Pabst, Patrea L.
CC        REGISTRATION NUMBER:  31,284
CC        REFERENCE/DOCKET NUMBER:  WU106
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (404) 815-6508
CC        TELEFAX:  (404) 815-6555
CC    INFORMATION FOR SEQ ID NO:  5:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2771 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  Genes & Dev.
CC        VOLUME:  2
CC        PAGES:  1318-1332
CC        DATE:  1988
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 561 TO 629
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Seeburg, et al.
CC        JOURNAL:  DNA
CC        VOLUME:  1
CC        PAGES:  239-249
CC        DATE:  1982
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 620 TO 2771
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  J. Biol. Chem.
CC        VOLUME:  261
CC        PAGES:  5553-5561
CC        DATE:  1986
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 1 TO 617
SQ   Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;

  Query Match           25.1%;  Score 288;  DB 7;  Length 2771;
  Best Local Similarity  95.6%;  Pred. No. 8.12e-218;
  Matches   323;  Conservative    0;  Mismatches  11;  Indels   4;  Gaps   3;

Db    680 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db    740 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTGAATG--AG 797
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||  ||
Qy     66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTTTGAATGTGAG 125

Db    798 TATCGCCATGTAAGCCCAGTATG-GCC-AATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 855
          ||| ||||||||||||||||||  ||| ||||||||||||||||||||||||||||||||
Qy    126 TATGGCCATGTAAGCCCAGTATTTGCCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 185

Db    856 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 915
          |||||||||||||||||||||||||||||||| | | ||||||||||||||| ||||
Qy    186 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGACACTCCTGGCCTCTTGCTCTGCGGC 245

Db    916 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 975
          ||| | |||||||| |||||||||||| ||||||||||||||||||||||||||||||||
Qy    246 TCCGTGTGTTGCCCTGTGGTTTCTCCCCACGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 305

Db    976 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1013
          |||||||||||||||||||||||||||||||||||||
Qy    306 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343


RESULT   11
ID   US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
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```
DE   Sequence 3, Application US/08343401A.
XX
CC   Sequence 3, Application US/08343401A
CC   Patent No. 5661132
CC    GENERAL INFORMATION:
CC      APPLICANT:  Swain, William F
CC      APPLICANT:  Macklin, Michael D
CC      APPLICANT:  Eriksson, Elof
CC      APPLICANT:  Andree, Christophe
CC      TITLE OF INVENTION:  Improved Wound Healing
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  PO Box 2113
CC        CITY:  Madison
CC        STATE:  WI
CC        COUNTRY:  USA
CC        ZIP:  53701-2113
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/343,401A
CC        FILING DATE:  22-NOV-1994
CC        CLASSIFICATION:  514
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Seay, Nicholas J
CC        REGISTRATION NUMBER:  27,386
CC        REFERENCE/DOCKET NUMBER:  11-229-9103-9
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  608-251-5000
CC        TELEFAX:  608-251-9166
CC     INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  4283 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  circular
CC      MOLECULE TYPE:  DNA (genomic)
CC      IMMEDIATE SOURCE:
CC        CLONE:  pWRG1630
CC      FEATURE:
CC        NAME/KEY:  exon
CC        LOCATION:  713..721
CC      FEATURE:
CC        NAME/KEY:  exon
CC        LOCATION:  981..1253
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  join(713..721, 981..1253)
CC      FEATURE:
CC        NAME/KEY:  sig_peptide
CC        LOCATION:  713..1049
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           25.0%;  Score 287;  DB 7;  Length 4283;
  Best Local Similarity  93.2%;  Pred. No. 5.86e-217;
  Matches   315;  Conservative    0;  Mismatches  22;  Indels   1;  Gaps   1;

Db    713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db    772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          |||||||||||||||||||||||||||||||||| || ||| || ||||||||||
Qy     66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTTTGAATGTGAG 125

Db    832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
          ||| ||||| |||||||||||||| ||||||||||||||||||  ||  |  ||||
Qy    126 TATGGCCATGTAAGCCCAGTATTTGCCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 185

Db    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
          |||||||||||||||||||||||||||||||||| | |  ||||||||||||| ||||
Qy    186 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGACACTCCTGGCCTCTTGCTCTGCGGC 245

Db    952 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          ||| | |||||||| |||||||||||| ||||||||||||||||||||||||||||||
Qy    246 TCCGTGTGTTGCCCTGTGGTTTCTCCCCACGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 305

Db   1012 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
          |||||||||||||||||||||||||||||||||||||
Qy    306 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343


RESULT   12
ID   US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08445265A.
XX
CC   Sequence 1, Application US/08445265A
CC   Patent No. 5697901
CC    GENERAL INFORMATION:
CC      APPLICANT:  Eriksson, Elof
CC      TITLE OF INVENTION:  GENE DELIVERY BY MICRONEEDLE INJECTION
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  1 South Pinckney Street
CC        CITY:  Madison
CC        STATE:  WI
CC        COUNTRY:  US
CC        ZIP:  53703
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/445,265A
CC        FILING DATE:
CC        CLASSIFICATION:  604
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Seay, Nicholas J
CC        REGISTRATION NUMBER:  27386
CC        REFERENCE/DOCKET NUMBER:  110229.91080
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  608-251-5000
CC        TELEFAX:  608-251-9166
CC     INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  4283 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  circular
CC      MOLECULE TYPE:  other nucleic acid
CC        DESCRIPTION:  /desc = "Plasmid DNA"
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  join(713..721, 981..1250)
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           25.0%;  Score 287;  DB 7;  Length 4283;
  Best Local Similarity  93.2%;  Pred. No. 5.86e-217;
  Matches   315;  Conservative    0;  Mismatches  22;  Indels   1;  Gaps   1;

Db    713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65
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Db    772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          ||||||||||||||||||||||||||||||||||||||| || ||| || ||||||||||
Qy     66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTTTGAATGTGAG 125

Db    832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
          ||| ||||| |||||||||||||| ||||||||||||||||||||  ||  |  ||||
Qy    126 TATGGCCATGTAAGCCCAGTATTTGCCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 185

Db    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
          |||||||||||||||||||||||||||||||| | |  |||||||||||||| ||||
Qy    186 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGACACTCCTGGCCTCTTGCTCTGCGGC 245

Db    952 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          ||| | ||||||||| |||||||||||| |||||||||||||||||||||||||||||
Qy    246 TCCGTGTGTTGCCCTGTGGTTTCTCCCCACGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 305

Db   1012 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
          |||||||||||||||||||||||||||||||||||||
Qy    306 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343
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RESULT 13
ID US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 53, Application US/08050319B.
XX
CC Sequence 53, Application US/08050319B
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 53:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 477 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..474
SQ Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

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  Query Match           22.2%;  Score 255;  DB 7;  Length 477;
  Best Local Similarity  98.9%;  Pred. No. 1.56e-189;
  Matches   258;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTACCTGC 381
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Qy    584 CGGGACACCGTGTGTGGCTGC 604
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RESULT 14
ID US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

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AC xxxxxx
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DT 01-JAN-1900
XX
DE Sequence 51, Application US/08050319B.
XX
CC Sequence 51, Application US/08050319B
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 51:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 462 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear

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CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..459
SQ   Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

  Query Match           18.6%;  Score 213;  DB 7;  Length 462;
  Best Local Similarity  97.8%;  Pred. No. 1.02e-153;
  Matches   218;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db    240 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
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Qy    601 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 660

Db    300 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 359
          || ||||||||||||||||||||||||||||||||| |||||||||||||||||||| ||
Qy    661 CACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAGAAACAGAACACCGTCTG 720

Db    360 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAA 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAA 780

Db    420 GAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTTAG 462
          |||||||||||||||||||||||| |||||||||||| ||
Qy    781 GAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823


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ID   US-08-187-756C-3 STANDARD; DNA; UNC; 534 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 3, Application US/08187756C.
XX
CC   Sequence 3, Application US/08187756C
CC   Patent No. 5597709
CC    GENERAL INFORMATION:
CC      APPLICANT:  ROSEN, ET AL.
CC      TITLE OF INVENTION:  Human Growth Hormone
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
CC        ADDRESSEE:  CECCHI, STEWART & OLSTEIN
CC        STREET:  6 BECKER FARM ROAD
CC        CITY:  ROSELAND
CC        STATE:  NEW JERSEY
CC        COUNTRY:  USA
CC        ZIP:  07068
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5 INCH DISKETTE
CC        COMPUTER:  IBM PS/2
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WORD PERFECT 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/187,756C
CC        FILING DATE:  January 27, 1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  FERRARO, GREGORY D.
CC        REGISTRATION NUMBER:  36,134
CC        REFERENCE/DOCKET NUMBER:  325800-55
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  201-994-1700
CC        TELEFAX:  201-994-1744
CC     INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  534 BASE PAIRS
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  SINGLE
CC        TOPOLOGY:  LINEAR
CC      MOLECULE TYPE:  cDNA
SQ   Sequence 534 BP; 108 A; 166 C; 143 G; 117 T; 0 other;

  Query Match            5.8%;  Score 67;  DB 6;  Length 534;
  Best Local Similarity  97.2%;  Pred. No. 4.70e-33;
  Matches    69;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      8 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAG 67
          || |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    273 CACGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAG 332

Db     68 AGGGCAGTGCC 78
          ||||||||||||
Qy    333 AGGGCAGTGCC 343


Search completed: Wed May  6 10:57:34 1998
Job time : 87 secs.
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:20:59 1998; MasPar time 4.78 Seconds
367.559 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 30.606; Variance 140.802; scale 0.217

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	48.0	455	7	US-08-321-	Sequence 2, Applicatio	4.13e-91
2	1124	48.0	455	7	US-08-050-	Sequence 25, Applicati	4.13e-91
3	1115	47.6	199	7	US-08-050-	Sequence 48, Applicati	2.79e-90
4	1025	43.8	145	6	US-08-425-	Sequence 2, Applicatio	5.45e-82
5	1025	43.8	145	6	US-08-425-	Sequence 1, Applicatio	5.45e-82
6	1020	43.6	145	7	US-08-298-	Sequence 1, Applicatio	1.57e-81
7	995	42.5	145	6	US-08-425-	Sequence 10, Applicati	3.13e-79
8	996	42.5	167	7	US-08-050-	Sequence 57, Applicati	2.54e-79
9	996	42.5	167	7	US-08-050-	Sequence 2, Applicatio	2.54e-79
10	981	41.9	124	7	US-08-050-	Sequence 4, Applicatio	6.07e-78
11	800	34.2	157	7	US-08-050-	Sequence 50, Applicati	2.36e-61
12	740	31.6	114	6	US-08-425-	Sequence 9, Applicatio	7.01e-56
13	734	31.4	114	6	US-08-425-	Sequence 7, Applicatio	2.47e-55
14	714	30.5	117	6	US-08-425-	Sequence 11, Applicati	1.63e-53
15	684	29.2	114	6	US-08-425-	Sequence 8, Applicatio	8.72e-51
16	666	28.4	158	7	US-08-050-	Sequence 54, Applicati	3.76e-49
17	651	27.8	117	6	US-08-425-	Sequence 12, Applicati	8.62e-48
18	613	26.2	149	6	US-08-425-	Sequence 5, Applicatio	2.38e-44
19	477	20.4	153	7	US-08-050-	Sequence 52, Applicati	4.02e-32
20	339	14.5	41	7	US-08-050-	Sequence 36, Applicati	6.36e-20
21	324	13.8	40	7	US-08-050-	Sequence 26, Applicati	1.29e-18
22	318	13.6	43	7	US-08-050-	Sequence 31, Applicati	4.28e-18
23	296	12.6	45	1	5451527-1	Patent No. 5451527.	3.43e-16
24	287	12.3	111	6	US-08-425-	Sequence 3, Applicatio	2.04e-15
25	287	12.3	111	6	US-08-425-	Sequence 4, Applicatio	2.04e-15
26	282	12.0	112	6	US-08-425-	Sequence 6, Applicatio	5.49e-15
27	268	11.4	46	5	US-08-086-	Sequence 14, Applicati	8.68e-14
28	261	11.1	46	5	US-08-086-	Sequence 12, Applicati	3.43e-13
29	260	11.1	131	1	5177193-3	Patent No. 5177193.	4.17e-13
30	249	10.6	46	5	US-08-086-	Sequence 11, Applicati	3.59e-12
31	249	10.6	46	5	US-08-086-	Sequence 13, Applicati	3.59e-12
32	230	9.8	41	5	US-08-086-	Sequence 17, Applicati	1.44e-10
33	227	9.7	34	1	5451527-4	Patent No. 5451527.	2.57e-10
34	227	9.7	39	1	5451527-8	Patent No. 5451527.	2.57e-10
35	227	9.7	39	1	5451527-12	Patent No. 5451527.	2.57e-10
36	227	9.7	39	13	PCT-US94-0	Sequence 29, Applicati	2.57e-10
37	225	9.6	325	10	PCT-US91-0	Sequence 2, Applicatio	3.78e-10
38	225	9.6	325	5	US-08-292-	Sequence 2, Applicatio	3.78e-10
39	221	9.4	326	10	PCT-US91-0	Sequence 4, Applicatio	8.16e-10
40	221	9.4	326	5	US-08-292-	Sequence 4, Applicatio	8.16e-10
41	212	9.1	41	5	US-08-086-	Sequence 15, Applicati	4.59e-09
42	212	9.1	474	1	5395760-4	Patent No. 5395760.	4.59e-09
43	210	9.0	355	5	US-08-292-	Sequence 6, Applicatio	6.72e-09
44	209	8.9	41	1	5451527-10	Patent No. 5451527.	8.14e-09
45	209	8.9	41	1	5451527-11	Patent No. 5451527.	8.14e-09

ALIGNMENTS

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ID   US-08-321-668-2     STANDARD;     PRT;   455 AA.
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 2, Application US/08321668.
XX
CC    Sequence 2, Application US/08321668
CC    Patent No. 5665859
CC     GENERAL INFORMATION:
CC       APPLICANT:  WALLACH, David
CC       APPLICANT:  BRAKEBUSCH, Cord
CC       APPLICANT:  VARFOLOMEEV, Eugene
CC       APPLICANT:  BATKIN, Michael
CC       TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC       TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC       NUMBER OF SEQUENCES:  42
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  BROWDY AND NEIMARK
CC         STREET:  419 Seventh Street, N.W., Suite 300
CC         CITY:  Washington
CC         STATE:  D.C.
CC         COUNTRY:  USA
CC         ZIP:  20004
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/321,668
CC         FILING DATE:  12-OCT-1994
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  IL 107268
CC         FILING DATE:  12-OCT-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  BROWDY, Roger L.
CC         REGISTRATION NUMBER:  25,618
CC         REFERENCE/DOCKET NUMBER:  WALLACH=13
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-628-5197
CC         TELEFAX:  202-737-3528
CC         TELEX:  248633
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CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50494 MW; 1048031 CN;

  Query Match           48.0%;  Score 1124;  DB 7;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 4.13e-91;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
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ID   US-08-050-319B-25     STANDARD;     PRT;   455 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 25, Application US/08050319B.
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CC    Sequence 25, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  25:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50579 MW; 1048388 CN;

  Query Match           48.0%;  Score 1124;  DB 7;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 4.13e-91;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
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ID   US-08-050-319B-48     STANDARD;     PRT;   199 AA.
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 48, Application US/08050319B.
XX
CC    Sequence 48, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  48:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  199 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   199 AA; 22186 MW; 195553 CN;

  Query Match           47.6%;  Score 1115;  DB 7;  Length 199;
  Best Local Similarity  98.6%;  Pred. No. 2.79e-90;
  Matches   141;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
          |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    4
ID   US-08-425-673-2     STANDARD;     PRT;   145 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08425673.
XX
CC    Sequence 2, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   145 AA; 15544 MW; 114662 CN;

  Query Match           43.8%;  Score 1025;  DB 6;  Length 145;
  Best Local Similarity  99.3%;  Pred. No. 5.45e-82;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||:
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    5
ID   US-08-425-673-1     STANDARD;     PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08425673.
XX
CC    Sequence 1, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  1:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   145 AA; 15544 MW; 114662 CN;

  Query Match           43.8%;  Score 1025;  DB 6;  Length 145;
  Best Local Similarity  99.3%;  Pred. No. 5.45e-82;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288
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Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    6
ID   US-08-298-189B-1     STANDARD;     PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08298189B.
XX
CC    Sequence 1, Application US/08298189B
CC    Patent No. 5674727
CC     GENERAL INFORMATION:
CC       APPLICANT:  Dr. Laurence A. Cole and Dr. Andrew Kardana
CC       TITLE OF INVENTION:  No. 5674727el Methods for Detecting Reproductive
CC       TITLE OF INVENTION:  Cancers or Tumors and Assay Products
CC       TITLE OF INVENTION:  Therefor
CC       NUMBER OF SEQUENCES:  1
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Dr. Laurence A. Cole , c/o Dept. of Obstetrics and
CC         STREET:  333 Cedar Street
CC         CITY:  New Haven
CC         STATE:  Connecticut
CC         COUNTRY:  USA
CC         ZIP:  06510
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  3.5" diskette
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  Windows 95
CC         SOFTWARE:  Microsoft Word 7.0
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/298,189B
CC         FILING DATE:  08/31/94
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Brian D. Voyce
CC         REGISTRATION NUMBER:  28,917
CC         REFERENCE/DOCKET NUMBER:  DSI1
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  919-638-3939 or 803-272-1471
CC         TELEFAX:  919-638-3939 or 803-272-1471
CC     INFORMATION FOR SEQ ID NO:  1:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  No. 5674727 applicable
CC         TOPOLOGY:  Unknown
CC       MOLECULE TYPE:  subunit of hormone, specifically the
CC       MOLECULE TYPE:  beta\subunit of hCG
CC       ORIGINAL SOURCE:  human urine
CC       FEATURE:
CC         NAME/KEY:  beta subunit of hCG that is nicked by GBNE
CC         LOCATION:  hCG
CC         IDENTIFICATION METHOD:  N-terminal sequence analysis
CC       PUBLICATION INFORMATION:
CC         AUTHORS:  Keutmann et alia
CC         TITLE:  "A Receptor-binding Region in Human        Choriogonadotrophin/Lutopr
CC         JOURNAL:  Proc Nat'l Acad Sci USA
CC         VOLUME:  84
CC         ISSUE:  No. 5674727 applicable
CC         PAGES:  2038-2042
CC         DATE:  1987
SQ   SEQUENCE   145 AA; 15476 MW; 116769 CN;

  Query Match           43.6%;  Score 1020;  DB 7;  Length 145;
  Best Local Similarity  98.6%;  Pred. No. 1.57e-81;
  Matches   137;  Conservative    2;  Mismatches   0;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCKKSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||::||||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    7
ID   US-08-425-673-10     STANDARD;     PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 10, Application US/08425673.
XX
CC    Sequence 10, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  10:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  145 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   145 AA; 15448 MW; 114931 CN;

  Query Match           42.5%;  Score 995;  DB 6;  Length 145;
  Best Local Similarity  96.4%;  Pred. No. 3.13e-79;
  Matches   134;  Conservative    1;  Mismatches   4;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
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Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||   :||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    8
ID   US-08-050-319B-57     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 57, Application US/08050319B.
XX
CC    Sequence 57, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  57:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           42.5%;  Score 996;  DB 7;  Length 167;
  Best Local Similarity 100.0%;  Pred. No. 2.54e-79;
  Matches   127;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
          |||||||
Qy    143 KQNTVCT 149


RESULT    9
ID   US-08-050-319B-2     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08050319B.
XX
CC    Sequence 2, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match           42.5%;  Score 996;  DB 7;  Length 167;
  Best Local Similarity 100.0%;  Pred. No. 2.54e-79;
  Matches   127;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCT 167
          |||||||
Qy    143 KQNTVCT 149


RESULT   10
ID   US-08-050-319B-4     STANDARD;     PRT;   124 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
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XX
DE   Sequence 4, Application US/08050319B.
XX
CC    Sequence 4, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC      INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  124 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   124 AA; 14047 MW; 75840 CN;

  Query Match           41.9%;  Score 981;  DB 7;  Length 124;
  Best Local Similarity 100.0%;  Pred. No. 6.07e-78;
  Matches   124;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db      61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db     121 NTVC 124
           ||||
Qy     145 NTVC 148


RESULT   11
ID   US-08-050-319B-50     STANDARD;     PRT;   157 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 50, Application US/08050319B.
XX
CC    Sequence 50, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC      INFORMATION FOR SEQ ID NO:  50:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  157 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   157 AA; 17570 MW; 122247 CN;

  Query Match           34.2%;  Score 800;  DB 7;  Length 157;
  Best Local Similarity 96.2%;  Pred. No. 2.36e-61;
  Matches   102;  Conservative    2;  Mismatches   2;  Indels   0;  Gaps   0;

Db      36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 95
           | : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119

Db      96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCS 141
           ||||||||||||||||||||||||||||||||||||||||||||||:
Qy     120 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165


RESULT   12
ID   US-08-425-673-9     STANDARD;     PRT;   114 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 9, Application US/08425673.
XX
CC    Sequence 9, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
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CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  9:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  114 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   114 AA; 12250 MW; 68564 CN;

  Query Match           31.6%;  Score 740;  DB 6;  Length 114;
  Best Local Similarity  93.3%;  Pred. No. 7.01e-56;
  Matches    97;  Conservative    1;  Mismatches   6;  Indels   0;  Gaps   0;

Db       7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Qy     169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db      67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDCGGPKDHPSYC 110
           |||||||||||||||||||||||||   :||||||||||  |
Qy     229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC 272


RESULT   13
ID   US-08-425-673-7     STANDARD;     PRT;   114 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 7, Application US/08425673.
XX
CC    Sequence 7, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  114 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   114 AA; 12401 MW; 67071 CN;

  Query Match           31.4%;  Score 734;  DB 6;  Length 114;
  Best Local Similarity  91.7%;  Pred. No. 2.47e-55;
  Matches    99;  Conservative    0;  Mismatches   9;  Indels   0;  Gaps   0;

Db       7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
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Qy     169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db      67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCTVRGLGPSYCDDPR 114
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ID   US-08-425-673-11     STANDARD;     PRT;   117 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 11, Application US/08425673.
XX
CC    Sequence 11, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
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CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  11:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  117 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   117 AA; 12890 MW; 72412 CN;

  Query Match           30.5%;  Score 714;  DB 6;  Length 117;
  Best Local Similarity  98.9%;  Pred. No. 1.63e-53;
  Matches    93;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 100
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Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262


RESULT   15
ID   US-08-425-673-8     STANDARD;     PRT;   114 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 8, Application US/08425673.
XX
CC    Sequence 8, Application US/08425673
CC    Patent No. 5508261
CC     GENERAL INFORMATION:
CC       APPLICANT:  Moyle, William R.
CC       APPLICANT:  Campbell, Robert K.
CC       TITLE OF INVENTION:  Analogs of Glycoprotein Hormones Having
CC       TITLE OF INVENTION:  Altered Receptor Binding Specificity and Activity and
CC       TITLE OF INVENTION:  Methods For Preparing and Using Same
CC       NUMBER OF SEQUENCES:  12
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Richard R. Muccino
CC         STREET:  P.O. Box 1267
CC         CITY:  Princeton
CC         STATE:  New Jersey
CC         COUNTRY:  USA
CC         ZIP:  08551
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/425,673
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/717,151
CC         FILING DATE:  18-JUN-1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Muccino, Richard R.
CC         REGISTRATION NUMBER:  32,538
CC         REFERENCE/DOCKET NUMBER:  UMD 1.0-004
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (609) 466-3407
CC         TELEFAX:  (609) 466-2760
CC     INFORMATION FOR SEQ ID NO:  8:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  114 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  peptide
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  NO
SQ   SEQUENCE   114 AA; 12242 MW; 69571 CN;

  Query Match           29.2%;  Score 684;  DB 6;  Length 114;
  Best Local Similarity  94.7%;  Pred. No. 8.72e-51;
  Matches    89;  Conservative    1;  Mismatches   4;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDC 100
          ||||||||||||||||||||||||||   :|||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262


Search completed: Wed May  6 08:21:12 1998
Job time : 13 secs.
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|  \/  |  ___/ ___||  _ \ / ___| | | |
| |\/| | |_ | |    | |_) | |   | |_| |
| |  | |  _|| |___ |  _ <| |___|  _  |
|_|  |_|_|   \____||_| \_\\____|_| |_|  (TM)
**************************************************************************

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                Distribution rights by Oxford Molecular Ltd

MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:          Wed May  6 10:28:56 1998;  MasPar time 67.26 Seconds
                                            941.976 Million cell updates/sec
Tabular output not generated.

Title:           >US-08-804-166-3
Description:     (1-1202) from US08804166.seq
Perfect Score:   1202
N.A. Sequence:        1 CTCGAGATGGCTACAGGTAA.........CCCCGATCCTCCCACAATAA 1202
     Comp:              GAGCTCTACCGATGTCCATT.........GGGGCTAGGAGGGTGTTATT

Scoring table:   TABLE default
                 Gap 6

Nmatch   STD :   Dbase 0;  Query 0

Searched:        102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        n-issued
                   1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                   10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics:      Mean 8.771;  Variance 4.649;  scale 1.887

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

                    %
Result              Query
  No.   Score       Match  Length DB  ID          Description            Pred. No.
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    1     424        35.3    2062  7  US-08-050-  Sequence 24, Applicati  0.00e+00
    2     424        35.3    2175  7  US-08-321-  Sequence 1, Applicatio  0.00e+00
    3     424        35.3    6889  6  US-08-286-  Sequence 2, Applicatio  0.00e+00
    4     424        35.3    6889 14  PCT-US95-0  Sequence 2, Applicatio  0.00e+00
    5     420        34.9     600  7  US-08-050-  Sequence 47, Applicati  0.00e+00
    6     381        31.7     504  7  US-08-050-  Sequence 56, Applicati  6.06e-276
    7     379        31.5     501  7  US-08-050-  Sequence 1, Applicatio  2.43e-274
    8     370        30.8     372  7  US-08-050-  Sequence 3, Applicatio  3.96e-267
    9     302        25.1    2771  7  US-08-273-  Sequence 5, Applicatio  8.84e-213
   10     300        25.0     474  7  US-08-050-  Sequence 49, Applicati  3.47e-211
   11     301        25.0    4283  7  US-08-343-  Sequence 3, Applicatio  5.54e-212
   12     301        25.0    4283  7  US-08-445-  Sequence 1, Applicatio  5.54e-212
   13     255        21.2     477  7  US-08-050-  Sequence 53, Applicati  2.07e-175
   14     169        14.1     462  7  US-08-050-  Sequence 51, Applicati  1.03e-107
   15     103         8.6     138  5  US-08-086-  Sequence 2, Applicatio  5.77e-57
   16      99         8.2     138  5  US-08-086-  Sequence 1, Applicatio  5.92e-54
   17      88         7.3    7218  7  US-08-232-  Sequence 14, Applicati  9.89e-46
   18      69         5.7     534  6  US-08-187-  Sequence 3, Applicatio  8.57e-32
   19      69         5.7     654  6  US-08-187-  Sequence 1, Applicatio  8.57e-32
   20      59         4.9     321  4  US-07-920-  Sequence 23, Applicati  1.20e-24
   21      59         4.9     321  6  US-08-314-  Sequence 23, Applicati  1.20e-24
   22      59         4.9     597  6  US-08-187-  Sequence 2, Applicatio  1.20e-24
   23      52         4.3    2248  7  US-08-636-  Sequence 1, Applicatio  9.36e-20
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c  27      45         3.7    7218  7  US-08-232-  Sequence 14, Applicati  5.54e-15
c  28      40         3.3     215  6  US-08-238-  Sequence 5, Applicatio  1.14e-11
   29      38         3.2     633  7  US-08-388-  Sequence 1, Applicatio  2.26e-10
   30      36         3.0    4810  7  US-08-453-  Sequence 7, Applicatio  4.31e-09
   31      36         3.0    4810 13  PCT-US94-0  Sequence 3, Applicatio  4.31e-09
   32      36         3.0    4810 12  PCT-US93-0  Sequence 7, Applicatio  4.31e-09
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   35      36         3.0    5125 12  PCT-US93-0  Sequence 11, Applicati  4.31e-09
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   37      36         3.0    5323  7  US-08-453-  Sequence 9, Applicatio  4.31e-09
   38      36         3.0    5323 12  PCT-US93-0  Sequence 9, Applicatio  4.31e-09
   39      32         2.7     196  1  5177193-2   Patent No. 5177193.     1.36e-06
   40      32         2.7     215  6  US-08-238-  Sequence 5, Applicatio  1.36e-06
   41      32         2.7    1006  6  US-08-239-  Sequence 1, Applicatio  1.36e-06
   42      30         2.5      33  7  US-08-050-  Sequence 14, Applicati  2.21e-05
   43      26         2.2      74 14  PCT-US95-1  Sequence 94, Applicati  4.79e-03
   44      27         2.2      81 14  PCT-US95-1  Sequence 92, Applicati  1.29e-03
   45      26         2.2      82 14  PCT-US95-1  Sequence 97, Applicati  4.79e-03

                               ALIGNMENTS

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ID   US-08-050-319B-24 STANDARD; DNA; UNC; 2062 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 24, Application US/08050319B.
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CC   Sequence 24, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  24:
CC      SEQUENCE CHARACTERISTICS:
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CC        LENGTH:  2062 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  155..1519
SQ   Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

  Query Match           35.3%;  Score 424;  DB 7;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy     345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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Qy     405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db     395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy     465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db     455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy     525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db     515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy     705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db     695 TCCTGT 700
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Qy     765 TCCTGT 770


RESULT    2
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 1, Application US/08321668.
XX
CC   Sequence 1, Application US/08321668
CC   Patent No. 5665859
CC    GENERAL INFORMATION:
CC      APPLICANT:  WALLACH, David
CC      APPLICANT:  BRAKEBUSCH, Cord
CC      APPLICANT:  VARFOLOMEEV, Eugene
CC      APPLICANT:  BATKIN, Michael
CC      TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC      TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC      NUMBER OF SEQUENCES:  42
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  BROWDY AND NEIMARK
CC        STREET:  419 Seventh Street, N.W., Suite 300
CC        CITY:  Washington
CC        STATE:  D.C.
CC        COUNTRY:  USA
CC        ZIP:  20004
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/321,668
CC        FILING DATE:  12-OCT-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  IL 107268
CC        FILING DATE:  12-OCT-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  BROWDY, Roger L.
CC        REGISTRATION NUMBER:  25,618
CC        REFERENCE/DOCKET NUMBER:  WALLACH=13
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  202-628-5197
CC        TELEFAX:  202-737-3528
CC        TELEX:  248633
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2175 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  256..1620
SQ   Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

  Query Match           35.3%;  Score 424;  DB 7;  Length 2175;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

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Db     436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Db     496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy     465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db     556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db     616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db     676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db     736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db     796 TCCTGT 801
           ||||||
Qy     765 TCCTGT 770


RESULT    3
ID   US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.
```

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XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08286740.
XX
CC   Sequence 2, Application US/08286740
CC   Patent No. 5561053
CC    GENERAL INFORMATION:
CC      APPLICANT:  Crowley, Craig W.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/286,740
CC        FILING DATE:  05-AUG-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:
CC        REFERENCE/DOCKET NUMBER:  798
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           35.3%;  Score 424;  DB 6;  Length 6889;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 TCCTGT 2150
           ||||||
Qy    765 TCCTGT 770


RESULT    4
ID   PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application PC/TUS9509576.
XX
CC   Sequence 2, Application PC/TUS9509576
CC    GENERAL INFORMATION:
CC      APPLICANT:  GENENTECH, INC.
CC      TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION:  HOST CELLS
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genentech, Inc.
CC        STREET:  460 Point San Bruno Blvd
CC        CITY:  South San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94080
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/09576
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/286740
CC        FILING DATE:  05-AUG-1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Lee, Wendy M.
CC        REGISTRATION NUMBER:  00,000
CC        REFERENCE/DOCKET NUMBER:  798PCT
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415/225-1994
CC        TELEFAX:  415/952-9881
CC        TELEX:  910/371-7168
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6889 bases
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

  Query Match           35.3%;  Score 424;  DB 14;  Length 6889;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 TCCTGT 2150
          ||||||
Qy    765 TCCTGT 770


RESULT    5
ID   US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 47, Application US/08050319B.
XX
CC   Sequence 47, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  47:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  600 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..597
SQ   Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

  Query Match           34.9%;  Score 420;  DB 7;  Length 600;
  Best Local Similarity  99.3%;  Pred. No. 0.00e+00;
  Matches   423;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCACAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    541 TCCTGT 546
          ||||||
Qy    765 TCCTGT 770


RESULT    6
ID   US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 56, Application US/08050319B.
XX
CC   Sequence 56, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
```

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CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  56:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  504 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

  Query Match           31.7%;  Score 381;  DB 7;  Length 504;
  Best Local Similarity  99.7%;  Pred. No. 6.06e-276;
  Matches   382;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
        |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACCTG 503
        |||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTG 727


RESULT    7
ID   US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08050319B.
XX
CC   Sequence 1, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  501 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..501
SQ   Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

  Query Match           31.5%;  Score 379;  DB 7;  Length 501;
  Best Local Similarity  99.7%;  Pred. No. 2.43e-274;
  Matches   380;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
        |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACC 501
        |||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACC 725


RESULT    8
ID   US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.
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XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08050319B.
XX
CC   Sequence 3, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  372 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..372
SQ   Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

  Query Match           30.8%;  Score 370;  DB 7;  Length 372;
  Best Local Similarity  99.7%;  Pred. No. 3.96e-267;
  Matches   371;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      1 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    351 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 410

Db     61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    411 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG 470

Db    121 GAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 180
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Qy    471 GAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC 530

Db    181 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    531 TCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGAC 590

Db    241 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    591 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAG 650

Db    301 TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    651 TGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAG 710

Db    361 AACACCGTGTGC 372
          ||||||||||||
Qy    711 AACACCGTGTGC 722


RESULT    9
ID   US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 5, Application US/08273411.
XX
CC   Sequence 5, Application US/08273411
CC   Patent No. 5625124
CC    GENERAL INFORMATION:
CC      APPLICANT:  Falk, Per
CC      APPLICANT:  Gordon, Jeffrey I.
CC      TITLE OF INVENTION:  Animal Model for Gastro-Intestinal
CC      TITLE OF INVENTION:  Disease
CC      NUMBER OF SEQUENCES:  10
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Patrea L. Pabst
CC        STREET:  1100 Peachtree Street, Suite 2800
CC        CITY:  Atlanta
CC        STATE:  Georgia
CC        COUNTRY:  USA
CC        ZIP:  30309-4530
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/273,411
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Pabst, Patrea L.
CC        REGISTRATION NUMBER:  31,284
CC        REFERENCE/DOCKET NUMBER:  WU106
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (404) 815-6508
CC        TELEFAX:  (404) 815-6555
CC     INFORMATION FOR SEQ ID NO:  5:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2771 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  Genes & Dev.
CC        VOLUME:  2
CC        PAGES:  1318-1332
CC        DATE:  1988
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 561 TO 629
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Seeburg, et al.
CC        JOURNAL:  DNA
CC        VOLUME:  1
CC        PAGES:  239-249
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CC        DATE:  1982
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 620 TO 2771
CC      PUBLICATION INFORMATION:
CC        AUTHORS:  Sweetser, et al.
CC        JOURNAL:  J. Biol. Chem.
CC        VOLUME:  261
CC        PAGES:  5553-5561
CC        DATE:  1986
CC        RELEVANT RESIDUES IN SEQ ID NO:  5: FROM 1 TO 617
SQ   Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;

  Query Match           25.1%;  Score 302;  DB 7;  Length 2771;
  Best Local Similarity  97.6%;  Pred. No. 8.84e-213;
  Matches   330;  Conservative    0;  Mismatches   4;  Indels   4;  Gaps   2;

Db    680 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      7 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Db    740 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTGAATG--AG 797
          |||||||||||||||||||||||||||||| |||||||||||||||||||  ||
Qy     67 TAGCGACCTGTAGATGGGACGGGGGCACTAACCCTGAGGTTTGGGGCTTCTGAATGTGAG 126

Db    798 TATCGCCATGTAAGCCCAGTAT--GGCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 855
          |||||||||||||||||||||  |||||| ||||||||||||||||||||||||||||
Qy    127 TATCGCCATGTAAGCCCAGTATTTGGCCAATGTCAGAAAGCTCCTGGTCCCTGGAGGGAT 186

Db    856 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 915
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    187 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 246

Db    916 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 975
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    247 TCCCTCTGTTGCCCTGTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306

Db    976 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1013
          |||||||||||||||||||||||||||||||||||||
Qy    307 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 344


RESULT   10
ID   US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 49, Application US/08050319B.
XX
CC   Sequence 49, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC    INFORMATION FOR SEQ ID NO:  49:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  474 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..471
SQ   Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;

  Query Match           25.0%;  Score 300;  DB 7;  Length 474;
  Best Local Similarity  97.5%;  Pred. No. 3.47e-211;
  Matches   308;  Conservative    0;  Mismatches   8;  Indels   0;  Gaps   0;

Db    105 GGACAGGGAGAAGAGAGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 164
          ||| | |||    || ||||||||||||||| ||||||||||||||||||||||||||
Qy    455 GGATACGGACTGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAG 514

Db    165 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 224
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    515 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 574

Db    225 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG 284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    575 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG 634

Db    285 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    635 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 694

Db    345 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    695 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 754

Db    405 CGAGTGTGTCTCCTGT 420
          ||||||||||||||||
Qy    755 CGAGTGTGTCTCCTGT 770


RESULT   11
ID   US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08343401A.
XX
CC   Sequence 3, Application US/08343401A
CC   Patent No. 5661132
CC    GENERAL INFORMATION:
CC      APPLICANT:  Swain, William F
CC      APPLICANT:  Macklin, Michael D
CC      APPLICANT:  Eriksson, Elof
CC      APPLICANT:  Andree, Christophe
CC      TITLE OF INVENTION:  Improved Wound Healing
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  PO Box 2113
CC        CITY:  Madison
CC        STATE:  WI
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CC         COUNTRY:  USA
CC         ZIP:  53701-2113
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/343,401A
CC         FILING DATE:  22-NOV-1994
CC         CLASSIFICATION:  514
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Seay, Nicholas J
CC         REGISTRATION NUMBER:  27,386
CC         REFERENCE/DOCKET NUMBER:  11-229-9103-9
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  608-251-5000
CC         TELEFAX:  608-251-9166
CC     INFORMATION FOR SEQ ID NO:  3:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  4283 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  double
CC         TOPOLOGY:  circular
CC       MOLECULE TYPE:  DNA (genomic)
CC       IMMEDIATE SOURCE:
CC         CLONE:  pWRG1630
CC       FEATURE:
CC         NAME/KEY:  exon
CC         LOCATION:  713..721
CC       FEATURE:
CC         NAME/KEY:  exon
CC         LOCATION:  981..1253
CC       FEATURE:
CC         NAME/KEY:  CDS
CC         LOCATION:  join(713..721, 981..1253)
CC       FEATURE:
CC         NAME/KEY:  sig_peptide
CC         LOCATION:  713..1049
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           25.0%;  Score 301;  DB 7;  Length 4283;
  Best Local Similarity  95.3%;  Pred. No. 5.54e-212;
  Matches   322;  Conservative    0;  Mismatches  15;  Indels   1;  Gaps   1;

Db    713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy      7 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Db    772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          |||||||||||||||||||||||||||||||||| ||| || ||| ||||||||||||||
Qy     67 TAGCGACCTGTAGATGGGACGGGGGCACTAACCCTGAGGTTTGGGGCTTCTGAATGTGAG 126

Db    832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
          |||||||| |||||||||||||||||| |||||||||||||||  ||  |  ||||
Qy    127 TATCGCCATGTAAGCCCAGTATTTGGCCAATGTCAGAAAGCTCCTGGTCCCTGGAGGGAT 186

Db    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    187 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 246

Db    952 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    247 TCCCTCTGTTGCCCTGTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306

Db   1012 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
          |||||||||||||||||||||||||||||||||||||
Qy    307 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 344


RESULT   12
ID   US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08445265A.
XX
CC   Sequence 1, Application US/08445265A
CC   Patent No. 5697901
CC    GENERAL INFORMATION:
CC      APPLICANT:  Eriksson, Elof
CC      TITLE OF INVENTION:  GENE DELIVERY BY MICRONEEDLE INJECTION
CC      NUMBER OF SEQUENCES:  4
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Quarles & Brady
CC        STREET:  1 South Pinckney Street
CC        CITY:  Madison
CC        STATE:  WI
CC        COUNTRY:  US
CC        ZIP:  53703
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/445,265A
CC        FILING DATE:
CC        CLASSIFICATION:  604
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Seay, Nicholas J
CC        REGISTRATION NUMBER:  27386
CC        REFERENCE/DOCKET NUMBER:  110229.91080
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  608-251-5000
CC        TELEFAX:  608-251-9166
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  4283 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  circular
CC      MOLECULE TYPE:  other nucleic acid
CC        DESCRIPTION:  /desc = "Plasmid DNA"
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  join(713..721, 981..1250)
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

  Query Match           25.0%;  Score 301;  DB 7;  Length 4283;
  Best Local Similarity  95.3%;  Pred. No. 5.54e-212;
  Matches   322;  Conservative    0;  Mismatches  15;  Indels   1;  Gaps   1;

Db    713 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy      7 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Db    772 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          |||||||||||||||||||||||||||||||||| ||| || ||| ||||||||||||||
Qy     67 TAGCGACCTGTAGATGGGACGGGGGCACTAACCCTGAGGTTTGGGGCTTCTGAATGTGAG 126

Db    832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGCTCCCTGGAGGAT 891
          |||||||| |||||||||||||||||| |||||||||||||||  ||  |  ||||
Qy    127 TATCGCCATGTAAGCCCAGTATTTGGCCAATGTCAGAAAGCTCCTGGTCCCTGGAGGGAT 186

Db    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    187 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 246

Db    952 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    247 TCCCTCTGTTGCCCTGTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306
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Db   1012 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 1049
          |||||||||||||||||||||||||||||||||||||
Qy    307 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 344


RESULT   13
ID   US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 53, Application US/08050319B.
XX
CC   Sequence 53, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  53:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  477 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..474
SQ   Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

  Query Match           21.2%;  Score 255;  DB 7;  Length 477;
  Best Local Similarity  98.9%;  Pred. No. 2.07e-175;
  Matches   258;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTACCTGC 381
          |||||||||||||||  ||||
Qy    585 CGGGACACCGTGTGTGGCTGC 605


RESULT   14
ID   US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 51, Application US/08050319B.
XX
CC   Sequence 51, Application US/08050319B
CC   Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT:  M.Feldmann, P.W. Gray,
CC      APPLICANT:  M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Reed & Robbins
CC        STREET:  635 Bryant Street
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/050,319B
CC        FILING DATE:  10-May-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Robbins, Roberta L.
CC        REGISTRATION NUMBER:  33,208
CC        REFERENCE/DOCKET NUMBER:  5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 617-8999
CC        TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  51:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  462 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..459
SQ   Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

  Query Match           14.1%;  Score 169;  DB 7;  Length 462;
  Best Local Similarity 100.0%;  Pred. No. 1.03e-107;
  Matches   169;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    240 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
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Qy    602 CTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 661

Db    300 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 359
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Qy    662 CAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 721

Db    360 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGT 408
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Qy    722 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGT 770


RESULT   15
ID   US-08-086-915-2 STANDARD; DNA; UNC; 138 BP.

XX
AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 2, Application US/08086915.
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CC   Sequence 2, Application US/08086915
CC   Patent No. 5444167
CC    GENERAL INFORMATION:
CC      APPLICANT:  Pettersson, Kim SI
CC      TITLE OF INVENTION:  Variant Luteinizing Hormone Encoding DNA
CC      NUMBER OF SEQUENCES:  17
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Adduci, Mastriani, Schaumberg & Schill
CC        STREET:  1140 Connecticut Avenue, N.W., Suite 250
CC        CITY:  Washington
CC        STATE:  D.C.
CC        COUNTRY:  U.S.A.
CC        ZIP:  20036
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/086,915
CC        FILING DATE:  07-JUL-1993
CC        CLASSIFICATION:  536
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Kubovcik, Ronald J.
CC        REGISTRATION NUMBER:  25,401
CC        REFERENCE/DOCKET NUMBER:  15873005
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  202-467-6300
CC        TELEFAX:  202-466-2006
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  138 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  double
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      ORIGINAL SOURCE:
CC        ORGANISM:  Homo sapiens
CC        DEVELOPMENTAL STAGE:  Adult
SQ   Sequence 138 BP; 24 A; 51 C; 42 G; 21 T; 0 other;

  Query Match             8.6%;  Score 103;  DB 5;  Length 138;
  Best Local Similarity  99.0%;  Pred. No. 5.77e-57;
  Matches   104;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     34 CCACGGTGCCACCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 93
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Db     94 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATG 138
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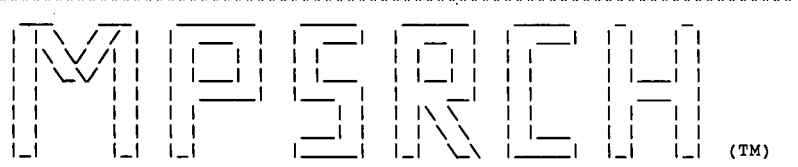

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:20:06 1998; MasPar time 1075.89 Seconds
1491.095 Million cell updates/sec

Tabular output not generated.

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Description: (1-1049) from US08804166.seq
Perfect Score: 1049
N.A. Sequence: 1 TCCACATGGCTACAGGTAAG.....TTATTATCACAAATCTTAAG 1049
Comp: AGGTGTACCGATGTCCATTC.....AATAATAGTGTTTAGAATTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl53
1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
13:em_pat
Database: genbank105
14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
26:gb_htg 27:gb_prl 28:gb_pr2

Statistics: Mean 11.026; Variance 4.973; scale 2.217

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	424	40.4	483	25	A29099	Synthetic DNA for TNF-	0.00e+00
2	424	40.4	510	25	A21525	oligonucleotide probe.	0.00e+00
3	424	40.4	600	25	A20257	Synthetic nucleotide s	0.00e+00
4	424	40.4	1331	25	A29103	H.sapiens mRNA for TNF	0.00e+00
5	424	40.4	1368	25	A29098	Synthetic DNA for TNF-	0.00e+00
6	424	40.4	2050	27	HUMTNFRP	Human tumor necrosis f	0.00e+00
7	424	40.4	2062	25	I43805	Sequence 24 from paten	0.00e+00
8	424	40.4	2062	25	A21522	TNF alpha gene.	0.00e+00
9	424	40.4	2087	27	HUMTNFR	Human tumor necrosis f	0.00e+00
10	424	40.4	2111	27	HUMTNFRB	Homo sapiens tumor nec	0.00e+00
11	424	40.4	2111	25	A26412	cDNA for (55kD TNF-BP)	0.00e+00
12	424	40.4	2112	27	HUMTNFRC	Human tumor necrosis f	0.00e+00
13	424	40.4	2161	27	HSTNFR1A	H.sapiens TNF-R mRNA f	0.00e+00
14	424	40.4	2175	25	A43873	Sequence 1 from Patent	0.00e+00
15	424	40.4	2175	25	I64751	Sequence 1 from patent	0.00e+00
16	424	40.4	2176	25	A19907	Synthetic nucleotide s	0.00e+00
17	424	40.4	6889	25	I26928	Sequence 2 from patent	0.00e+00
18	420	40.0	600	25	I43808	Sequence 47 from paten	0.00e+00
19	417	39.8	2061	25	A20255	55kD receptor gene for	0.00e+00
20	381	36.3	504	25	A20713	Synthetic nucleotide s	0.00e+00
21	381	36.3	504	25	I43813	Sequence 56 from paten	0.00e+00
22	379	36.1	501	25	I43786	Sequence 1 from patent	0.00e+00
23	372	35.5	500	25	A20254	Synthetic nucleotide 5	0.00e+00
24	370	35.3	372	25	I43787	Sequence 3 from patent	0.00e+00
25	370	35.3	372	25	A20253	Synthetic nucleotide 5	0.00e+00
26	326	31.1	66495	27	HUMGHCSA	Human growth hormone (	1.10e-264
27	304	29.0	581	15	FCU72344	Felis catus tumour nec	3.28e-244
28	302	28.8	474	25	A20259	Synthetic nucleotide s	2.37e-242
29	302	28.8	474	25	I43809	Sequence 49 from paten	2.37e-242
30	300	28.6	1826	25	I02855	Sequence 1 from Patent	1.71e-240
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33	300	28.6	2771	25	I41411	Sequence 5 from patent	1.71e-240
34	298	28.4	2657	27	HUMGHN	Human growth hormone g	1.23e-238
35	298	28.4	4283	25	I63120	Sequence 3 from patent	1.23e-238
36	297	28.3	2004	15	SSU19994	Sus scrofa p55 TNF rec	1.05e-237
37	258	24.6	621	27	HSGONA	Human messenger RNA fo	1.39e-201
38	255	24.3	477	25	I43811	Sequence 53 from paten	8.20e-199
39	255	24.3	477	25	A20263	Synthetic nucleotide s	8.20e-199
40	250	23.8	2740	27	HUMCS3	Human chorionic somato	3.37e-194
41	248	23.6	2301	27	HUMCS1	Human chorionic somato	2.35e-192
42	245	23.4	1841	25	I02856	Sequence 2 from Patent	1.37e-189
43	245	23.4	2967	27	HUMPLA	Human placental lactog	1.37e-189
44	240	22.9	2440	15	BTU90937	Bos taurus tumor necro	5.52e-185
45	239	22.8	2734	27	HUMCS5	Human chorionic somato	4.60e-184

ALIGNMENTS

RESULT 1
LOCUS A29099 483 bp DNA PAT 03-JUL-1995

DEFINITION Synthetic DNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION A29099
NID g1248893
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 483)
AUTHORS Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL Patent: EP 0393438-A 49 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES Location/Qualifiers
source 1..483
/organism="unidentified"
/db_xref="taxon:32644"
source 1..483
/organism="artificial sequence"
/db_xref="taxon:29278"
BASE COUNT 130 a 124 c 123 g 106 t
ORIGIN

Query Match 40.4%; Score 424; DB 25; Length 483;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    121 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 180
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    301 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 360
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    361 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 420
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    421 TCCTGT 426
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Qy    764 TCCTGT 769


RESULT    2
LOCUS       A21525        510 bp    DNA             PAT       26-JUL-1994

DEFINITION  oligonucleotide probe.
ACCESSION   A21525
NID         g583574
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   .
  JOURNAL   Patent: GB 2246569-A 4 05-FEB-1992;
FEATURES             Location/Qualifiers
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                     /organism="Artificial sequences"
BASE COUNT      136 a    132 c    133 g    109 t
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  Query Match           40.4%;  Score 424;  DB 25;  Length 510;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    214 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 273
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Db    274 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 333
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    334 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 393
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    394 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 453
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    454 TCCTGT 459
          ||||||
Qy    764 TCCTGT 769


RESULT    3
LOCUS       A20257        600 bp    DNA             PAT       20-SEP-1995

DEFINITION  Synthetic nucleotide sequence of plasmid p-TNFRecd.
ACCESSION   A20257
NID         g1247896
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   .
  TITLE     MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL   Patent: WO 9207076-A 25 30-APR-1992;
FEATURES             Location/Qualifiers
     source          1. .600
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     source          1. .600
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BASE COUNT      148 a    157 c    162 g    133 t
ORIGIN

  Query Match           40.4%;  Score 424;  DB 25;  Length 600;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    541 TCCTGT 546
          ||||||
Qy    764 TCCTGT 769


RESULT    4
LOCUS       A29103        1331 bp    DNA             PAT       03-JUL-1995

DEFINITION  H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29103
```

```
NID         g1247517
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1331)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 53 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1. .1331
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      298 a    407 c    343 g    283 t
ORIGIN

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  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    333 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 392
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    393 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 452
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    453 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 512
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    513 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 572
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    633 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 692
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    693 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 752
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    753 TCCTGT 758
          ||||||
Qy    764 TCCTGT 769


RESULT    5
LOCUS       A29098       1368 bp    DNA             PAT       03-JUL-1995

DEFINITION  Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION   A29098
NID         g1248892
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1368)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 48 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1. .1368
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BASE COUNT      293 a    424 c    375 g    276 t
ORIGIN

  Query Match           40.4%;  Score 424;  DB 25;  Length 1368;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    541 TCCTGT 546
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Qy    764 TCCTGT 769


RESULT    6
LOCUS       HUMTNFRP     2050 bp    mRNA            PRI       11-OCT-1991

DEFINITION  Human tumor necrosis factor receptor(TNF) mRNA, complete cds.
ACCESSION   M60275 M37764
NID         g339759
KEYWORDS    TNF receptor; transmembrane receptor; tumor necrosis factor
            receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2050)
  AUTHORS   Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.
  TITLE     Cloning of human tumor necrosis factor (TNF) receptor cDNA and
            expression of recombinant soluble TNF-binding protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
  MEDLINE   91017509
COMMENT     Draft entry and computer-readable sequence for [Proc. Natl. Acad.
            Sci. U.S.A. (1990) In press] kindly submitted
            by P.W.Gray, 13-AUG-1990.
FEATURES             Location/Qualifiers
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                     /tissue_type="placenta"
     sig_peptide     155. .274
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BASE COUNT      429 a    611 c    566 g    444 t
ORIGIN

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  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGT 700
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Qy    764 TCCTGT 769


RESULT    7
LOCUS       I43805       2062 bp    DNA             PAT       10-JUL-1997

DEFINITION  Sequence 24 from patent US 5633145.
ACCESSION   I43805
NID         g2468903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE     TNF.alpha. receptor-derived binding protein
  JOURNAL   Patent: US 5633145-A 24 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .2062
                     /organism="unknown"
BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

  Query Match           40.4%;  Score 424;  DB 25;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGT 700
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Qy    764 TCCTGT 769


RESULT    8
LOCUS       A21522       2062 bp    RNA             PAT       26-JUL-1994

DEFINITION  TNF alpha gene.
ACCESSION   A21522
NID         g579599
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   .
  JOURNAL   Patent: GB 2246569-A 1 05-FEB-1992;
FEATURES             Location/Qualifiers
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                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
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BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

  Query Match           40.4%;  Score 424;  DB 25;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGT 700
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Qy    764 TCCTGT 769


RESULT    9
LOCUS       HUMTNFR      2087 bp    mRNA            PRI       10-NOV-1993

DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61, 361-370 (1990)
  MEDLINE   90235285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
FEATURES             Location/Qualifiers
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
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BASE COUNT      433 a    624 c    581 g    449 t
ORIGIN

  Query Match           40.4%;  Score 424;  DB 27;  Length 2087;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    302 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 361
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    362 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 421
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    422 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 481
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    482 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 541
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    542 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 601
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    662 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 721
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    722 TCCTGT 727
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Qy    764 TCCTGT 769


RESULT   10
LOCUS       HUMTNFRB     2111 bp    mRNA            PRI       14-NOV-1990

DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID         g339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cell line HL60, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
  TITLE     Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
  JOURNAL   Cell 61, 351-359 (1990)
  MEDLINE   90235284
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
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BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           40.4%;  Score 424;  DB 27;  Length 2111;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
        ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 546
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    547 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 606
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 726
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    727 TCCTGT 732
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Qy    764 TCCTGT 769


RESULT   11
LOCUS       A26412       2111 bp    DNA             PAT       26-APR-1995

DEFINITION  cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
            patent EP0417563.
ACCESSION   A26412
NID         g904968
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 24 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .2111
                     /organism="Artificial sequences"
     CDS             187. .1554
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BASE COUNT      445 a    629 c    587 g    450 t
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  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

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Qy    764 TCCTGT 769


RESULT   12
LOCUS       HUMTNFRC     2112 bp    mRNA            PRI       30-SEP-1991

DEFINITION  Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
            cds.
ACCESSION   M63121 M75861
NID         g339755
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2112)
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  AUTHORS   Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
            Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C. and
            Adolf,G.R.
  TITLE     Molecular cloning and expression of human and rat tumor necrosis
            factor receptor chain (p60) and its soluble derivative, tumor
            necrosis factor-binding protein
  JOURNAL   DNA Cell Biol. 9, 705-715 (1990)
  MEDLINE   91090841
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  Query Match           40.4%;  Score 424;  DB 27;  Length 2112;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     327 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 386
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Qy     344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db     387 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 446
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Qy     404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db     447 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 506
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DEFINITION  H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION   X55313
NID         g37223
KEYWORDS    TNF-R gene; tumor necrosis factor receptor 1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2161)
  AUTHORS   Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
            Aderka,D., Holtmann,H. and Wallach,D.
  TITLE     Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
            for the type I TNF-R, cloned using amino acid sequence data of its
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            the receptor
  JOURNAL   EMBO J. 9 (10), 3269-3278 (1990)
  MEDLINE   91006021
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  Query Match           40.4%;  Score 424;  DB 27;  Length 2161;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Db     496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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DEFINITION  Sequence 1 from Patent EP0657536.
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KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Proteases capable of shedding the soluble TNF-receptor and TNF-R
            derived peptides and antibodies against the proteases inhibiting
            the shedding
  JOURNAL   Patent: EP 0657536-A 1 14-JUN-1995;
            YEDA RES & DEV (IL)
COMMENT     Other publication ZA 9407962 951121
            Other publication JP 7194376 950801
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  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 TCCTGT 801
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Qy    764 TCCTGT 769


RESULT   15
LOCUS       I64751       2175 bp    DNA             PAT       26-SEP-1997

DEFINITION  Sequence 1 from patent US 5665859.
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NID         g2481645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Molecules influencing the shedding of the TNF receptor, their
            preparation and their use
  JOURNAL   Patent: US 5665859-A 1 09-SEP-1997;
FEATURES             Location/Qualifiers
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  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

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Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 TCCTGT 801
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Qy    764 TCCTGT 769


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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:55:12 1998; MasPar time 137.48 Seconds
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Searched: 159651 seqs, 57698962 bases x 2

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Listing first 45 summaries

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19:part19 20:part20 21:part21 22:part22 23:part23
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Statistics: Mean 9.090; Variance 5.026; scale 1.809

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	424	40.4	1368	8	Q49932	Lambda-derived TNF-R	2.42e-296
4	424	40.4	2062	4	Q24440	Encodes TNF-alpha 55k	2.42e-296
5	424	40.4	2062	3	Q20973	TNF-alpha binding pro	2.42e-296
6	424	40.4	2088	2	Q10883	30kD TNF inhibitor pr	2.42e-296
7	424	40.4	2111	2	Q10955	Encodes human 55kD TN	2.42e-296
8	424	40.4	2141	1	Q06285	Human Tumour Necrosis	2.42e-296
9	424	40.4	2175	15	Q90513	p55 TNF-R gene.	2.42e-296
10	424	40.4	6889	18	T15931	DHFR/intron (WTrasSD)	2.42e-296
11	422	40.2	2170	9	Q50870	p55 Tumour necrosis f	8.37e-295
12	422	40.2	2176	2	Q12215	Type I TNF receptor.	8.37e-295
13	381	36.3	504	4	Q24445	Encodes truncated TNF	2.76e-263
14	302	28.8	474	4	Q24442	Encodes truncated TNF	8.62e-203
15	300	28.6	2771	31	T76770	Rat Fabpl gut-specifi	2.90e-201
16	298	28.4	2160	33	T62826	Human growth hormone	9.73e-200
17	291	27.7	336	6	Q41459	Human growth hormone	2.12e-194
18	259	24.7	707	17	T03236	Single chain gonadotr	4.80e-170
19	259	24.7	719	17	T03235	Single chain gonadotr	4.80e-170
20	259	24.7	728	17	T03224	Single chain gonadotr	4.80e-170
21	259	24.7	743	17	T03219	Single chain gonadotr	4.80e-170
22	259	24.7	743	17	T03233	Single chain gonadotr	4.80e-170
23	259	24.7	743	17	T03231	Single chain gonadotr	4.80e-170
24	259	24.7	744	17	T03221	Single chain gonadotr	4.80e-170
25	259	24.7	752	17	T03227	Single chain gonadotr	4.80e-170
26	259	24.7	752	17	T03229	Single chain gonadotr	4.80e-170
27	259	24.7	836	17	T03212	Single chain gonadotr	4.80e-170
28	258	24.6	592	2	Q10075	Engineered human alph	2.76e-169
29	258	24.6	592	24	T41695	Dimeric glycoprotein	2.76e-169
30	255	24.3	477	4	Q24444	Encodes truncated TNF	5.24e-167
31	251	23.9	312	17	T03237	Gonadotropin alpha su	5.69e-164
32	251	23.9	836	17	T03243	Single chain gonadotr	5.69e-164
33	230	21.9	2173	1	Q06284	Rat Tumour Necrosis F	4.62e-148
34	206	19.6	2660	4	N30032	Sequence of gene for	6.00e-130
35	176	16.8	608	1	Q03846	Porcine alpha subunit	1.95e-107
36	169	16.1	462	4	Q24443	Encodes truncated TNF	3.28e-102
37	166	15.8	716	2	Q10059	Ovine FSH alpha subun	5.66e-100
38	164	15.6	731	1	Q03843	Bovine alpha subunit	1.75e-98
39	150	14.3	480	1	Q03849	Equine alpha subunit	4.39e-88
40	146	13.9	482	1	Q03820	Gene encoding equine	4.02e-85
41	132	12.6	1027	2	Q10878	Partial sequence of c	8.45e-75
42	103	9.8	345	11	Q65374	Fish gonadotropic hor	1.12e-53
43	101	9.6	340	2	N91174	Sequence encoding fis	3.09e-52
44	80	7.6	360	11	Q65373	Fish gonadotropic hor	2.70e-37
45	79	7.5	267	3	N50521	Sequence encoding sal	1.36e-36

ALIGNMENTS

RESULT 1
ID Q24441 standard; DNA; 608 BP.
AC Q24441;
DT 05-NOV-1992 (first entry)
DE Encodes truncated TNF-alpha 55kD receptor (197 amino acids).
KW tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningits; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
PN WO9207076-A.
PD 30-APR-1992.
PF 18-OCT-1991; G01826.
PR 18-OCT-1990; GB-022648.
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR WPI; 92-167156/20.
DR P-PSDB; R24080.
PT New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
PS Example; Fig 7; 43pp; English.
CC This sequence encodes the designed TNF-alpha 55kD receptor
CC derivative, as present in pTNFRecd. This was produced as described in
CC Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC the cytoplasmic domain. The derivative could be used in the
CC regulation of TNF-alpha mediated responses by binding and
CC sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC diseases, septic shock, HIV infection, malaria, viral meningitis,
CC graft versus host disease and autoimmune diseases, esp. rheumatoid
CC arthritis.
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ Sequence 608 BP; 148 A; 159 C; 165 G; 136 T;

Query Match 40.4%; Score 424; DB 4; Length 608;
Best Local Similarity 99.8%; Pred. No. 2.42e-296;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 129 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 188

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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    189 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    249 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    309 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    369 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 428
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    429 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    489 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    549 tcctgt 554
          ||||||
Qy    764 TCCTGT 769


RESULT    2
ID   Q06282 standard; DNA; 1334 BP.
AC   Q06282;
DT   29-JAN-1991  (first entry)
DE   Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             213..1325
FT   /*tag=  a
FT   /product=TNF-BP
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   P-PSDB; R07449.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   pTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC   from induced TNF-induced fibrosarcoma cells.  A TNF-BP had been
CC   isolated from the urine of patients with uraemia and probes/primers
CC   were constructed from the determined amino acid sequence.
CC   To produce a vector expressing a soluble form of TNF-binding
CC   protein, this plasmid was cut with XmmI, amplified by PCR and the
CC   amplified DNA cut with BamHI and EcoRI.
CC   The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC   (BRL) cut with the same enzymes to recover pTNF-BP.  This was cut
CC   with BamHI and EcoRI, and the recovered fragment inserted into
CC   pAD-CMV1 (Q06283) to give the required plasmid pADTNF-BP.
CC   See also Q06282-Q06285.
SQ   Sequence   1334 BP;    299 A;    409 C;    342 G;    284 T;

  Query Match           40.4%;  Score 424;  DB 1;  Length 1334;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 392
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    753 tcctgt 758
          ||||||
Qy    764 TCCTGT 769


RESULT    3
ID   Q49932 standard; cDNA to mRNA; 1368 BP.
AC   Q49932;
DT   29-APR-1994  (first entry)
DE   Lambda-derived TNF-R cDNA.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction; ss.
OS   Homo sapiens.
OS   Lambda-gt10-7-ctnfbp.
FH   Key             Location/Qualifiers
FT   CDS             1..1366
FT   /*tag=  a
FT   /product= hTNF-R
FT   sig_peptide     1..120
FT   /*tag=  b
FT   mat_peptide     121..1363
FT   /*tag=  c
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   P-PSDB; R42059.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.
CC   The sequences given in Q49931-32 encode human tumour necrosis factor
CC   receptor (TNF-R) and the sequences in Q49933-34 encode human
CC   interleukin-1 receptor (IL-1R).  These sequences were used in the
CC   production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
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CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence   1368 BP;    292 A;    424 C;    376 G;    276 T;

  Query Match           40.4%;  Score 424;  DB 8;  Length 1368;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 180
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 420
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    481 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    541 tcctgt 546
          ||||||
Qy    764 TCCTGT 769


RESULT    4
ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-NOV-1992  (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             156..1517
FT   /*tag=  a
FT   /product= human TNF-alpha
FT   mat_peptide     1265..1267
FT   /*tag=  b
FT   /note= "3"
FT   mat_peptide     1265..1267
FT   /*tag=  c
FT   /codon= seq:"TGG", aa:Thr
FT   mat_peptide     1258..1260
FT   /*tag=  d
FT   /codon= Seq"AAG", aa:Leu
FT   mat_peptide     1433..1435
FT   /*tag=  e
FT   /codon= Seq:"GAC", aa:Asn
FT   sig_peptide     156..274
FT   /*tag=  f
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24000
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Claim 4; Fig 1; 43pp; English.
CC   This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC   library in gt10 was screened with probe Q29236. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in prTNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain. PCR with primers Q29237,8 generated a 300bp
CC   restriction fragment which was cloned into prTNFR, giving pTNFRecd.
CC   DNA sequencing confirmed this contained the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   2062 BP;    429 A;    618 C;    572 G;    443 T;

  Query Match           40.4%;  Score 424;  DB 4;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 tcctgt 700
          ||||||
Qy    764 TCCTGT 769
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RESULT    5
ID   Q20973 standard; DNA; 2062 BP.
AC   Q20973;
DT   11-MAY-1992  (first entry)
DE   TNF-alpha binding protein gene.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             155..1522
FT   /*tag=  a
FT   sig_peptide     155..274
FT   /*tag=  b
FT   mat_peptide     275..1522
FT   /*tag=  c
FT   misc_feature    473..532
FT   /*tag=  d
FT   /note= "homologous to probe Q20974"
FT   misc_feature    242..751
FT   /*tag=  e
FT   /note= "encodes the extracellular domain of human
FT   TNF alpha receptor"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding tumour necrosis factor alpha
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence   2062 BP;    429 A;    616 C;    573 G;    444 T;

  Query Match           40.4%;  Score 424;  DB 3;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 tcctgt 700
          ||||||
Qy    764 TCCTGT 769


RESULT    6
ID   Q10883 standard; cDNA; 2088 BP.
AC   Q10883;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
KW   Tumour necrosis factor; inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             171..1536
FT   /*tag=  a
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   P-PSDB; R10986.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also Q10878, Q10884 and Q10907.
SQ   Sequence   2088 BP;    439 A;    626 C;    578 G;    445 T;

  Query Match           40.4%;  Score 424;  DB 2;  Length 2088;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    289 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 348
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    349 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    409 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    469 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    529 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    589 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    649 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    709 tcctgt 714
          ||||||
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Qy    764 TCCTGT 769


RESULT    7
ID   Q10955 standard; cDNA; 2111 BP.
AC   Q10955;
DT   24-MAY-1991  (first entry)
DE   Encodes human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   sig_peptide     187..273
FT   /*tag= a
FT   mat_peptide     274..1551
FT   /*tag= b
FT   /product= 55kD TNF-BP
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   P-PSDB; R11082.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 4; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   2111 BP;    445 A;    628 C;    588 G;    450 T;

  Query Match           40.4%;  Score 424;  DB 2;  Length 2111;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    307 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    367 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    427 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    487 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    547 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    607 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    667 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    727 tcctgt 732
          ||||||
Qy    764 TCCTGT 769


RESULT    8
ID   Q06285 standard; DNA; 2141 BP.
AC   Q06285;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   lambdaTNF-R2; raTNF-R8; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             213..1577
FT   /*tag= a
FT   /label=huTNF-R
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   P-PSDB; R07451.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).
CC   See also Q06282-Q06285.
SQ   Sequence   2141 BP;    455 A;    633 C;    593 G;    460 T;

  Query Match           40.4%;  Score 424;  DB 1;  Length 2141;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    753 tcctgt 758
          ||||||
Qy    764 TCCTGT 769
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RESULT    9
ID   Q90513 standard; DNA; 2175 BP.
AC   Q90513;
DT   19-JAN-1996  (first entry)
DE   p55 TNF-R gene.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT   /*tag= a
FT   /product= p55 TNF-R
FT   misc_signal     2143..2149
FT   /*tag= b
FT   /note= "possible poly-A signal"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
DR   WPI; 95-194342/26.
DR   P-PSDB; R75084.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor  - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment.  The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type.  The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain.  This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain.  The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11.  This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.  The
CC   mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3.  These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence   2175 BP;    474 A;    642 C;    603 G;    456 T;

  Query Match           40.4%;  Score 424;  DB 15;  Length 2175;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 tcctgt 801
          ||||||
Qy    764 TCCTGT 769


RESULT   10
ID   T15931 standard; DNA; 6889 BP.
AC   T15931;
DT   20-JUN-1996  (first entry)
DE   DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.
KW   Recombinant host cell; dihydrofolate reductase; selectable marker;
KW   DHFR; ras splice donor; dicistronic vector; gene expression;
KW   immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
OS   Synthetic.
PN   WO9604391-A1.
PD   15-FEB-1996.
PF   28-JUL-1995; U09576.
PR   05-AUG-1994; US-286740.
PA   (GETH ) GENENTECH INC.
PI   Crowley CW;
DR   WPI; 96-129407/13.
PT   Improved process for the selection of recombinant host cells
PT   expressing high level of a desired product - uses eukaryotic host
PT   cells contg. a DNA construct comprising a selectable gene
PS   Example 2; Page 36-42; 137pp; English.
CC   A dicistronic vector (T15930) comprises a regulatory region
CC   derived from the cytomegalovirus immediate-early gene, a
CC   selectable dihydrofolate reductase gene positioned within an
CC   intron having a 5' wild-type ras splice donor site, a downstream
CC   sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
CC   tumour necrosis factor, and a poly-A sequence.  Transfection of CHO
CC   DHFR- cells and subsequent methotrexate amplification and growth of
CC   the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC   ug/ml (15-fold higher compared to conventional vector amplified
CC   pools).
SQ   Sequence   6889 BP;    1729 A;    1826 C;    1681 G;    1653 T;

  Query Match           40.4%;  Score 424;  DB 18;  Length 6889;
  Best Local Similarity  99.8%;  Pred. No. 2.42e-296;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1725 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 1784
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db   1785 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 1844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db   1845 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 1904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db   1905 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   1965 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db   2025 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 2084
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db   2085 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 2144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db   2145 tcctgt 2150
          ||||||
Qy    764 TCCTGT 769


RESULT   11
ID   Q50870 standard; DNA; 2170 BP.
AC   Q50870;
DT   13-MAY-1994  (first entry)
DE   p55 Tumour necrosis factor receptor coding sequence.
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT   /*tag= a
FT   /product= p55 Tumour necrosis factor receptor.
PN   EP-568925-A.
PD   10-NOV-1993.
PF   29-APR-1993; 106981.
PR   03-MAY-1992; IL-101769.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Brakebusch C,  Wallach D;
DR   WPI; 93-353057/45.
DR   P-PSDB; R42197.
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
PS   Claim 2; Figure 1; 17pp; English.
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor.  This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock.  They can also
CC   be used to treat overdoses of exogenous TNF.
SQ   Sequence   2170 BP;    474 A;    657 C;    584 G;    455 T;

  Query Match           40.2%;  Score 422;  DB 9;  Length 2170;
  Best Local Similarity  99.5%;  Pred. No. 8.37e-295;
  Matches   424;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgcgaccgtgcacctctcctgccaggag 735
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 tcctgt 801
          ||||||
Qy    764 TCCTGT 769


RESULT   12
ID   Q12215 standard; DNA; 2176 BP.
AC   Q12215;
DT   12-SEP-1991  (first entry)
DE   Type I TNF receptor.
KW   Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   terminator      244..246
FT   /*tag= a
FT   /note= "in-frame termination codon"
FT   CDS             256..1620
FT   /*tag= a
FT   /product= type I TNF receptor
FT   sig_peptide     256..318
FT   /*tag= b
FT   mat_peptide     319..1620
FT   /*tag= c
FT   misc_RNA        319..864
FT   /*tag= d
FT   /label= soluble_domain
FT   /note= "may be 2 codons shorter or a few codons
FT   longer"
FT   misc_feature    376..414
FT   /*tag= e
FT   /note= "TBP-I derived sequence"
FT   misc_feature    583..627
FT   /*tag= f
FT   /note= "TBP-I derived sequence"
FT   misc_feature    850..858
FT   /*tag= g
FT   /note= "TBP-I derived sequence"
FT   misc_RNA        889..957
FT   /*tag= h
FT   /label= transmembrane_domain
FT   repeat_unit     385..504
FT   /*tag= i
FT   /number= 1
FT   repeat_unit     505..633
FT   /*tag= j
FT   /number= 2
FT   repeat_unit     634..756
FT   /*tag= k
FT   /number= 3
FT   repeat_unit     757..858
FT   /*tag= l
FT   /number= 4
FT   polyA_signal    2145..2150
FT   /*tag= m
PN   EP-433900-A.
PD   26-JUN-1991.
PF   13-DEC-1990; 124133.
PR   13-DEC-1989; IL-092697.
PR   12-JUL-1990; IL-095064.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI   Aderka D;
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```
DR   WPI; 91-186774/26.
DR   P-PSDB; R12550.
PT   Recombinant tumour necrosis factor binding protein I - prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PT   acid encoding human type T TNF receptor or soluble domain
PS   Disclosure; Fig 1(D); 30pp; English.
CC   The Tumour Necrosis Factor Binding Protein I is the soluble form of
CC   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA.  The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also Q12212-15.
SQ   Sequence   2176 BP;    475 A;    644 C;    602 G;    455 T;

  Query Match           40.2%;  Score 422;  DB 2;  Length 2176;
  Best Local Similarity  99.5%;  Pred. No. 8.37e-295;
  Matches   424;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgcagtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 tcctgt 801
          ||||||
Qy    764 TCCTGT 769


RESULT   13
ID   Q24445 standard; DNA; 504 BP.
AC   Q24445;
DT   05-NOV-1992  (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (165 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24084.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 11; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
CC   derivative, as present in pdeltaIV. This construct was generated by
CC   cloning of the BglII/HindIII digested product of a PCR using
CC   primers 5A and 4D into BglII/HindIII 5'-deltaCla. This introduced
CC   a termination codon after amino acid 167, to yield pdeltaIV.
CC   This derivative lacks the membrane proximal 4th subdomain, yet
CC   retains the ability to bind TNF-alpha with high affinity
CC   (10power8 - 10power9 Mpower-1) The deriv. can be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis. The deriv. is given at 10-100ug/dose.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   504 BP;    122 A;    137 C;    138 G;    107 T;

  Query Match           36.3%;  Score 381;  DB 4;  Length 504;
  Best Local Similarity  99.7%;  Pred. No. 2.76e-263;
  Matches   382;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db    181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db    241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db    481 aaacagaacaccgtgtgcacctg 503
          |||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTG 726


RESULT   14
ID   Q24442 standard; DNA; 474 BP.
AC   Q24442;
DT   05-NOV-1992  (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (155 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24081.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 8; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
```

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CC   derivative, as present in pdeltaI. This construct was generated by
CC   joining PCR fragments by means of overlaps introduced into the
CC   primers used for PCR. Gel purified products of PCR's using
CC   5'Cla, IA, IB, and 5D primers were mixed and subjected to further
CC   amplification using 5'Cla and 5D as primers. The resulting fragment
CC   was digested with ClaI and BglII and cloned into ClaI/BglII
CC   digested pTNFRecd, to yield pdeltaI, containing the sequence given.
CC   This derivative could be used to regulate TNF-alpha mediated responses
CC   by binding and sequestering human TNF-alpha e.g. in the treatment of
CC   pulmonary diseases, septic shock, HIV infection, malaria, viral
CC   meningitis, graft versus host disease and autoimmune diseases, esp.
CC   rheumatoid arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   474 BP;    110 A;    126 C;    132 G;    106 T;

  Query Match           28.8%;  Score 302;  DB 4;  Length 474;
  Best Local Similarity  97.8%;  Pred. No. 8.62e-203;
  Matches   309;  Conservative    0;  Mismatches   7;  Indels   0;  Gaps   0;

Db    105 ggacagggagaagagagagtgtgagagcggctccttcaccgcttcagaaaaccacctcag 164
          ||| | |||    || ||||||||||||||||||||||||||||||||||||||||||||
Qy    454 GGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAG 513

Db    165 acactgcctcagctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttg 224
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    514 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 573

Db    225 cacagtggaccgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggag 284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    574 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAG 633

Db    285 tgaaaacctttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctc 344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    634 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTC 693

Db    345 ctgccaggagaaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaa 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    694 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 753

Db    405 cgagtgtgtctcctgt 420
          ||||||||||||||||
Qy    754 CGAGTGTGTCTCCTGT 769


RESULT   15
ID   T76770 standard; cDNA; 2771 BP.
AC   T76770;
DT   15-SEP-1997  (first entry)
DE   Rat Fabpl gut-specific promoter and human growth hormone exon 1.
KW   Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
KW   GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase;
KW   alpha 1,2 FT; alpha 1,3/4 FT; tissue-specific promoter;
KW   rat liver fatty acid binding protein; transgene; transgenic mouse;
KW   animal model; intestinal adhesion; Helicobacter pylori infection;
KW   stomach; small intestine; gut; epithelial cell; surface receptor;
KW   carbohydrate antigen; gastritis; peptic ulcer; neoplasia;
KW   gastric adenocarcinoma; Lewis antigen; fucosylation; ds.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Rattus sp.
FH   Key             Location/Qualifiers
FT   promoter        1..617
FT   /*tag= a
FT   /note= "Corresponds to nucleotides -596 to +21 of
FT   the rat liver fatty acid binding protein
FT   gene"
FT   exon            620..2771
FT   /*tag= b
FT   /number= 1
FT   /note= "Corresponds to nucleotides +3 to +2150 of
FT   the human growth hormone (hGH) gene; it is
FT   desirable for cDNA coding for a human
FT   fucosyltransferase to be inserted into
FT   exon 1 of the hGH gene"
PN   US5625124-A.
PD   29-APR-1997.
PF   11-JUL-1994; 273411.
PR   11-JUL-1994; US-273411.
PA   (UNIW ) UNIV WASHINGTON.
PI   Falk P,  Gordon JI;
DR   WPI; 97-258275/23.
PT   Animal model for Helicobacter pylori infection - comprising
PT   transgenic mouse expressing human enzyme promoting intestinal
PT   adhesion
PS   Example 2; Columns 25-28; 24pp; English.
CC   A claimed transgenic mouse expresses, in its intestinal epithelial
CC   cells, the enzyme human GDP-L-fucose:beta-D-galactoside 2-alpha-L-
CC   fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose:
CC   beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also
CC   called alpha 1,3/4 FT). The enzyme is expressed under the
CC   control of a gut epithelial cell-specific promoter and Helicobacter
CC   pylori adheres to the transgenic cells. The transgenic mouse and
CC   intestinal epithelial cells from it are useful as models for screening
CC   compounds for the ability to inhibit adhesion of H. pylori to gut
CC   epithelial cells. The first 617 nucleotides of the present chimeric
CC   sequence encode the promoter from rat liver fatty acid binding protein
CC   (Fabpl) which can direct foreign gene expression to the pit cell
CC   lineage of the mouse gastric epithelium, to proliferating and non-
CC   proliferating cells in intestinal crypts, as well as to the four
CC   principal differentiated cell lineages along the crypt-to-villus axis
CC   of the small intestine. The remainder of the chimeric sequence
CC   corresponds to exon 1 of the human growth hormone (hGH) gene, into
CC   which a sequence coding for a human fucosyltransferase (hFT) can be
CC   inserted. No hGH will be produced because the initiator Met codon
CC   and the first translation stop codon will be from the hFT sequence
CC   and there is no ribosome re-entry sequence. The hGH exon 1 ensures
CC   efficient splicing of the transgene primary transcript, improves
CC   stability of the cytoplasmic hFT mRNA and allows transgene
CC   expression to be monitored by in situ hybridisation using a
CC   digoxigenin-labelled hGH oligonucleotide.
SQ   Sequence   2771 BP;    666 A;    718 C;    704 G;    683 T;

  Query Match           28.6%;  Score 300;  DB 31;  Length 2771;
  Best Local Similarity  97.3%;  Pred. No. 2.90e-201;
  Matches   329;  Conservative    0;  Mismatches   5;  Indels   4;  Gaps   2;

Db    680 atggctacaggtaagcgcccctaaaatccctttgggcacaatgtgtcctgaggggagagg 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db    740 cagcgacctgtagatgggacgggggcactaaccctcaggtttggggcttctgaatg--ag 797
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||   |
Qy     66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db    798 tatcgccatgtaagcccagtat--ggccaatctcagaaagctcctggtccctggagggat 855
          |||||||||||||||||||||  ||||||||||||||||||  ||||||||||||
Qy    126 TATCGCCATGTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTCCTCCCTGGAGGGAT 185

Db    856 ggagagagaaaaacaaacagctcctggagcagggagagtgctggcctcttgctctccggc 915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    186 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC 245

Db    916 tccctctgttgccctctggtttctccccaggctcccggacgtccctgctcctggctttttg 975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    246 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 305

Db    976 gcctgctctgcctgccctggcttcaagagggcagtgcc 1013
          ||||||||||||||||||||||||||||||||||||||
Qy    306 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343


Search completed: Wed May  6 12:57:36 1998
Job time : 144 secs.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:38:32 1998; MasPar time 969.27 Seconds
1315.719 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-1
Description: (1-1049) from US08804166.seq
Perfect Score: 1049
N.A. Sequence: 1 TCCACATGGCTACAGGTAAG.....TTATTATCACAAATCTTAAG 1049
Comp: AGGTGTACCGATGTCCATTC.....AATAATAGTGTTTAGAATTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est8 8:em_gss 9:em_est13
Database: genbank-est
10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13
25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.127; Variance 1.959; scale 5.680

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	258	24.6	373	23	HUM505B08B	Human placenta cDNA 5'	0.00e+00
2	258	24.6	379	23	C18240	Human placenta cDNA 5'	0.00e+00
3	258	24.6	392	11	R76249	yi72b05.r1 Homo sapien	0.00e+00
4	258	24.6	464	23	C17209	Human placenta cDNA 5'	0.00e+00
5	258	24.6	467	11	R71429	yi51d03.r1 Homo sapien	0.00e+00
6	257	24.5	423	12	H00861	yj31h01.r1 Homo sapien	0.00e+00
7	256	24.4	433	11	R23843	yh48c04.r1 Homo sapien	0.00e+00
8	256	24.4	452	12	H00781	yj30d01.r1 Homo sapien	0.00e+00
9	254	24.2	478	23	C17142	Human placenta cDNA 5'	0.00e+00
10	251	23.9	330	23	C18403	Human placenta cDNA 5'	0.00e+00
11	250	23.8	458	11	R77385	yi75d11.r1 Homo sapien	0.00e+00
12	248	23.6	482	12	H03289	yj44h10.r1 Homo sapien	0.00e+00
13	245	23.4	336	23	HUM530G10B	Human placenta cDNA 5'	0.00e+00
14	236	22.5	519	23	C18044	Human placenta cDNA 5'	0.00e+00
c 15	234	22.3	519	31	AA779136	zj46h11.s1 Soares feta	0.00e+00
16	232	22.1	423	23	C17966	Human placenta cDNA 5'	0.00e+00
17	229	21.8	471	12	H47149	yp73d07.r1 Homo sapien	0.00e+00
18	227	21.6	403	11	R65664	yi16a09.r1 Homo sapien	0.00e+00
19	227	21.6	430	12	H00795	yj30f02.r1 Homo sapien	0.00e+00
20	226	21.5	386	17	W86567	zh63h08.r1 Soares feta	0.00e+00
21	226	21.5	439	12	H01069	yj26c09.r1 Homo sapien	0.00e+00
22	221	21.1	513	23	AA441787	zw62b09.s1 Soares tota	0.00e+00
23	219	20.9	336	11	R79875	yi85a07.r1 Homo sapien	0.00e+00
24	219	20.9	468	11	R23095	yh31g05.r1 Homo sapien	0.00e+00
25	216	20.6	365	23	HUM505C02B	Human placenta cDNA 5'	0.00e+00
26	216	20.6	526	16	H94810	yu21c05.r1 Soares feta	0.00e+00
c 27	215	20.5	527	31	AA777267	zi96b03.s1 Soares feta	0.00e+00
28	214	20.4	294	10	T48916	yb07c06.r1 Homo sapien	0.00e+00
29	214	20.4	348	11	R33236	yh84d10.r1 Homo sapien	0.00e+00
30	213	20.3	429	13	H77743	yu23f09.r1 Homo sapien	0.00e+00
c 31	212	20.2	478	31	AA778170	zf45c10.s1 Soares feta	0.00e+00
32	210	20.0	420	10	T49525	ya76f03.r1 Homo sapien	0.00e+00
33	205	19.5	291	23	HUM511F08B	Human placenta cDNA 5'	0.00e+00
34	203	19.4	365	11	R23453	yh39b02.r1 Homo sapien	0.00e+00
35	203	19.4	393	11	R33285	yh81d04.r1 Homo sapien	0.00e+00
c 36	203	19.4	465	29	AA704477	zj19d06.s1 Soares feta	0.00e+00
37	202	19.3	261	23	HUM525D05B	Human placenta cDNA 5'	0.00e+00
38	201	19.2	438	14	N57230	yw65f07.r1 Homo sapien	0.00e+00
39	197	18.8	465	14	W01919	za35c04.r1 Soares feta	0.00e+00
40	196	18.7	479	11	R68866	yi37d02.r1 Homo sapien	0.00e+00
41	195	18.6	347	11	R34458	yh85b04.r1 Homo sapien	0.00e+00
c 42	194	18.5	450	12	H04324	yj20g12.s1 Homo sapien	0.00e+00
c 43	194	18.5	450	29	AA677403	zj62g07.s1 Soares feta	0.00e+00
44	192	18.3	344	11	R27121	yh52h07.r1 Homo sapien	0.00e+00
45	188	17.9	267	13	N40676	yw79b10.r1 Homo sapien	0.00e+00

ALIGNMENTS

RESULT 1
LOCUS HUM505B08B 373 bp mRNA EST 21-MAY-1996

DEFINITION Human placenta cDNA 5'-end GEN-505B08.
ACCESSION D58574
NID g968208
KEYWORDS EST; EST(expressed sequence tag); Human placenta; similar to known(May 29,1995).
SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human placenta polyA+ mRNA (#6518).
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 373)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
TITLE Unpublished(004)
JOURNAL Unpublished (1995)
REFERENCE 2 (bases 1 to 373)
AUTHORS Fujiwara,T.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035)
COMMENT Submitted (30-May-1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888

```
          Fax  : 0886-37-1035.
FEATURES             Location/Qualifiers
     source          1. .373
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                     /db_xref="taxon:9606"
                     /clone_lib="Clontech human placenta polyA+ mRNA (#6518)"
BASE COUNT       94 a     88 c     84 g    107 t
ORIGIN

  Query Match           24.6%;  Score 258;  DB 23;  Length 373;
  Best Local Similarity  99.2%;  Pred. No. 0.00e+00;
  Matches   260;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      47 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db     107 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     167 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 226
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Qy     907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db     227 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 286
           |||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Qy     967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db     287 TTGTTATTATCACAAATCTTAA 308
           |||||||||||||||||||||
Qy    1027 TTGTTATTATCACAAATCTTAA 1048


RESULT    2
LOCUS       C18240        379 bp    mRNA            EST       09-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-559D08.
ACCESSION   C18240
NID         g1579842
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:559D08.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 379)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1. .379
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                     /db_xref="taxon:9606"
                     /clone="559D08"
                     /tissue_type="placenta"
BASE COUNT       94 a     95 c     85 g    104 t      1 others
ORIGIN

  Query Match           24.6%;  Score 258;  DB 23;  Length 379;
  Best Local Similarity  98.9%;  Pred. No. 0.00e+00;
  Matches   259;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db      67 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 126
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Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db     127 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTARGGTCCAAGAAGAC 186
           ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     187 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 246
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Qy     907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db     247 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 306
           |||||||||||| |||||||||||||||||||||||||||||| |||||||||||||||||
Qy     967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db     307 TTGTTATTATCACAAATCTTAA 328
           |||||||||||||||||||||
Qy    1027 TTGTTATTATCACAAATCTTAA 1048


RESULT    3
LOCUS       R76249        392 bp    mRNA            EST       06-JUN-1995

DEFINITION  yi72b05.r1 Homo sapiens cDNA clone 144753 3' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R76249
NID         g850931
KEYWORDS    EST.
SOURCE      human clone=144753 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=Promega -21m13 Rsite1=Not I Rsite2=Eco RI Female
            placenta obtained at birth (full term). 1st strand cDNA was primed
            with a Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 328
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .392
                     /organism="Homo sapiens"
                     /clone="144753"
BASE COUNT      100 a     90 c     89 g    112 t      1 others
ORIGIN

  Query Match           24.6%;  Score 258;  DB 11;  Length 392;
  Best Local Similarity  99.2%;  Pred. No. 0.00e+00;
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Db      35 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 94
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Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db      95 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 154
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Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     155 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 214
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Qy     907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db     215 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 274
           ||||||||||||| |||||||||||||||||||||||||||||| |||||||||||||||
Qy     967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db     275 TTGTTATTATCACAAATCTTAA 296
           |||||||||||||||||||||
Qy    1027 TTGTTATTATCACAAATCTTAA 1048


RESULT    4
LOCUS       C17209        464 bp    mRNA            EST       04-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-541F08.
ACCESSION   C17209
NID         g1571916
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:541F08.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 464)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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BASE COUNT      114 a    117 c     95 g    138 t
ORIGIN

  Query Match           24.6%;  Score 258;  DB 23;  Length 464;
  Best Local Similarity  99.2%;  Pred. No. 0.00e+00;
  Matches   260;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      39 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 98
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Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db      99 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 158
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Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     159 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 218
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Qy     907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db     219 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 278
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Qy     967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db     279 TTGTTATTATCACAAATCTTAA 300
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Qy    1027 TTGTTATTATCACAAATCTTAA 1048


RESULT    5
LOCUS       R71429        467 bp    mRNA            EST       01-JUN-1995

DEFINITION  yi51d03.r1 Homo sapiens cDNA clone 142757 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R71429
NID         g844946
KEYWORDS    EST.
SOURCE      human clone=142757 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 386
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
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BASE COUNT      113 a    114 c     98 g    139 t      3 others
ORIGIN

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  Matches   260;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

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Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db     110 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 169
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Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     170 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 229
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Qy    907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db    230 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 289
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Qy    967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db    290 TTGTTATTATCACAAATCTTAA 311
          |||||||||||||||||||||||
Qy   1027 TTGTTATTATCACAAATCTTAA 1048


RESULT    6
LOCUS       H00861        423 bp    mRNA            EST       19-JUN-1995

DEFINITION  yj31h01.r1 Homo sapiens cDNA clone 150385 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00861
NID         g863794
KEYWORDS    EST.
SOURCE      human clone=150385 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 344
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .423
                      /organism="Homo sapiens"
                      /clone="150385"
BASE COUNT      109 a     95 c     95 g    119 t      5 others
ORIGIN

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  Best Local Similarity  98.9%;  Pred. No. 0.00e+00;
  Matches   259;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db     18 TTGCCCAGAATGCACGCTACAGGANAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 77
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Qy    787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db     78 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 137
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Qy    847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db    138 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db    198 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 257
          |||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Qy    967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db    258 TTGTTATTATCACAAATCTTAA 279
          |||||||||||||||||||||||
Qy   1027 TTGTTATTATCACAAATCTTAA 1048


RESULT    7
LOCUS       R23843        433 bp    mRNA            EST       20-APR-1995

DEFINITION  yh48c04.r1 Homo sapiens cDNA clone 132966 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R23843
NID         g778731
KEYWORDS    EST.
SOURCE      human clone=132966 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 334
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .433
                      /organism="Homo sapiens"
                      /clone="132966"
BASE COUNT      111 a    104 c     90 g    127 t      1 others
ORIGIN

  Query Match           24.4%;  Score 256;  DB 11;  Length 433;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   261;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db      2 CAGGATTGCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAA 61
          |||| |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    783 CAGGTTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAA 842

Db     62 TACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    843 TACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 902
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Db    122 AGACGATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCAT 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    903 AGACGATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCAT 962

Db    182 ATAACAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCA 241
          |||||||||||||||| |||||||||||||||||||||||||||||| ||||||||||||
Qy    963 ATAACAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCA 1022

Db    242 GTACTTGTTATTATCACAAATCTTAA 267
          |||||||||||||||||||||||||
Qy   1023 GTACTTGTTATTATCACAAATCTTAA 1048


RESULT    8
LOCUS       H00781        452 bp    mRNA            EST       19-JUN-1995

DEFINITION  yj30d01.r1 Homo sapiens cDNA clone 150241 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00781
NID         g863714
KEYWORDS    EST.
SOURCE      human clone=150241 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 322
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .452
                      /organism="Homo sapiens"
                      /clone="150241"
BASE COUNT       107 a    104 c    103 g    133 t      5 others
ORIGIN

  Query Match           24.4%;  Score 256;  DB 12;  Length 452;
  Best Local Similarity  99.2%;  Pred. No. 0.00e+00;
  Matches   258;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db     44 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db    104 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db    164 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db    224 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 283
          |||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Qy    967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db    284 TTGTTATTATCACAAATCTT 303
          ||||||||||||||||||||
Qy   1027 TTGTTATTATCACAAATCTT 1046


RESULT    9
LOCUS       C17142        478 bp    mRNA            EST       04-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-539G04.
ACCESSION   C17142
NID         g1571849
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:539G04.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 478)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES              Location/Qualifiers
     source           1. .478
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="539G04"
                      /tissue_type="placenta"
BASE COUNT       125 a    113 c     96 g    144 t
ORIGIN

  Query Match           24.2%;  Score 254;  DB 23;  Length 478;
  Best Local Similarity  99.2%;  Pred. No. 0.00e+00;
  Matches   256;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 CCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    791 CCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAG 850

Db     61 TGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    851 TGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATG 910

Db    121 TTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    911 TTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGG 970

Db    181 GTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGT 240
          |||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Qy    971 GTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTACTTGT 1030

Db    241 TATTATCACAAATCTTAA 258
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Qy   1031 TATTATCACAAATCTTAA 1048


RESULT   10
LOCUS       C18403        330 bp    mRNA            EST       09-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-561H02.
ACCESSION   C18403
NID         g1580005
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:561H02.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 330)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="561H02"
                     /tissue_type="placenta"
BASE COUNT       82 a     87 c     73 g     88 t
ORIGIN

  Query Match           23.9%;  Score 251;  DB 23;  Length 330;
  Best Local Similarity  98.9%;  Pred. No. 0.00e+00;
  Matches   259;  Conservative    0;  Mismatches   2;  Indels   1;  Gaps   1;

Db      67 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db     127 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     187 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db     247 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGA-CCACACGGCGTGCCACTGCAGTAC 305
           |||||||||||| |||||||||||||||||||||| |||||||| ||||||||||||||
Qy     967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db     306 TTGTTATTATCACAAATCTTAA 327
           |||||||||||||||||||||
Qy    1027 TTGTTATTATCACAAATCTTAA 1048


RESULT   11
LOCUS       R77385        458 bp    mRNA            EST       06-JUN-1995

DEFINITION  yi75d11.r1 Homo sapiens cDNA clone 145077 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R77385
NID         g852017
KEYWORDS    EST.
SOURCE      human clone=145077 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 458)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 393
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .458
                     /organism="Homo sapiens"
                     /clone="145077"
BASE COUNT      119 a    109 c     97 g    133 t
ORIGIN

  Query Match           23.8%;  Score 250;  DB 11;  Length 458;
  Best Local Similarity  99.2%;  Pred. No. 0.00e+00;
  Matches   252;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      16 AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAGTGCA 75
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     795 AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAGTGCA 854

Db      76 TGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATGTTGG 135
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     855 TGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATGTTGG 914

Db     136 TCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCA 195
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     915 TCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCA 974

Db     196 CAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTTATT 255
           |||| |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Qy     975 CAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTACTTGTTATT 1034

Db     256 ATCACAAATCTTAA 269
           ||||||||||||||
Qy    1035 ATCACAAATCTTAA 1048


RESULT   12
LOCUS       H03289        482 bp    mRNA            EST       20-JUN-1995

DEFINITION  yj44h10.r1 Homo sapiens cDNA clone 151651 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H03289
NID         g866222
KEYWORDS    EST.
```

```
SOURCE      human clone=151651 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 482)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 301
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .482
                     /organism="Homo sapiens"
                     /clone="151651"
BASE COUNT      111 a    106 c    118 g    142 t      5 others
ORIGIN

  Query Match           23.6%;  Score 248;  DB 12;  Length 482;
  Best Local Similarity  98.9%;  Pred. No. 0.00e+00;
  Matches   261;  Conservative    0;  Mismatches   1;  Indels   2;  Gaps   2;

Db      51 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

Db     111 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     171 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db     231 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGGAGAACCACACGGGCGTGCCACTGCAGT 290
           |||||||||||| |||||||||||||||||| |||||||||||| ||||||||||||
Qy     967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGG-AGAACCACACGGG-GTGCCACTGCAGT 1024

Db     291 ACTTGTTATTATCACAAATCTTAA 314
           |||||||||||||||||||||||||
Qy    1025 ACTTGTTATTATCACAAATCTTAA 1048


RESULT   13
LOCUS       HUM530G10B    336 bp    mRNA            EST       13-DEC-1995

DEFINITION  Human placenta cDNA 5'-end GEN-530G10.
ACCESSION   D79076
NID         g1180949
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone_lib:human placenta
            polyA+.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
  TITLE     Large-scale sequencing project at Otsuka GEN Research Institute
  JOURNAL   Unpublished (1995)
REFERENCE   2  (bases 1 to 336)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan
COMMENT     Submitted (7-Nov-1995) to DDBJ by:
            Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical CO.,Ltd
            463-10 Kagasuno Kawauchi-cho
            Tokushima, Tokushima
            771-01
            Japan
            Phone:0886-65-2888
            Fax  :0886-37-1035.
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                     /tissue_type="placenta"
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  Matches   250;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db      47 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 106
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Qy     787 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 846

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Qy     847 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db     167 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 226
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Qy     907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db     227 CAGGGTCACAGTAATGGGGGGTTTCATAGTGGGGACCCACACGGCGTGCCACTGCAGTAC 286
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Qy     967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCACTGCAGTAC 1026

Db     287 TTGTTATTATCACAA 301
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Qy    1027 TTGTTATTATCACAA 1041


RESULT   14
LOCUS       C18044        519 bp    mRNA            EST       09-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-556F06.
ACCESSION   C18044
NID         g1579646
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:556F06.
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  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 519)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
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                     /clone="556F06"
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  Matches   305;  Conservative    0;  Mismatches  31;  Indels   7;  Gaps   6;

Db      40 ATGGCTGCAGGTAAGCGCCCCTAAAANNNNTTTGGGCACAACGTGTCCTGAGGGGAGAGG 99
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Qy       6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db     100 CGGCGCCCTGCAGATGGGACGGGGGCACTAACC-TCAGGTTTGGGGCTTCTGAATGTGAA 158
           | ||| |||| |||||||||||||||||||||| ||||||||||||||||| ||| | |
Qy      66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db     159 TATCGCCATCTAAGGCCAGATATTTGGCCAATCTCTGAATGTTCCTGGTCCCTGGAGGGA 218
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Qy     126 TATCGCCATGTAAGCCCAG-TATTTGGCCAATCTCAGAAAGCTCCTCCTCCCTGGAGGGA 184

Db     219 TGGAGAGAGAGAAAAAGAAAACAGCTCCTGGAACAGGGAGAGTACTGGCCTCTTGCTCTG 278
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Qy     185 TGGAGAGAGA--AAAACAAA-CAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTC 241

Db     279 CGGCTCCCT-TCTTGCCCTCCGGTTTCTCCCCAGGCTCCCGGACGTCCCTTCTCCTGGCT 337
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Qy     242 CGGCTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCT 301

Db     338 TTTGCCCTGCTCTGCCTGCCCTGGCTTCA-GAGGCTGGTGCCG 379
           |||| |||||||||||||||||||||||| ||||   ||||||
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RESULT   15
LOCUS       AA779136      519 bp    mRNA            EST       05-FEB-1998

DEFINITION  zj46h11.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA
            clone 453381 3' similar to gb:V00518 GLYCOPROTEIN HORMONES ALPHA
            CHAIN PRECURSOR (HUMAN);.
ACCESSION   AA779136
NID         g2838467
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 519)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 316.
FEATURES             Location/Qualifiers
     source          1. .519
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                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.  1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
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                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
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ORIGIN

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  Best Local Similarity  95.9%;  Pred. No. 0.00e+00;
  Matches   255;  Conservative    0;  Mismatches   9;  Indels   2;  Gaps   2;

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Db     313 ACCCCCCATTACTGTGACCCTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 372
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Cp     988 ACCCCCCATGACTGTGACCCTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 929

Db     373 GACGTTCTTTTGGACCAACATCGTCTTCTTGGACCTTAGTGGAGTGGGATATGCTCTAGA 432
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Db     433 GAAGCAGCAGCCCATGCACTGAAGTAGTGGGGCACCGGGCTCGTAGAAGAATGGGGTTTC 492
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Cp     868 GAAGCAGCAGCCCATGCACTGAAGTATTGGGGCACCCGGCTGGGAGAAGAATGGGTTTTC 809

Db     493 CTG-AGCGTG-ATTCTGGGGAATCTG 516
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Cp     808 CTGTAGCGTGCATTCTGGGCAACCTG 783


Search completed: Wed May  6 12:54:51 1998
Job time : 979 secs.
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:50:59 1998; MasPar time 8.51 Seconds
449.440 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150
Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 31.442; Variance 119.617; scale 0.263

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1994	100.0	256	26	W33357	TBP(20-161)/hCG-alpha	1.90e-207
2	1667	83.6	285	26	W33359	TBP(20-190)/hCG-alpha	1.11e-170
3	1321	66.2	307	26	W33358	TBP(20-161)/hCG-beta	6.46e-132
4	1291	64.7	336	26	W33360	TBP(20-190)/hCG-beta	1.46e-128
5	1124	56.4	161	5	R27496	Native 30 kD TNF inhi	6.19e-110
6	1124	56.4	199	4	R24080	Truncated TNF-alpha 5	6.19e-110
7	1124	56.4	309	13	R70108	TNF-R-GBPH fusion pro	6.19e-110
8	1124	56.4	371	2	R07449	Tumour Necrosis Facto	6.19e-110
9	1124	56.4	451	13	R70107	TNF-R-GBP 130 fusion	6.19e-110
10	1124	56.4	455	8	R42059	Lambda derived TNF-R.	6.19e-110
11	1124	56.4	455	2	R10986	30kD TNF inhibitor pr	6.19e-110
12	1124	56.4	455	4	R20787	TNF-alpha binding pro	6.19e-110
13	1124	56.4	455	14	R75084	p55 TNF-R.	6.19e-110
14	1124	56.4	455	2	R07451	Human Tumour Necrosis	6.19e-110
15	1124	56.4	455	2	R11082	Human 55kD TNF-bindin	6.19e-110
16	1124	56.4	455	4	R24000	TNF-alpha 55kD recept	6.19e-110
17	1124	56.4	547	13	R70104	TNF-R-GBPH fusion pro	6.19e-110
18	1124	56.4	884	13	R70109	TNF-R-GBP 130 fusion	6.19e-110
19	1124	56.4	900	13	R70103	TNF-R-GBP 130 fusion	6.19e-110
20	1124	56.4	1245	13	R70106	TNF-R-Pl. vivax Duffy	6.19e-110
21	1124	56.4	1604	13	R70105	TNF-R-EBA 175 fusion	6.19e-110
22	1118	56.1	433	8	R51032	Mutant p55 tumour nec	2.88e-109
23	1118	56.1	443	8	R51033	Mutant p55 tumour nec	2.88e-109
24	1118	56.1	455	8	R51034	Mutant p55 tumour nec	2.88e-109
25	1118	56.1	455	8	R42197	p55 Tumour necrosis f	2.88e-109
26	1110	55.7	455	3	R12550	Type I TNF receptor.	2.24e-108
27	996	49.9	168	4	R24084	Truncated TNF-alpha 5	1.06e-95
28	800	40.1	158	4	R24081	Truncated TNF-alpha 5	5.13e-74
29	788	39.5	461	2	R07450	Rat Tumour Necrosis F	1.08e-72
30	672	33.7	96	3	R15182	hCG/bCG alpha subunit	5.96e-60
31	667	33.5	92	1	P92146	Beta subunit of urina	2.10e-59
32	667	33.5	96	3	R15195	hCG alpha subunit mut	2.10e-59
33	667	33.5	116	26	W31665	Secreted protein huma	2.10e-59
34	667	33.5	116	2	R10095	Engineered human alph	2.10e-59
35	667	33.5	116	19	R99417	Dimeric glycoprotein	2.10e-59
36	667	33.5	222	15	R86268	Partially deglycosyla	2.10e-59
37	667	33.5	222	15	R86256	Single chain gonadotr	2.10e-59
38	667	33.5	226	15	R86255	Single chain gonadotr	2.10e-59
39	667	33.5	229	15	R86250	Single chain gonadotr	2.10e-59
40	667	33.5	234	15	R86254	Single chain gonadotr	2.10e-59
41	667	33.5	234	15	R86249	Single chain gonadotr	2.10e-59
42	667	33.5	234	15	R86248	Single chain gonadotr	2.10e-59
43	667	33.5	234	15	R86253	Single chain gonadotr	2.10e-59
44	667	33.5	237	15	R86251	Single chain gonadotr	2.10e-59
45	667	33.5	265	15	R86247	Single chain gonadotr	2.10e-59

ALIGNMENTS

RESULT 1
ID W33357 standard; Protein; 256 AA.
AC W33357;
DT 19-MAR-1998 (first entry)
DE TBP(20-161)/hCG-alpha fusion protein.
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW alpha subunit; hCG-alpha.
OS Homo sapiens.
PN WO9730161-A1.
PD 21-AUG-1997.
PF 20-FEB-1997; U02315.
PR 20-FEB-1996; US-011936.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PI Campbell RK, Chappel SC, Jameson BA;
DR WPI; 97-425036/39.
DR N-PSDB; T94007.
PT Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation
PS Example; Pages 32-33; 60pp; English.
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein hormone capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC (hCG-alpha) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed..
SQ Sequence 256 AA;

Query Match 100.0%; Score 1994; DB 26; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.90e-207;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
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Db     121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscagaapgcpectlqenp 180
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Db     181 ffsqpgapilqcmgccfsrayptplrskktmlvqknvtsestccvaksynrvtvmggfkv 240
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Qy     181 FFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKV 240

Db     241 enhtgchcstcyyhks 256
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Qy     241 ENHTGCHCSTCYYHKS 256


RESULT    2
ID   W33359 standard; Protein; 285 AA.
AC   W33359;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94021.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 37-38; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   285 AA;

  Query Match           83.6%;  Score 1667;  DB 26;  Length 285;
  Best Local Similarity  89.1%;  Pred. No. 1.11e-170;
  Matches   254;  Conservative    2;  Mismatches   0;  Indels  29;  Gaps   1;

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Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
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Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfnctclclngtvhlscqekqntvctchagfflrenecvscsnckkslectklslpq 180
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Qy    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSC---------------- 164

Db    181 ienvkgtedsgttagaapgcpectlqenpffsqpgapilqcmgccfsrayptplrskktm 240
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Qy    165 -------------AGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTM 211

Db    241 lvqknvtsestccvaksynrvtvmggfkvenhtachcstcyyhks 285
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Qy    212 LVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT    3
ID   W33358 standard; Protein; 307 AA.
AC   W33358;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             279..1202
FT                   /*tag=  a
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94008.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 34-35; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   307 AA;

  Query Match           66.2%;  Score 1321;  DB 26;  Length 307;
  Best Local Similarity  98.8%;  Pred. No. 6.46e-132;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscagaggprc 171
          ||||||||||||||||||||||||||||||||||||||||||||:| |
Qy    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCAGAAPGC 171


RESULT    4
ID   W33360 standard; Protein; 336 AA.
AC   W33360;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94022.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 39-40; 60pp; English.
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CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   336 AA;

  Query Match           64.7%;  Score 1291;  DB 26;  Length 336;
  Best Local Similarity  99.4%;  Pred. No. 1.46e-128;
  Matches   164;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscs 165
          |||||||||||||||||||||||||||||||||||||||||||:
Qy    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165


RESULT    5
ID   R27496 standard; protein; 161 AA.
AC   R27496;
DT   09-MAR-1993  (first entry)
DE   Native 30 kD TNF inhibitor.
KW   Tumour necrosis factor; ethylene glycol; pharmokinetic;
KW   adult respiratory distress syndrome; rheumatoid arthritis;
KW   septic shock; pulmonary fibrosis; spacer.
OS   Homo sapiens.
PN   WO9216221-A.
PD   01-OCT-1992.
PF   13-MAR-1992; U02122.
PR   15-MAR-1991; US-669862.
PR   17-JAN-1992; US-822296.
PA   (SYND ) SYNERGEN INC.
PI   Armes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;
DR   WPI; 92-348933/42.
PT   New ethylene glycolated polypeptide(s) with improved
PT   pharmacokinetic properties - for treating e.g. TNF and IL-1
PT   mediated diseases, e.g. adult respiratory distress syndrome,
PT   rheumatoid arthritis, septic shock etc.
PS   Claim 54; Fig 2; 100pp; English.
CC   The sequence shows a native 30 kD TNF inhibitor which may be
CC   modified to contain at least one non-native cysteine residue, pref.
CC   at positions 1, 14, 105, 111 and/or 165.  The non-native cysteine is
CC   joined to a non-peptidic polymer, pref. monomethoxy PEG via
CC   thio-ether bonds.  Two such TNF inhibitor mols. may be linked via
CC   this non-peptidic spacer.  The modified polypeptides show improved
CC   pharmokinetic properties, i.e. increased mol. wt. hence reduced
CC   clearance rate following s.c. or systemic administration, increased
CC   sol. of native TNF inhibitors, and reduced antigenicity.  The
CC   polypeptides may be used for treatment of TNF mediated diseases such
CC   as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
CC   arthritis,inflammatory bowel disease and septic shock.  The same
CC   method may be applied to the interleukin-1 receptor antagonist
CC   IL-1ra.            See also R27495.
SQ   Sequence   161 AA;

  Query Match           56.4%;  Score 1124;  DB 5;  Length 161;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     61 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    121 kqntvctchagfflrenecvscs 143
          |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    6
ID   R24080 standard; Protein; 199 AA.
AC   R24080;
DT   05-NOV-1992  (first entry)
DE   Truncated TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   N-PSDB; Q24441.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence is a truncated TNF-alpha receptor derivative, as encoded
CC   in pTNFRecd. This was produced as described in Q24440.
CC   This derivative lacks the 81 carboxyl terminal residues of the
CC   cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   199 AA;

  Query Match           56.4%;  Score 1124;  DB 4;  Length 199;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
          |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    7
ID   R70108 standard; Protein; 309 AA.
AC   R70108;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
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OS   Chimeric Plasmodium falciparum.
FH   Key             Location/Qualifiers
FT   misc_difference 230..269
FT                   /label= repeat_region
FT                   /note= "can be repeated n times, where n is a real
FT                   number"
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 54-55; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The
CC   use of cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   309 AA;

  Query Match           56.4%;  Score 1124;  DB 13;  Length 309;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscs 162
           |||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    8
ID   R07449 standard; protein; 371 AA.
AC   R07449;
DT   29-JAN-1991  (first entry)
DE   Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06282.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of
CC   e.g. COS7 cells.  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   371 AA;

  Query Match           56.4%;  Score 1124;  DB 2;  Length 371;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    9
ID   R70107 standard; Protein; 451 AA.
AC   R70107;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 53-54; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence   451 AA;

  Query Match           56.4%;  Score 1124;  DB 13;  Length 451;
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  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db      80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     140 kqntvctchagfflrenecvscs 162
           |||||||||||||||||||||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   10
ID   R42059 standard; Protein; 455 AA.
AC   R42059;
DT   29-APR-1994  (first entry)
DE   Lambda derived TNF-R.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction.
OS   Homo sapiens.
OS   Lambda-gt10-7ctnfbp.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "Signal peptide"
FT   protein         41..455
FT                   /note= "Mature hTNF-R"
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   N-PSDB; Q49932.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.
CC   The sequences given in R42058-59 repressent human tumour necrosis
CC   factor receptor (TNF-R) and the sequences in R42060-61 represent
CC   human interleukin-1 receptor (IL-1R).  These sequences were used in
CC   the production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence   455 AA;

  Query Match           56.4%;  Score 1124;  DB 8;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   11
ID   R10986 standard; Protein; 455 AA.
AC   R10986;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor.
KW   Tumour necrosis factor; inhibitor.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cleavage_site   40..41
FT                   note=" cleavage gives active protein "
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   N-PSDB; Q10883.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC   from which the sequence was deduced was isolated from a cDNA
CC   library prepd. from RNA form U937 cells treated with PMA/PHA.
CC   The whole gene can be inserted into expression vectors for prepn.
CC   of TNF inhibitor for use in the treatment of inflammatory and
CC   degenerative diseases.  The active protein is claimed (Claim 8).
CC   See also R10984 and R11001.
SQ   Sequence   455 AA;

  Query Match           56.4%;  Score 1124;  DB 2;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   12
ID   R20787 standard; Protein; 455 AA.
AC   R20787;
DT   11-MAY-1992  (first entry)
DE   TNF-alpha binding protein.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "signal peptide"
FT   peptide         41..455
FT                   /note= "mature peptide"
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FT   domain          30..199
FT                   /note= "extracellular domain"
FT   domain          212..234
FT                   /note= "transmembrane domain"
FT   modified_site   145..147
FT                   /note= "potential N-glycosylation site"
FT   modified_site   151..153
FT                   /note= "potential N-glycosylation site"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   N-PSDB; Q20973.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
CC   can therefore be used therapeutically to treat disorders such as
CC   cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC   arthritis.
SQ   Sequence   455 AA;

  Query Match           56.4%;  Score 1124;  DB 4;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
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Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   13
ID   R75084 standard; Protein; 455 AA.
AC   R75084;
DT   19-JAN-1996  (first entry)
DE   p55 TNF-R.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         41..53
FT                   /note= "N terminus of soluble p55 TNF-R"
FT   modified_site   54..56
FT                   /note= "glycosylation site"
FT   modified_site   145..147
FT                   /note= "glycosylation site"
FT   modified_site   161..163
FT                   /note= "glycosylation site"
FT   peptide         193..210
FT                   /note= "peptide used in creation of chimeras"
FT   region          198..210
FT                   /note= "spacer region"
FT   misc_difference 201
FT                   /note= "major C terminus for soluble p55 TNF-R"
FT   misc_difference 202
FT                   /note= "essential for shedding reaction"
FT   misc_difference 203
FT                   /note= "minor C terminus for soluble p55 TNF-R"
FT   region          212..234
FT                   /note= "transmembrane region"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
DR   WPI; 95-194342/26.
DR   N-PSDB; Q90513.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor  - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R).
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment.  The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type.  The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain.  This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain.  The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11.  This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.
CC   The mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3.  These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence   455 AA;

  Query Match           56.4%;  Score 1124;  DB 14;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
         |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   14
ID   R07451 standard; protein; 455 AA.
AC   R07451;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
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DR   WPI; 90-321987/43.
DR   N-PSDB; Q06285.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   455 AA;

  Query Match           56.4%;  Score 1124;  DB 2;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   15
ID   R11082 standard; Protein; 455 AA.
AC   R11082;
DT   24-MAY-1991  (first entry)
DE   Human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   modified_site   54
FT                   /label= putative N-glycosylation site
FT   modified_site   145
FT                   /label= putative N-glycosylation site
FT   modified_site   151
FT                   /label= putative N-glycosylation site
FT   modified_site   270
FT                   /label= putative N-glycosylation site
FT   region          212..230
FT                   /label= transmembrane region
FT   peptide         1..28
FT                   /label= signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   455 AA;

  Query Match           56.4%;  Score 1124;  DB 2;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 6.19e-110;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


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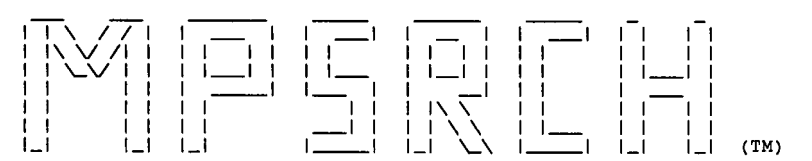

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:50:01 1998; MasPar time 11.89 Seconds
786.633 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150
Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 40.411; Variance 71.735; scale 0.563

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	56.4	158	5	1EXTB	tumor necrosis factor	2.23e-230
2	1124	56.4	455	1	GQHUT1	tumor necrosis factor	2.23e-230
3	1118	56.1	160	5	1EXTA	tumor necrosis factor	5.83e-229
4	1114	55.9	142	5	1NCFB	tumor necrosis factor	5.14e-228
5	1105	55.4	139	5	1TNRR	tumor necrosis factor	6.85e-226
6	1098	55.1	140	5	1NCFA	tumor necrosis factor	3.08e-224
7	962	48.2	461	2	JC4302	tumor necrosis factor	3.26e-192
8	841	42.2	454	2	I57826	tumor necrosis factor	7.05e-164
9	841	42.2	454	1	GQMST1	tumor necrosis factor	7.05e-164
10	809	40.6	461	1	GQRTT1	tumor necrosis factor	2.05e-156
11	667	33.5	116	1	TTHUAP	glycoprotein hormones	1.71e-123
12	647	32.4	86	5	1HRPA	chorionic gonadotropi	6.89e-119
13	645	32.3	85	5	1XULA	chorionic gonadotropi	1.99e-118
14	645	32.3	85	5	1HCNA	Human chorionic gonad	1.99e-118
15	551	27.6	120	2	A39555	glycoprotein hormones	6.48e-97
16	548	27.5	120	1	TTBOA	glycoprotein hormones	3.12e-96
17	548	27.5	120	1	UTSHA	glycoprotein hormones	3.12e-96
18	546	27.4	96	2	A05096	glycoprotein hormones	8.89e-96
19	544	27.3	120	1	TTRTA	glycoprotein hormones	2.53e-95
20	541	27.1	96	2	PN0138	glycoprotein hormones	1.22e-94
21	541	27.1	120	1	UTPGA	glycoprotein hormones	1.22e-94
22	541	27.1	120	1	TTMSA	glycoprotein hormones	1.22e-94
23	539	27.0	120	2	G00021	chorionic gonadotropi	3.47e-94
24	537	26.9	120	2	A45585	glycoprotein hormones	9.87e-94
25	537	26.9	120	2	I51241	pituitary glycoprotei	9.87e-94
26	507	25.4	118	2	A40554	glycoprotein hormones	6.20e-87
27	503	25.2	120	2	S53062	glycoprotein hormones	4.97e-86
28	501	25.1	96	1	TTHOA	glycoprotein hormones	1.41e-85
29	500	25.1	118	2	S16762	gonadotropin alpha ch	2.37e-85
30	500	25.1	118	1	UTCAA	glycoprotein hormones	2.37e-85
31	500	25.1	118	2	A60626	glycoprotein hormones	2.37e-85
32	478	24.0	93	2	S07091	glycoprotein hormones	2.15e-80
33	476	23.9	97	2	S20287	lutropin alpha chain	6.06e-80
34	474	23.8	117	2	A37198	glycoprotein hormones	1.71e-79
35	451	22.6	119	2	I51229	gonadotropin alpha 1	2.46e-74
36	448	22.5	114	2	B60627	glycoprotein hormones	1.15e-73
37	447	22.4	108	2	A60627	glycoprotein hormones	1.93e-73
38	446	22.4	114	2	I51230	gonadotropin alpha 2	3.23e-73
39	440	22.1	117	2	I50992	gonadotropin alpha-su	7.08e-72
40	231	11.6	435	2	I54182	tumor necrosis factor	8.52e-27
41	228	11.4	38	2	A60583	glycoprotein hormones	3.48e-26
42	225	11.3	325	2	B43692	T2 protein - rabbit f	1.42e-25
43	221	11.1	326	1	GQVZML	T2 protein - myxoma v	9.18e-25
44	214	10.7	349	2	D36858	gene G4R protein - va	2.37e-23
45	212	10.6	474	2	B38634	tumor necrosis factor	5.96e-23

ALIGNMENTS

RESULT 1
ENTRY 1EXTB #type complete

TITLE tumor necrosis factor receptor extracellular domain, chain B
PDB_TITLE extracellular domain of the 55kda tumor necrosis factor receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM #formal_name Homo sapiens #common_name man
#note expressed in Escherichia coli, the construct contains residues 12 to 172 of the mature sequence of the entire receptor. residue 11 is mutated to met as a result of the expression system
REFERENCE A65560
#authors Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
REFERENCE TN026251
#authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal J. Biol. Chem. (1995) 270:13303
#title Crystallographic evidence for dimerization of unliganded tumor necrosis factor receptor.
REFERENCE TN026252
#authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale, K.; Naismith, J.H.; Sprang, S.R.
#journal J. Mol. Biol. (1994) 239:332
#title Two crystal forms of the extracellular domain of type i tumor necrosis factor receptor.
REFERENCE A40737
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld, H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal Cell (1993) 73:431-445
#title Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for TNF receptor activation.
COMMENT Resolution: 1.85 angstroms
COMMENT Determination: X-ray diffraction
COMMENT R-value: no refinement
KEYWORDS binding protein; cytokine; signalling protein
FEATURE
68-70 #region helix (right hand 3-10)\
143-145 #region helix (right hand 3-10)\
9-11,19-21 #region beta sheet\
133-136,139-142 #region beta sheet\
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5-19 #disulfide_bonds\

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   45-60              #disulfide_bonds\
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   66-86              #disulfide_bonds\
   88-104             #disulfide_bonds\
   107-119            #disulfide_bonds\
   110-127            #disulfide_bonds\
   129-140            #disulfide_bonds\
   143-156            #disulfide_bonds\
   146-152            #disulfide_bonds
SUMMARY           #length 158  #molecular-weight 17827  #checksum 5022

  Query Match           56.4%;  Score 1124;  DB 5;  Length 158;
  Best Local Similarity  99.3%;  Pred. No. 2.23e-230;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

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Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
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Db    122 KQNTVCTCHAGFFLRENECVSCS 144
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Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    2
ENTRY             GQHUT1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAMES
CONTAINS          tumor necrosis factor alpha inhibitor; tumor necrosis factor
                    binding protein 1 (TNF blocking factor)
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    24-Oct-1997
ACCESSIONS        A38208; A34899; A34900; A36555; C36555; A38281; S12057;
                    JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE         A38208
   #authors       Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
   #journal       Genomics (1992) 13:219-224
   #title         Structure of the human TNF receptor 1 (p60) gene (TNRF1) and
                    localization to chromosome 12p13.
   #accession     A38208
      ##molecule_type DNA
      ##residues       1-455 ##label FUC
      ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
                          PID:g339750
REFERENCE         A34899
   #authors       Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
                    M.; Tabuchi, H.; Lesslauer, W.
   #journal       Cell (1990) 61:351-359
   #title         Molecular cloning and expression of the human 55 kd tumor
                    necrosis factor receptor.
   #cross-references MUID:90235284
   #accession     A34899
      ##molecule_type mRNA
      ##residues       1-455 ##label LOE
      ##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
      ##experimental_source placenta
      ##note           part of this sequence, including the amino end of the
                        mature protein, confirmed by protein sequencing
REFERENCE         A34900
   #authors       Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
                    Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
                    H.; Kohr, W.J.; Goeddel, D.V.
   #journal       Cell (1990) 61:361-370
   #title         Molecular cloning and expression of a receptor for human
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      ##molecule_type mRNA
      ##residues       1-455 ##label SCH
      ##cross-references GB:M33294; NID:g339744; PID:g339745
REFERENCE         A36555
   #authors       Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                    Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                    Stratowa, C.; Adolf, G.R.
   #journal       DNA Cell Biol. (1990) 9:705-715
   #title         Molecular cloning and expression of human and rat tumor
                    necrosis factor receptor chain (p60) and its soluble
                    derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
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      ##molecule_type mRNA
      ##residues       1-455 ##label HIM
      ##cross-references GB:M63121; NID:g339755; PID:g339756
   #accession     C36555
      ##molecule_type protein
      ##residues       30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
                        107-128;162-167,'X',169-201 ##label HI2
      ##note           the purified protein, called tumor necrosis factor
                        binding protein, is a soluble derivative of the
                        receptor
REFERENCE         A38281
   #authors       Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
                    M.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
   #title         Cloning of human tumor necrosis factor (TNF) receptor cDNA
                    and expression of recombinant soluble TNF-binding protein.
   #cross-references MUID:91017509
   #accession     A38281
      ##molecule_type mRNA
      ##residues       1-455 ##label GRA
      ##cross-references GB:M37764
      ##note           the authors translated the codon TGG for residue 371 as
                        Thr, AAG for residue 372 as Leu, and GAC for residue
                        427 as Asn
REFERENCE         S12057
   #authors       Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
                    R.; Aderka, D.; Holtmann, H.; Wallach, D.
   #journal       EMBO J. (1990) 9:3269-3278
   #title         Soluble forms of tumor necrosis factor receptors (TNF-Rs).
                    The cDNA for the type I TNF-R, cloned using amino acid
                    sequence data of its soluble form, encodes both the cell
                    surface and a soluble form of the receptor.
   #cross-references MUID:91006021
   #accession     S12057
      ##molecule_type mRNA
      ##residues       1-455 ##label NOP
      ##cross-references EMBL:X55313; NID:g37223; PID:g37224
      ##note           parts of soluble TNF binding protein 1, including its
                        amino and carboxyl ends, were confirmed by protein
                        sequencing
REFERENCE         JT0758
   #authors       Kemper, O.; Wallach, D.
   #journal       Gene (1993) 134:209-216
   #title         Cloning and partial characterization of the promoter for the
                    human p55 tumor necrosis factor (TNF) receptor.
   #accession     JT0758
      ##molecule_type DNA
      ##residues       1-13 ##label KEM
REFERENCE         A60231
   #authors       Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
                    J.M.
   #journal       Eur. J. Immunol. (1990) 20:1167-1174
   #title         Tumor necrosis factor inhibitor: purification, NH-2-terminal
                    amino acid sequence and evidence for anti-inflammatory and
                    immunomodulatory activities.
   #cross-references MUID:90292116
   #accession     A60231
      ##molecule_type protein
      ##residues       41-43,'X',45-53,'X',55-57 ##label SEC
```

```
REFERENCE       A38258
  #authors      Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
                  J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
                  R.S.; Granger, G.A.
  #journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
  #title        Purification and characterization of an inhibitor (soluble
                  tumor necrosis factor receptor) for tumor necrosis factor
                  and lymphotoxin obtained from the serum ultrafiltrates of
                  human cancer patients.
  #cross-references MUID:91062364
  #accession    A38258
    ##molecule_type protein
    ##residues      41-60 ##label GAT
    ##experimental_source cancer patient serum
REFERENCE       A60594
  #authors      Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
                  Grubb, A.; Adolf, G.
  #journal      Eur. J. Haematol. (1989) 42:270-275
  #title        Isolation and characterization of a tumor necrosis factor
                  binding protein from urine.
  #accession    A60594
    ##molecule_type protein
    ##residues      41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
    ##experimental_source renal failure patient urine
REFERENCE       A35010
  #authors      Engelmann, H.; Novick, D.; Wallach, D.
  #journal      J. Biol. Chem. (1990) 265:1531-1536
  #title        Two tumor necrosis factor-binding proteins purified from
                  human urine. Evidence for immunological cross-reactivity
                  with cell surface tumor necrosis factor receptors.
  #cross-references MUID:90110215
  #accession    A35010
    ##molecule_type protein
    ##residues      41-45 ##label ENG
    ##experimental_source normal urine
REFERENCE       JC2404
  #authors      Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
  #journal      Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
  #title        Amino acid sequence of natural tumor necrosis factor alpha
                  inhibitor purified from human urine.
  #accession    JC2404
    ##molecule_type protein
    ##residues      41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
                     ##label KAJ
    ##experimental_source urine
COMMENT     This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
GENETICS
  #gene         GDB:TNFR1
    ##cross-references GDB:125913; OMIM:191190
  #map_position 12p13.2-12p13.2
  #introns      13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                  receptor repeat homology
KEYWORDS        duplication; glycoprotein; receptor; transmembrane protein
FEATURE
  1-21              #domain signal sequence #status predicted #label SIG\
  22-455            #product tumor necrosis factor receptor type 1 #status
                      predicted #label MAT\
  30-211            #domain extracellular #status predicted #label EXT\
  41-201            #product TNF binding protein 1 (tumor necrosis factor
                      alpha inhibitor) #status experimental #label TBP1\
  44-82             #domain NGF receptor repeat homology #label NG1\
  84-126            #domain NGF receptor repeat homology #label NG2\
  127-167           #domain NGF receptor repeat homology #label NG3\
  168-196           #domain NGF receptor repeat homology #label NG4\
  212-234           #domain transmembrane #status predicted #label MEM\
  235-455           #domain intracellular #status predicted #label INT\
  54,145,151        #binding_site carbohydrate (Asn) (covalent) #status
                      predicted
SUMMARY         #length 455  #molecular-weight 50494  #checksum 153

  Query Match           56.4%;  Score 1124;  DB 1;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 2.23e-230;
  Matches  142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCTCHAGFFLRENECVSCS 183
           |||||||||||||||||||||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    3
ENTRY           1EXTA      #type complete

TITLE           tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE       extracellular domain of the 55kda tumor necrosis factor
                  receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM        #formal_name Homo sapiens #common_name man
  #note         expressed in Escherichia coli, the construct contains
                  residues 12 to 172 of the mature sequence of the entire
                  receptor. residue 11 is mutated to met as a result of the
                  expression system
REFERENCE       A65560
  #authors      Naismith, J.H.; Sprang, S.R.
  #submission   submitted to the Brookhaven Protein Data Bank, July 1996
  #cross-references PDB:1EXT
REFERENCE       TN026248
  #authors      Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
  #journal      J. Biol. Chem. (1995) 270:13303
  #title        Crystallographic evidence for dimerization of unliganded
                  tumor necrosis factor receptor.
REFERENCE       TN026249
  #authors      Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                  K.; Naismith, J.H.; Sprang, S.R.
  #journal      J. Mol. Biol. (1994) 239:332
  #title        Two crystal forms of the extracellular domain of type i tumor
                  necrosis factor receptor.
REFERENCE       A40737
  #authors      Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
  #journal      Cell (1993) 73:431-445
  #title        Crystal structure of the soluble human 55 kd TNF
                  receptor-human TNFbeta complex: implications for TNF
                  receptor activation.
COMMENT     Resolution: 1.85 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS        binding protein; cytokine; signalling protein
FEATURE
  66-68             #region helix (right hand 3-10)\
  141-143           #region helix (right hand 3-10)\
  151-154           #region helix (right hand alpha)\
  7-9,17-19         #region beta sheet\
  131-134,137-140   #region beta sheet\
  25-29,39-42       #region beta sheet\
  71-74,83-85       #region beta sheet\
  90-96,99-104      #region beta sheet\
  111-115,124-127   #region beta sheet\
  3-17              #disulfide_bonds\
  18-31             #disulfide_bonds\
  21-40             #disulfide_bonds\
  43-58             #disulfide_bonds\
  61-76             #disulfide_bonds\
  64-84             #disulfide_bonds\
  86-102            #disulfide_bonds\
  105-117           #disulfide_bonds\
  108-125           #disulfide_bonds\
  127-138           #disulfide_bonds\
```

```
   141-154            #disulfide_bonds\
   144-150            #disulfide_bonds
SUMMARY           #length 160  #molecular-weight 18065  #checksum 2297

  Query Match           56.1%;  Score 1118;  DB 5;  Length 160;
  Best Local Similarity  99.3%;  Pred. No. 5.83e-229;
  Matches   141;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     24 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 83

Db     61 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     84 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 143

Db    121 QNTVCTCHAGFFLRENECVSCS 142
          |||||||||||||||||||||:
Qy    144 QNTVCTCHAGFFLRENECVSCA 165


RESULT    4
ENTRY             1NCFB      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain B - hu
ALTERNATE_NAMES   stnfr1; type i receptor
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029041
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   2-16               #disulfide_bonds\
   17-30              #disulfide_bonds\
   20-39              #disulfide_bonds\
   42-57              #disulfide_bonds\
   60-75              #disulfide_bonds\
   63-83              #disulfide_bonds\
   85-101             #disulfide_bonds\
   104-116            #disulfide_bonds\
   107-124            #disulfide_bonds\
   126-137            #disulfide_bonds
SUMMARY           #length 142  #molecular-weight 16046  #checksum 1225

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  Best Local Similarity  99.3%;  Pred. No. 5.14e-228;
  Matches   140;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db     61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db    121 NTVCTCHAGFFLRENECVSCS 141
          |||||||||||||||||||||:
Qy    145 NTVCTCHAGFFLRENECVSCA 165


RESULT    5
ENTRY             1TNRR      #type complete

TITLE             tumor necrosis factor receptor type 1 (P55 extracellular
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          recombinant form expressed in Baculovirus SF9
REFERENCE         A52442
   #authors       Banner, D.W.
   #submission    submitted to the Brookhaven Protein Data Bank, May 1994
   #cross-references PDB:1TNR
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
REFERENCE         TN034093
   #authors       D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
                    Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
                    Lesslauer, W.
   #journal       J. Mol. Biol. (1993) 229:555
   #title         Crystallization and preliminary analysis of tnf-beta and a
                    tnf-beta-55 kd tnf receptor complex.
COMMENT     Resolution: 2.85 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS          Complex(lymphokineRECEPTOR)
FEATURE
   1-15               #disulfide_bonds\
   16-29              #disulfide_bonds\
   19-38              #disulfide_bonds\
   41-56              #disulfide_bonds\
   59-74              #disulfide_bonds\
   62-82              #disulfide_bonds\
   84-100             #disulfide_bonds\
   103-115            #disulfide_bonds\
   106-123            #disulfide_bonds\
   125-136            #disulfide_bonds
SUMMARY           #length 139  #molecular-weight 15746  #checksum 5235

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  Best Local Similarity 100.0%;  Pred. No. 6.85e-226;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db     61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db    121 TVCTCHAGFFLRENECVSC 139
          |||||||||||||||||||
Qy    146 TVCTCHAGFFLRENECVSC 164


RESULT    6
ENTRY             1NCFA      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain A - hu
ALTERNATE_NAMES   stnfr1; type i receptor
```

```
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029039
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   5-19                #disulfide_bonds\
   20-33               #disulfide_bonds\
   23-42               #disulfide_bonds\
   45-60               #disulfide_bonds\
   63-78               #disulfide_bonds\
   66-86               #disulfide_bonds\
   88-104              #disulfide_bonds\
   107-119             #disulfide_bonds\
   110-127             #disulfide_bonds\
   129-140             #disulfide_bonds
SUMMARY           #length 140  #molecular-weight 15889  #checksum 6622

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  Best Local Similarity 100.0%;  Pred. No. 3.08e-224;
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Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENEC 140
          |||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENEC 161


RESULT    7
ENTRY             JC4302     #type complete

TITLE             tumor necrosis factor receptor p55 - pigORGANISM        #formal_name S
DATE              29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                    12-Dec-1997
ACCESSIONS        JC4302; PC4093
REFERENCE         JC4302
   #authors       Suter, B.; Pauli, U.
   #journal       Gene (1995) 163:263-266
   #title         Cloning of the cDNA encoding the porcine p55 tumor necrosis
                    factor receptor.
   #accession     JC4302
      ##molecule_type mRNA
      ##residues      1-461 ##label SUT
      ##cross-references GB:U19994; NID:g1141752; PID:g1141753
   #accession     PC4093
      ##molecule_type protein
      ##residues      1-7 ##label SU2
      ##experimental_source kidney cell line 15
GENETICS
   #gene          tnfr
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
   1-29               #domain signal sequence #status predicted #label SIG\
   30-461             #product tumor necrosis factor receptor p55 #status
                        predicted #label MAT\
   44-194             #domain extracellular cysteine rich #status predicted
                        #label EXT\
   44-82              #domain NGF receptor repeat homology #label NG1\
   211-231            #domain transmembrane #status predicted #label TMM\
   361-447            #domain signal transduction #status predicted #label
                        SIT\
   54,145,151         #binding_site carbohydrate (Asn) (covalent) #status
                        predicted
SUMMARY           #length 461  #molecular-weight 50696  #checksum 8079

  Query Match           48.2%;  Score 962;  DB 2;  Length 461;
  Best Local Similarity 69.8%;  Pred. No. 3.26e-192;
  Matches   120;  Conservative   22;  Mismatches  26;  Indels   4;  Gaps   4;

Db     41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|:|||||| |||| ||||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |||||| ||:|||||:||||||||||||||| |||| ||||:||||| ||||:|:| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQDTICNCHSGFFLRDKECVSCVNCKNADCKNLCPATSETRNDFQDTGTTVL 212
          ||:|:| ||:|||||::|||||     : | : | :  |    | : |: :|
Qy    143 KQNTVCTCHAGFFLRENECVSCAG-AAPGCPE-C-TLQENPF-FSQPGAPIL 190


RESULT    8
ENTRY             I57826     #type complete

TITLE             tumor necrosis factor receptor - mouseORGANISM         #formal_name
DATE              02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                    23-May-1997
ACCESSIONS        I57826
REFERENCE         I57826
   #authors       Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
                    Steinmetz, M.
   #journal       Mol. Immunol. (1993) 30:165-176
   #title         Genomic organization and promoter function of the murine
                    tumor necrosis factor receptor beta gene.
   #cross-references MUID:93156721
   #accession     I57826
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-454 ##label RES
      ##cross-references GB:M76656; NID:g202100; PID:g202102
GENETICS
   #gene          TNFR-2
   #introns       13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          cytokine receptor
SUMMARY           #length 454  #molecular-weight 50030  #checksum 4267

  Query Match           42.2%;  Score 841;  DB 2;  Length 454;
  Best Local Similarity 70.6%;  Pred. No. 7.05e-164;
  Matches   101;  Conservative   23;  Mismatches  19;  Indels   0;  Gaps   0;

Db     41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
```

```
          ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 TQNTVCNCHAGFFLRESECVPCS 183
           ||||| |||||||||:|||:|:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    9
ENTRY             GQMST1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    05-Sep-1997
ACCESSIONS        A38634; B40254; S16677; S19021; I54532
REFERENCE         A38634
   #authors       Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
                    G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
   #title         Cloning and expression of cDNAs for two distinct murine tumor
                    necrosis factor receptors demonstrate one receptor is
                    species specific.
   #cross-references MUID:91187885
   #accession     A38634
      ##molecule_type mRNA
      ##residues       1-454 ##label LEW
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         A40254
   #authors       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
                    C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
   #journal       Mol. Cell. Biol. (1991) 11:3020-3026
   #title         Molecular cloning and expression of the type 1 and type 2
                    murine receptors for tumor necrosis factor.
   #cross-references MUID:91246168
   #accession     B40254
      ##molecule_type mRNA
      ##residues       1-454 ##label GO2
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         S16677
   #authors       Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis,
                    A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
   #journal       Eur. J. Immunol. (1991) 21:1649-1656
   #title         Cloning, expression and cross-linking analysis of the murine
                    p55 tumor necrosis factor receptor.
   #cross-references MUID:91285014
   #accession     S16677
      ##molecule_type mRNA
      ##residues       1-454 ##label BAR
      ##cross-references EMBL:X59238; NID:g53578; PID:g53579
REFERENCE         S19021
   #authors       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
   #journal       Immunogenetics (1991) 34:338-340
   #title         Molecular cloning and expression of the mouse Tnf receptor
                    type b.
   #cross-references MUID:92039815
   #accession     S19021
      ##molecule_type mRNA
      ##residues       1-454 ##label ROT
      ##cross-references EMBL:X57796; NID:g54848; PID:g54849
REFERENCE         I54532
   #authors       Bebo, B.F.
   #journal       Immunogenetics (1994) 39:450-451
   #title         Nucleotide sequence of the TNF type I receptor from a mouse
                    endothelioma cell line.
   #cross-references MUID:94245292
   #accession     I54532
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-454 ##label RES
      ##cross-references GB:L26349; NID:g430732; PID:g430733
COMMENT     This protein is one of two distantly related receptors for both
              TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                 #domain signal sequence #status predicted #label SIG\
   30-454               #product tumor necrosis factor receptor type 1 #status
                          predicted #label MAT\
   30-212               #domain extracellular #status predicted #label EXT\
   44-82                #domain NGF receptor repeat homology #label NG1\
   84-126               #domain NGF receptor repeat homology #label NG2\
   127-167              #domain NGF receptor repeat homology #label NG3\
   168-204              #domain NGF receptor repeat homology #label NG4\
   213-235              #domain transmembrane #status predicted #label MEM\
   236-454              #domain intracellular #status predicted #label INT\
   54,151,202           #binding_site carbohydrate (Asn) (covalent) #status
                          predicted
SUMMARY           #length 454  #molecular-weight 50129  #checksum 4839

  Query Match           42.2%;  Score 841;  DB 1;  Length 454;
  Best Local Similarity  70.6%;  Pred. No. 7.05e-164;
  Matches   101;  Conservative   23;  Mismatches  19;  Indels   0;  Gaps   0;

Db      41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
           ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 TQNTVCNCHAGFFLRESECVPCS 183
           ||||| |||||||||:|||:|:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   10
ENTRY             GQRTT1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
                    05-Sep-1997
ACCESSIONS        B36555
REFERENCE         A36555
   #authors       Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                    Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                    Stratowa, C.; Adolf, G.R.
   #journal       DNA Cell Biol. (1990) 9:705-715
   #title         Molecular cloning and expression of human and rat tumor
                    necrosis factor receptor chain (p60) and its soluble
                    derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
   #accession     B36555
      ##molecule_type mRNA
      ##residues       1-461 ##label HIM
      ##cross-references GB:M63122; NID:g207361; PID:g207362
COMMENT     This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                 #domain signal sequence #status predicted #label SIG\
   30-461               #product tumor necrosis factor receptor type 1 #status
                          predicted #label MAT\
   30-211               #domain extracellular #status predicted #label EXT\
   30-201               #product tumor necrosis factor binding protein #status
                          predicted #label TBP\
   44-82                #domain NGF receptor repeat homology #label NG1\
   84-126               #domain NGF receptor repeat homology #label NG2\
   127-167              #domain NGF receptor repeat homology #label NG3\
   168-204              #domain NGF receptor repeat homology #label NG4\
   212-234              #domain transmembrane #status predicted #label MEM\
```

```
   235-461           #domain intracellular #status predicted #label INT\
   54,151,201        #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
SUMMARY          #length 461  #molecular-weight 50969  #checksum 1617

  Query Match           40.6%;  Score 809;  DB 1;  Length 461;
  Best Local Similarity  68.5%;  Pred. No. 2.05e-156;
  Matches    98;  Conservative   21;  Mismatches  24;  Indels   0;  Gaps   0;

Db     41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
          |::|||||| || |||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  ||||| |||||:|  | ||||||:|||:::| ||  ||| :|| |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCNCHAGFFLSGNECTPCS 183
          |||||| |||||||  ||| :|:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   11
ENTRY            TTHUAP     #type complete

TITLE            glycoprotein hormones alpha chain precursor - humanALTERNATE_NAMES  cho
                   alpha chain; follitropin alpha chain; interstitial
                   cell-stimulating hormone alpha chain; luteinizing hormone
                   alpha chain; lutropin alpha chain; thyroid-stimulating
                   hormone alpha chain; thyrotropin alpha chain
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             13-Jul-1981 #sequence_revision 23-Oct-1981 #text_change
                   05-Sep-1997
ACCESSIONS       A93213; A92832; B92303; A90751; A90179; A91461; A92184;
                   A94552; B92181; A92141; I58200; A01481
REFERENCE        A93213
   #authors      Fiddes, J.C.; Goodman, H.M.
   #journal      Nature (1979) 281:351-356
   #title        Isolation, cloning and sequence analysis of the cDNA for the
                   alpha-subunit of human chorionic gonadotropin.
   #cross-references MUID:80011660
   #accession    A93213
      ##molecule_type mRNA
      ##residues      1-116 ##label FID
      ##cross-references GB:V00518; NID:g31868; PID:g31869
REFERENCE        A92832
   #authors      Fiddes, J.C.; Goodman, H.M.
   #journal      J. Mol. Appl. Genet. (1981) 1:3-18
   #title        The gene encoding the common alpha subunit of the four human
                   glycoprotein hormones.
   #cross-references MUID:82267643
   #accession    A92832
      ##molecule_type DNA
      ##residues      1-98 ##label FI2
      ##cross-references GB:V00484
REFERENCE        A92303
   #authors      Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
   #journal      J. Biol. Chem. (1981) 256:1816-1823
   #title        The amino acid sequences of the prepeptides contained in the
                   alpha and beta subunits of human choriogonadotropin.
   #cross-references MUID:81117268
   #accession    B92303
      ##molecule_type protein
      ##residues      1-24 ##label BIR
      ##note          restriction endonuclease evidence indicates that a
                       single gene codes for the alpha chain common to the
                       four dimeric hormones: thyrotropin, lutropin,
                       follitropin, and choriogonadotropin
      ##note          previously the mature alpha chain (residues 25-116) was
                       isolated from each of the hormones and its sequence
                       was determined, as documented below
REFERENCE        A90751
   #authors      Sairam, M.R.; Li, C.H.
   #journal      Can. J. Biochem. (1977) 55:755-760
   #title        Human pituitary thyrotropin. The primary structure of the
                   alpha and beta subunits.
   #cross-references MUID:77243687
   #accession    A90751
      ##molecule_type protein
      ##residues      28-107,'SC',110-116 ##label SAI
REFERENCE        A90179
   #authors      Sairam, M.R.; Papkoff, H.; Li, C.H.
   #journal      Biochem. Biophys. Res. Commun. (1972) 48:530-537
   #title        Human pituitary interstitial cell stimulating hormone:
                   primary structure of the alpha subunit.
   #cross-references MUID:72242988
   #accession    A90179
      ##molecule_type protein
      ##residues      28-107,'SC',110-116 ##label SA2
REFERENCE        A91461
   #authors      Keutmann, H.T.; Williams, R.M.; Bishop, W.H.; Ryan, R.J.
   #journal      Fed. Proc. (1978) 37:1828
   #title        Structure of human luteninizing hormone.
   #accession    A91461
      ##molecule_type protein
      ##residues      28-116 ##label KEU
REFERENCE        A92184
   #authors      Rathnam, P.; Saxena, B.B.
   #journal      J. Biol. Chem. (1975) 250:6735-6746
   #title        Primary amino acid sequence of follicle-stimulating hormone
                   from human pituitary glands.
   #cross-references MUID:76005558
   #accession    A92184
      ##molecule_type protein
      ##residues      25-28,'E',30-116 ##label RAT
REFERENCE        A94552
   #authors      Shome, B.; Parlow, A.F.
   #submission   submitted to the Atlas, April 1975
   #accession    A94552
      ##molecule_type protein
      ##residues      28-116 ##label SHO
REFERENCE        A92181
   #authors      Morgan, F.J.; Birken, S.; Canfield, R.E.
   #journal      J. Biol. Chem. (1975) 250:5247-5258
   #title        The amino acid sequence of human chorionic gonadotropin. The
                   alpha subunit and beta subunit.
   #cross-references MUID:75211304
   #accession    B92181
      ##molecule_type protein
      ##residues      25-116 ##label MOR
      ##note          heterogeneity is found at the amino end. Approximately
                       10 and 30% of the chains lack residues 1-2 and 1-3,
                       respectively
REFERENCE        A92141
   #authors      Bellisario, R.; Carlsen, R.B.; Bahl, O.P.
   #journal      J. Biol. Chem. (1973) 248:6796-6809
   #title        Human chorionic gonadotropin. Linear amino acid sequence of
                   the alpha subunit.
   #cross-references MUID:74011266
   #accession    A92141
      ##molecule_type protein
      ##residues      25-116 ##label BEL
REFERENCE        A92760
   #authors      Shome, B.; Parlow, A.F.
   #journal      J. Clin. Endocrinol. Metab. (1974) 39:199-202
   #title        Human follicle stimulating hormone (hFSH): first proposal for
                   the amino acid sequence of the alpha-subunit (hFSHalpha)
                   and first demonstration of its identity with the
                   alpha-subunit of human luteinizing hormone (hLHalpha).
   #cross-references MUID:74262937
   #contents     annotation
REFERENCE        A90632
   #authors      Fujiki, Y.; Rathnam, P.; Saxena, B.B.
   #journal      Biochim. Biophys. Acta (1980) 624:428-435
   #title        Studies on the disulfide bonds in human pituitary
                   follicle-stimulating hormone.
```

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   #cross-references MUID:81021713
   #contents      annotation; preliminary disulfide bonds
REFERENCE         A44674
   #authors       Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                    J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                    N.W.
   #journal       Nature (1994) 369:455-461
   #title         Crystal structure of human chorionic gonadotropin.
   #contents      annotation; X-ray crystallography, 3.0 angstroms; correction
                    of disulfide bonds
REFERENCE         I58200
   #authors       Miyoshi, I.; Kasai, N.; Hayashizaki, Y.
   #journal       Nippon Rinsho (1994) 52:940-947
   #title         [Structure and regulation of human thyroid-stimulating
                    hormone (TSH) gene].
   #cross-references MUID:94254248
   #accession     I58200
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-116 ##label RES
      ##cross-references GB:S70585; NID:g546844; PID:g546845
GENETICS
   #gene          GDB:CGA
      ##cross-references GDB:119774; OMIM:118850
   #map_position 6q14-6q21
   #introns       30/1; 91/3
CLASSIFICATION    #superfamily glycoprotein hormones alpha chain
KEYWORDS          glycoprotein; heterodimer; hormone; pituitary
FEATURE
   1-24                #domain signal sequence #status experimental #label SIG\
   25-116              #product glycoprotein hormones alpha chain #status
                         experimental #label MAT\
   31-55,34-84,52-106,
   56-108,83-111       #disulfide_bonds #status experimental\
   76,102              #binding_site carbohydrate (Asn) (covalent) #status
                         experimental
SUMMARY           #length 116  #molecular-weight 13075  #checksum 1664

  Query Match             33.5%;  Score 667;  DB 1;  Length 116;
  Best Local Similarity  93.5%;  Pred. No. 1.71e-123;
  Matches    86;  Conservative    1;  Mismatches   5;  Indels   0;  Gaps   0;

Db      25 APDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC 84
           |     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     165 AGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC 224

Db      85 VAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 116
           ||||||||||||||||||:||||||||||||
Qy     225 VAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT   12
ENTRY             1HRPA       #type complete

TITLE             chorionic gonadotropin, chain A - humanORGANISM          #formal_name Ho
   #note          placental origin, urinary extracted
REFERENCE         A52806
   #authors       Lapthorn, A.J.; Harris, D.C.; Isaacs, N.W.
   #submission    submitted to the Brookhaven Protein Data Bank, August 1994
   #cross-references PDB:1HRP
REFERENCE         TN022062
   #authors       Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                    J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                    N.W.
   #journal       Nature (1994) 369:455
   #title         Crystal structure of human chorionic gonadotropin.
REFERENCE         TN022063
   #authors       Harris, D.C.; Machin, K.J.; Evin, G.M.; Morgan, F.J.; Isaacs,
                    N.W.
   #journal       J. Biol. Chem. (1989) 264:6705
   #title         Preliminary x-ray diffraction analysis of human chorionic
                    gonadotropin.
COMMENT     Resolution: 3.0 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS          hormone
FEATURE
   4-28                #disulfide_bonds\
   7-57                #disulfide_bonds\
   25-79               #disulfide_bonds\
   29-81               #disulfide_bonds\
   56-84               #disulfide_bonds
SUMMARY           #length 86  #molecular-weight 9572  #checksum 1371

  Query Match             32.4%;  Score 647;  DB 5;  Length 86;
  Best Local Similarity  95.3%;  Pred. No. 6.89e-119;
  Matches    82;  Conservative    2;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 TQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 60
           : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     168 APGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 227

Db      61 SYNRVTVMGGFKVENHTACHCSTCYY 86
           ||||||||||||||||||:||||||||
Qy     228 SYNRVTVMGGFKVENHTGCHCSTCYY 253


RESULT   13
ENTRY             1XULA       #type complete

TITLE             chorionic gonadotropin, chain A - humanPDB_TITLE          theoretical
                    receptor complexed with human chorionic gonadotropin
ORGANISM          #formal_name Homo sapiens #common_name man
REFERENCE         A66957
   #authors       Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                    Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #submission    submitted to the Brookhaven Protein Data Bank, December 1996
   #cross-references PDB:1XUL
REFERENCE         TN032623
   #authors       Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                    Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #journal       Structure (London) (1996) 3:1341
   #title         Structural predictions for the ligand-binding region of
                    glycoprotein hormone receptors and the nature of
                    hormone-receptor interactions structure.
REFERENCE         TN032624
   #authors       Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                    Hendrickson, W.A.
   #journal       Structure (London) (1994) 2:545
   #title         Structure of human chorionic gonadotropin at 2.6 a resolution
                    from mad analysis of the selenomethionyl protein.
COMMENT     Resolution: not applicable
COMMENT     Determination: theoretical model
KEYWORDS          complex; glycoprotein hormone receptor glycoprotein; hormone;
                    phosphorylation; receptor
FEATURE
   37-41               #region helix (right hand alpha)\
   7-10,22-25          #region beta sheet\
   49-53,26-34         #region beta sheet\
   61-65,71-75         #region beta sheet\
   55-60,77-81         #region beta sheet\
   3-27                #disulfide_bonds\
   6-56                #disulfide_bonds\
   24-78               #disulfide_bonds\
   28-80               #disulfide_bonds\
   55-83               #disulfide_bonds
SUMMARY           #length 85  #molecular-weight 9471  #checksum 9656

  Query Match             32.3%;  Score 645;  DB 5;  Length 85;
  Best Local Similarity  98.8%;  Pred. No. 1.99e-118;
  Matches    82;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db       3 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     171 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230

Db      63 RVTVMGGFKVENHTACHCSTCYY 85
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          ||||||||||||||:||||||||
Qy    231 RVTVMGGFKVENHTGCHCSTCYY 253


RESULT   14
ENTRY             1HCNA      #type complete

TITLE             Human chorionic gonadotropin, chain A - humanORGANISM         #formal_n
REFERENCE         A52587
   #authors       Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                    Hendrickson, W.A.
   #submission    submitted to the Brookhaven Protein Data Bank, July 1994
   #cross-references PDB:1HCN
REFERENCE         TN020262
   #authors       Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                    Hendrickson, W.A.
   #journal       Structure (1994) 2:545
   #title         Structure of human chorionic gonadotropin at 2.6 angstroms
                    resolution from mad analysis of the selenomethionyl
                    protein.
COMMENT     Resolution: 2.6 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS          Hormone
FEATURE
   36-43               #region helix (right hand alpha)\
   4-11,21-28          #region beta sheet\
   29-35,48-54         #region beta sheet\
   3-27                #disulfide_bonds\
   6-56                #disulfide_bonds\
   24-78               #disulfide_bonds\
   28-80               #disulfide_bonds\
   55-83               #disulfide_bonds
SUMMARY           #length 85  #molecular-weight 9471  #checksum 9656

  Query Match            32.3%;  Score 645;  DB 5;  Length 85;
  Best Local Similarity  98.8%;  Pred. No. 1.99e-118;
  Matches    82;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      3 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    171 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230

Db     63 RVTVMGGFKVENHTACHCSTCYY 85
          |||||||||||||:||||||||
Qy    231 RVTVMGGFKVENHTGCHCSTCYY 253


RESULT   15
ENTRY             A39555     #type complete

TITLE             glycoprotein hormones alpha chain precursor - rhesus macaqueORGANISM
DATE              08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change
                    13-Jan-1995
ACCESSIONS        A39555
REFERENCE         A39555
   #authors       Golos, T.G.; Durning, M.; Fisher, J.M.
   #journal       DNA Cell Biol. (1991) 10:367-380
   #title         Molecular cloning of the rhesus glycoprotein hormone
                    alpha-subunit gene.
   #cross-references MUID:91321740
   #accession     A39555
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type DNA
      ##residues      1-120 ##label GOL
CLASSIFICATION    #superfamily glycoprotein hormones alpha chain
KEYWORDS          glycoprotein
SUMMARY           #length 120  #molecular-weight 13785  #checksum 5074

  Query Match            27.6%;  Score 551;  DB 2;  Length 120;
  Best Local Similarity  83.5%;  Pred. No. 6.48e-97;
  Matches    71;  Conservative    4;  Mismatches  10;  Indels   0;  Gaps   0;

Db     35 CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94

          ||||  :|| ||| ||||| ||||||||||||:||||||||||||||||||||||
Qy    171 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230

Db     95 RVMVMGSVRVENHTECHCSTCYYHK 119
          || |||: :|||||  ||||||||||
Qy    231 RVTVMGGFKVENHTGCHCSTCYYHK 255

Search completed: Wed May  6 08:50:40 1998
Job time : 39 secs.
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FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      362    447       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD     86     86       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
SQ   SEQUENCE   461 AA;  50696 MW;  8E2C350A CRC32;

  Query Match           48.2%;  Score 962;  DB 1;  Length 461;
  Best Local Similarity  69.8%;  Pred. No. 3.53e-226;
  Matches   120;  Conservative   22;  Mismatches  26;  Indels   4;  Gaps   4;

Db     41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|:|||||| |||| |||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |||||| ||:|||||:|||||||||||||||| |||| ||||:||||| ||||:|:| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQDTICNCHSGFFLRDKECVSCVNCKNADCKNLCPATSETRNDFQDTGTTVL 212
          ||:|:| ||:||||||::||||||     : | : | :  |    | : |: :|
Qy    143 KQNTVCTCHAGFFLRENECVSCAG-AAPGCPE-C-TLQENPF-FSQPGAPIL 190


RESULT    3
ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL   MOL. CELL. BIOL. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL   EUR. J. IMMUNOL. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL   IMMUNOGENETICS 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RL   IMMUNOGENETICS 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL   MOL. IMMUNOL. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M60468; G199826; -.
DR   EMBL; M59377; G202097; -.
DR   EMBL; X59238; G53579; -.
DR   EMBL; X57796; G54849; -.
DR   EMBL; L26349; G430733; -.
DR   EMBL; M76656; G202102; -.
DR   EMBL; M88067; G202102; JOINED.
DR   EMBL; M76655; G202102; JOINED.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1TNR.
DR   MGD; MGI:98781; TNFR1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235       POTENTIAL.
FT   DOMAIN      236    454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      356    441       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    202    202       POTENTIAL.
FT   CONFLICT    394    394       R -> G (IN REF. 6).
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SQ   SEQUENCE   454 AA;  50129 MW;  4B6EEC09 CRC32;

  Query Match           42.2%;  Score 841;  DB 1;  Length 454;
  Best Local Similarity  70.6%;  Pred. No. 8.77e-193;
  Matches   101;  Conservative   23;  Mismatches  19;  Indels   0;  Gaps   0;

Db     41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 TQNTVCNCHAGFFLRESECVPCS 183
          ||||| |||||||||:|||:|:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    4
ID   TNR1_RAT       STANDARD;      PRT;   461 AA.
AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M63122; G207362; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      363    448       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    201    201       POTENTIAL.
SQ   SEQUENCE   461 AA;  50969 MW;  82F68B08 CRC32;

  Query Match           40.6%;  Score 809;  DB 1;  Length 461;
  Best Local Similarity  68.5%;  Pred. No. 5.45e-184;
  Matches    98;  Conservative   21;  Mismatches  24;  Indels   0;  Gaps   0;

Db     41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
          |::|||||| || |||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  ||||| ||||||:|  | ||||||:|||:::| ||  ||| :|| |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCNCHAGFFLSGNECTPCS 183
          |||||| |||||||  ||| :|:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    5
ID   GLHA_HUMAN     STANDARD;      PRT;   116 AA.
AC   P01215;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 80011660.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 281:351-356(1979).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94254248.
RA   MIYOSHI I., KASAI N., HAYASHIZAKI Y.;
RL   NIPPON RINSHO 52:940-947(1994).
RN   [3]
RP   SEQUENCE OF 1-98 FROM N.A.
RX   MEDLINE; 82267643.
RA   FIDDES J.C., GOODMAN H.M.;
RL   J. MOL. APPL. GENET. 1:3-18(1981).
RN   [4]
RP   SEQUENCE OF 1-24.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 77243687.
RA   SAIRAM M.R., LI C.H.;
RL   CAN. J. BIOCHEM. 55:755-760(1977).
RN   [6]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 72242988.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 48:530-537(1972).
RN   [7]
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RP   SEQUENCE, AND REVISIONS.
RA   KEUTMANN H.T., WILLIAMS R.M., BISHOP W.H., RYAN R.J.;
RL   FED. PROC. 37:1828-1828(1978).
RN   [8]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 76005558.
RA   RATHNAM P., SAXENA B.B.;
RL   J. BIOL. CHEM. 250:6735-6746(1975).
RN   [9]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 74262937.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 39:199-202(1974).
RN   [10]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 75211304.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [11]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 74011266.
RA   BELLISARIO R., CARLSEN R.B., BAHL O.P.;
RL   J. BIOL. CHEM. 248:6796-6809(1973).
RN   [12]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81021713.
RA   FUJIKI Y., RATHNAM P., SAXENA B.B.;
RL   BIOCHIM. BIOPHYS. ACTA 624:428-435(1980).
RN   [13]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81006887.
RA   MISE T., BAHL O.P.;
RL   J. BIOL. CHEM. 255:8516-8522(1980).
RN   [14]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 91122088.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
RN   [16]
RP   STRUCTURE BY NMR.
RX   MEDLINE; 97054614.
RA   DE BEER T., VAN ZUYLEN C.W.E.M., LEEFLANG B.R., HARD K., BOELENS R.,
RA   KAPTEIN R., KAMERLING J.P., VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 241:229-242(1996).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; J00152; G183319; -.
DR   EMBL; J00150; G183319; JOINED.
DR   EMBL; J00151; G183319; JOINED.
DR   EMBL; S70585; G546845; -.
DR   EMBL; S70583; G546845; JOINED.
DR   EMBL; S70584; G546845; JOINED.
DR   EMBL; V00518; G31869; -.
DR   EMBL; V00485; G669156; -.
DR   EMBL; V00486; G669156; JOINED.
DR   EMBL; V00487; G669156; JOINED.
DR   PIR; A01481; TTHUAP.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   MIM; 118850; -.
DR   MIM; 188530; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT   SIGNAL        1     24
FT   CHAIN        25    116       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     31     55
FT   DISULFID     34     84
FT   DISULFID     52    106
FT   DISULFID     56    108
FT   DISULFID     83    111
FT   CARBOHYD     63     63
FT   CARBOHYD     76     76
FT   CARBOHYD    102    102
FT   CONFLICT     29     29       Q -> E (IN REF. 8).
FT   CONFLICT    108    109       CS -> SC (IN REF. 5 AND 6).
SQ   SEQUENCE   116 AA;  13075 MW;  3BA19E2F CRC32;

  Query Match           33.5%;  Score 667;  DB 1;  Length 116;
  Best Local Similarity  93.5%;  Pred. No. 3.28e-145;
  Matches    86;  Conservative    1;  Mismatches   5;  Indels   0;  Gaps   0;

Db     25 APDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC 84
          |     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    165 AGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC 224

Db     85 VAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 116
          ||||||||||||||||||:||||||||||
Qy    225 VAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT    6
ID   GLHA_MACMU     STANDARD;      PRT;   120 AA.
AC   P22762;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   MACACA MULATTA (RHESUS MACAQUE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91321740.
RA   GOLOS T.G., DURNING M., FISHER J.M.;
RL   DNA CELL BIOL. 10:367-380(1991).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; A39555; A39555.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     67     67       BY SIMILARITY.
FT   CARBOHYD     80     80       BY SIMILARITY.
FT   CARBOHYD    106    106       BY SIMILARITY.
SQ   SEQUENCE   120 AA;  13785 MW;  85E1F9F4 CRC32;

  Query Match           27.6%;  Score 551;  DB 1;  Length 120;
  Best Local Similarity  83.5%;  Pred. No. 6.39e-114;
  Matches    71;  Conservative    4;  Mismatches  10;  Indels   0;  Gaps   0;

Db     35 CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94
          ||||  :|| ||| ||||| |||||||||||||:|||||||||||||||||||||
Qy    171 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230

Db     95 RVMVMGSVRVENHTECHCSTCYYHK 119
          || |||: :||||| ||||||||||
Qy    231 RVTVMGGFKVENHTGCHCSTCYYHK 255
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RESULT    7
ID   GLHA_BOVIN     STANDARD;      PRT;   120 AA.
AC   P01217;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84041490.
RA   GOODWIN R.G., MONCMAN C.L., ROTTMAN F.M., NILSON J.H.;
RL   NUCLEIC ACIDS RES. 11:6873-6882(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84024633.
RA   ERWIN C., CROYLE M.L., DONELSON J., MAURER R.;
RL   BIOCHEMISTRY 22:4856-4860(1983).
RN   [3]
RP   SEQUENCE OF 8-133 FROM N.A.
RX   MEDLINE; 83161058.
RA   NILSON J.H., THOMASON A.R., CSERBAK M.T., MONCMAN C.L., WOYCHIK R.P.;
RL   J. BIOL. CHEM. 258:4679-4682(1983).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 71111428.
RA   LIAO T.-H., PIERCE J.G.;
RL   J. BIOL. CHEM. 246:850-865(1971).
RN   [5]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 71111429.
RA   PIERCE J.G., LIAO T.-H., CARLSEN R.B., REIMO T.;
RL   J. BIOL. CHEM. 246:866-872(1971).
RN   [6]
RP   SEQUENCE OF 80-91 AND 100-120.
RX   MEDLINE; 72012932.
RA   MAGHUIN-ROGISTER G., HENNEN G.P.;
RL   EUR. J. BIOCHEM. 21:489-497(1971).
RN   [7]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 74307752.
RA   CORNELL J.S., PIERCE J.G.;
RL   J. BIOL. CHEM. 249:4166-4174(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X00003; E274391; -.
DR   EMBL; X00004; E274391; JOINED.
DR   EMBL; X00050; G607; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A05132; A05132.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80
FT   CARBOHYD    106    106
FT   CONFLICT     13     13       A -> T (IN REF. 2).
FT   CONFLICT     37     37       E -> Q (IN REF. 4).
FT   CONFLICT     52     52       P -> A (IN REF. 2).
FT   CONFLICT     84     87       EATC -> AZCT (IN REF. 6).
SQ   SEQUENCE   120 AA;  13616 MW;  99C153C5 CRC32;
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  Query Match           27.5%;  Score 548;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 4.06e-113;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | || :|| | ||| |||||||||||||| |||||||| ||:|||:|||||::
Qy     170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db      94 TKATVMGNVRVENHTECHCSTCYYHKS 120
              : ||||  :|||||  ||||||||||
Qy     230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT    8
ID   GLHA_SHEEP     STANDARD;      PRT;   120 AA.
AC   P01218;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   OVIS ARIES (SHEEP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90098887.
RA   BELLO P.A., MOUNTFORD P.S., BRANDON M.R., ADAMS T.E.;
RL   NUCLEIC ACIDS RES. 17:10494-10494(1989).
RN   [2]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 72211144.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., LAMKIN W.M., BAKER H.N.,
RA   WARD D.N.;
RL   J. BIOL. CHEM. 247:4351-4364(1972).
RN   [3]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 73190034.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:554-571(1972).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 82113052.
RA   SAIRAM M.R.;
RL   BIOCHEM. J. 197:535-539(1981).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RA   CHUNG D., SAIRAM M.R., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973).
RN   [6]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 91006170.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X16977; G1366; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A01484; UTSHA.
DR   PIR; S06935; S06935.
DR   PIR; S13200; S13200.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
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FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80
FT   CARBOHYD    106    106
FT   CONFLICT     27     27       D -> N (IN REF. 2).
FT   CONFLICT     29     29       E -> Q (IN REF. 2).
FT   CONFLICT     37     37       E -> Q (IN REF. 2 TO 4).
FT   CONFLICT    112    113       CS -> SC (IN REF. 3).
SQ   SEQUENCE   120 AA;  13588 MW;  13BA4DE1 CRC32;

  Query Match           27.5%;  Score 548;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 4.06e-113;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | || :|| | ||| ||||||||||||||| |||||||| ||:|||:||||||::
Qy     170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db      94 TKATVMGNVRVENHTECHCSTCYYHKS 120
             : ||||  :||||| ||||||||||
Qy     230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT    9
ID   GLHA_RABIT     STANDARD;      PRT;     96 AA.
AC   P07474;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN   CGA.
OS   ORYCTOLAGUS CUNICULUS (RABBIT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; LAGOMORPHA.
RN   [1]
RP   SEQUENCE.
RA   GLENN S.D., NAHM H.S., WARD D.N.;
RL   J. PROTEIN CHEM. 3:143-156(1984).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; A05096; A05096.
DR   HSSP; P01233; 1HRP.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID     11     35       BY SIMILARITY.
FT   DISULFID     14     64       BY SIMILARITY.
FT   DISULFID     32     86       BY SIMILARITY.
FT   DISULFID     36     88       BY SIMILARITY.
FT   DISULFID     63     91       BY SIMILARITY.
FT   CARBOHYD     56     56
FT   CARBOHYD     82     82
SQ   SEQUENCE   96 AA;  10663 MW;  CD56D255 CRC32;

  Query Match           27.4%;  Score 546;  DB 1;  Length 96;
  Best Local Similarity  76.7%;  Pred. No. 1.39e-112;
  Matches    69;  Conservative    6;  Mismatches  15;  Indels   0;  Gaps   0;

Db       7 AMQGCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVA 66
           |  ||||| | || :||  |||| |||||||||||||| |||||||| ||:|||:|||||
Qy     167 AAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVA 226

Db      67 KAFTKATVMGNAKVENHTECHCSTCYYHKS 96
             |:: : ||||  |||||| ||||||||||
Qy     227 KSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT   10
ID   GLH1_RAT       STANDARD;      PRT;   120 AA.
AC   P11962; P70516;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN 1 PRECURSOR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=PITUITARY;
RX   MEDLINE; 82214055.
RA   GODINE J.E., CHIN W.W., HABENER J.F.;
RL   J. BIOL. CHEM. 257:8368-8371(1982).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89196918.
RA   BURNSIDE J., BUCKLAND P.R., CHIN W.W.;
RL   GENE 70:67-74(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   ZOOL. SCI. 7:877-885(1990).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01252; G56580; -.
DR   EMBL; J00757; G206111; -.
DR   EMBL; M22829; -; NOT_ANNOTATED_CDS.
DR   EMBL; M25543; G204470; -.
DR   EMBL; M25544; G204471; -.
DR   EMBL; D00575; G220842; -.
DR   PIR; JT0408; TTRTA.
DR   PIR; S27385; S27385.
DR   HSSP; P01233; 1HRP.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN 1.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80       PROBABLE.
FT   CARBOHYD    106    106       PROBABLE.
FT   CONFLICT     84     84       E -> Q (IN G206111).
SQ   SEQUENCE   120 AA;  13453 MW;  5E507A0D CRC32;

  Query Match           27.3%;  Score 544;  DB 1;  Length 120;
  Best Local Similarity  78.2%;  Pred. No. 4.78e-112;
  Matches    68;  Conservative    6;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKSF 93
           ||||| | || :||  |||| |||||||||||||| |||||||| ||:|||:|||||||:
Qy     170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db      94 TKATVMGNARVENHTDCHCSTCYYHKS 120
             : ||||  :||||| ||||||||||
Qy     230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT   11
ID   GLHA_BALAC     STANDARD;      PRT;     96 AA.
AC   P37036;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN   CGA.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.
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RA   KARASEV V.S., PANKOV Y.A.;
RL   BIOKHIMIIA 50:1972-1986(1985).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; PN0138; PN0138.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID     11     35       BY SIMILARITY.
FT   DISULFID     14     64       BY SIMILARITY.
FT   DISULFID     32     86       BY SIMILARITY.
FT   DISULFID     36     88       BY SIMILARITY.
FT   DISULFID     63     91       BY SIMILARITY.
FT   CARBOHYD     56     56
FT   CARBOHYD     82     82
SQ   SEQUENCE   96 AA;  10720 MW;  E2CD30DF CRC32;

  Query Match           27.1%;  Score 541;  DB 1;  Length 96;
  Best Local Similarity  70.1%;  Pred. No. 3.03e-111;
  Matches    61;  Conservative   13;  Mismatches  13;  Indels   0;  Gaps   0;

Db     10 GCPZCKLKZBKYFSKLGAPIYZCMGCCFSRAYPTPARSKKTMLVPKNITSZATCCVAKAF 69
          |||:| | :: :||  |||| :|||||||||||||| |||||||| ||:||::||||||::
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db     70 TKATVMGBARVZNHTZCHCSTCYYHKS 96
          : ||||  :|:||| ||||||||||
Qy    230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT   12
ID   GLH2_RAT       STANDARD;      PRT;   120 AA.
AC   P11963;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN 2 PRECURSOR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 82214055.
RA   GODINE J.E., CHIN W.W., HABENER J.F.;
RL   J. BIOL. CHEM. 257:8368-8371(1982).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01253; G56583; -.
DR   PIR; S27386; S27386.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN 2.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80       PROBABLE.
FT   CARBOHYD    106    106       PROBABLE.
SQ   SEQUENCE   120 AA;  13565 MW;  4E4FAB2E CRC32;

  Query Match           27.1%;  Score 541;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 3.03e-111;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

, Db     34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
          ||||| | || :||  |||| |||||||||||||| |||||||| ||:|||:|||||::
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db     94 TKATVMGNARVENHTECHCSTCYYHKS 120
          : ||||  :||||| ||||||||||
Qy    230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT   13
ID   GLHA_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01216;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 82060239.
RA   CHIN W.W., KRONENBERG H.M., DEE P.C., MALOOF F., HABENER J.F.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:5329-5333(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89170115.
RA   GORDON D.F., WOOD W.M., RIDGWAY E.C.;
RL   DNA 7:679-690(1988).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; J00643; G202180; -.
DR   EMBL; V00852; G54799; -.
DR   EMBL; M22991; -; NOT_ANNOTATED_CDS.
DR   EMBL; M22992; G575520; -.
DR   PIR; A01482; TTMSA.
DR   PIR; A31598; A31598.
DR   HSSP; P01215; 1HCN.
DR   MGD; MGI:88390; CGA.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80       PROBABLE.
FT   CARBOHYD    106    106       PROBABLE.
SQ   SEQUENCE   120 AA;  13565 MW;  86F1F31A CRC32;

  Query Match           27.1%;  Score 541;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 3.03e-111;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db     34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
          ||||| | || :||  |||| |||||||||||||| |||||||| ||:|||:|||||::
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db     94 TKATVMGNARVENHTECHCSTCYYHKS 120
          : ||||  :||||| ||||||||||
Qy    230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT   14
ID   GLHA_PIG       STANDARD;      PRT;   120 AA.
AC   P01219;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
```

```
GN   CGA.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89325834.
RA   HIRAI T., TAKIKAWA H., KATO Y.;
RL   MOL. CELL. ENDOCRINOL. 63:209-217(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SEQUENCE OF 31-120.
RX   MEDLINE; 74075725.
RA   MAGHUIN-ROGISTER G., COMBARNOUS Y., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:255-263(1973).
RN   [4]
RP   PRELIMINARY SEQUENCE OF 25-120.
RA   CLOSSET J., MAGHUIN-ROGISTER G., HENNEN G.;
RL   ENDOCRINOL. EXP. 8:164(1974).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 75093922.
RA   COMBARNOUS Y., HENNEN G.;
RL   BIOCHEM. SOC. TRANS. 2:915-917(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; D00768; G217699; -.
DR   EMBL; D00767; G217699; JOINED.
DR   PIR; A01485; UTPGA.
DR   PIR; A30339; A30339.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80
FT   CARBOHYD    106    106
SQ   SEQUENCE   120 AA;  13532 MW;  8749DBA5 CRC32;

  Query Match           27.1%;  Score 541;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 3.03e-111;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | || :||  |||| ||||||||||||||| |||||||| ||:|||:||||||::
Qy     170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db      94 TKATVMGNARVENHTECHCSTCYYHKS 120
             : ||||  :||||| ||||||||||
Qy     230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT   15
ID   GLHA_STRCA     STANDARD;      PRT;    96 AA.
AC   P80665;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
OS   STRUTHIO CAMELUS (OSTRICH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES;
OC   PALAEOGNATHAE; STRUTHIONIFORMES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 97025333.
RA   KOIDE Y., PAPKOFF H., KAWAUCHI H.;
RL   EUR. J. BIOCHEM. 240:262-267(1996).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID     11     35       BY SIMILARITY.
FT   DISULFID     14     64       BY SIMILARITY.
FT   DISULFID     32     86       BY SIMILARITY.
FT   DISULFID     36     88       BY SIMILARITY.
FT   DISULFID     63     91       BY SIMILARITY.
FT   CARBOHYD     56     56       POTENTIAL.
FT   CARBOHYD     82     82       POTENTIAL.
SQ   SEQUENCE   96 AA;  10781 MW;  DDF7B4BB CRC32;

  Query Match           27.0%;  Score 538;  DB 1;  Length 96;
  Best Local Similarity  74.7%;  Pred. No. 1.92e-110;
  Matches    65;  Conservative   10;  Mismatches  12;  Indels   0;  Gaps   0;

Db      10 GCPECKLGENRFFSKPGAPVYQCTGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKAF 69
           ||||| | || ||| ||||: || ||||||||||||||||||| ||:|||:||||||::
Qy     170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db      70 TKITLKDNVKIENHTECHCSTCYYHKS 96
             ::|::   |:|||| ||||||||||
Qy     230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


Search completed: Wed May  6 08:48:07 1998
Job time : 35 secs.
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:47:32 1998; MasPar time 7.91 Seconds
811.687 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150
Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 42.029; Variance 63.165; scale 0.665

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	56.4	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	3.58e-271
2	962	48.2	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	3.53e-226
3	841	42.2	454	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	8.77e-193
4	809	40.6	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	5.45e-184
5	667	33.5	116	1	GLHA_HUMAN	GLYCOPROTEIN HORMONES	3.28e-145
6	551	27.6	120	1	GLHA_MACMU	GLYCOPROTEIN HORMONES	6.39e-114
7	548	27.5	120	1	GLHA_BOVIN	GLYCOPROTEIN HORMONES	4.06e-113
8	548	27.5	120	1	GLHA_SHEEP	GLYCOPROTEIN HORMONES	4.06e-113
9	546	27.4	96	1	GLHA_RABIT	GLYCOPROTEIN HORMONES	1.39e-112
10	544	27.3	120	1	GLH1_RAT	GLYCOPROTEIN HORMONES	4.78e-112
11	541	27.1	96	1	GLHA_BALAC	GLYCOPROTEIN HORMONES	3.03e-111
12	541	27.1	120	1	GLH2_RAT	GLYCOPROTEIN HORMONES	3.03e-111
13	541	27.1	120	1	GLHA_MOUSE	GLYCOPROTEIN HORMONES	3.03e-111
14	541	27.1	120	1	GLHA_PIG	GLYCOPROTEIN HORMONES	3.03e-111
15	538	27.0	96	1	GLHA_STRCA	GLYCOPROTEIN HORMONES	1.92e-110
16	539	27.0	120	1	GLHA_CALJA	GLYCOPROTEIN HORMONES	1.04e-110
17	537	26.9	120	1	GLHA_MELGA	GLYCOPROTEIN HORMONES	3.55e-110
18	535	26.8	96	1	GLHA_PHYCA	GLYCOPROTEIN HORMONES	1.22e-109
19	507	25.4	118	1	GLH2_CYPCA	GLYCOPROTEIN HORMONES	3.54e-102
20	503	25.2	120	1	GLHA_EQUAS	GLYCOPROTEIN HORMONES	4.10e-101
21	501	25.1	96	1	GLHA_HORSE	GLYCOPROTEIN HORMONES	1.39e-100
22	500	25.1	118	1	GLHA_HYPMO	GLYCOPROTEIN HORMONES	2.57e-100
23	500	25.1	118	1	GLH1_CYPCA	GLYCOPROTEIN HORMONES	2.57e-100
24	500	25.1	118	1	GLHA_CTEID	GLYCOPROTEIN HORMONES	2.57e-100
25	499	25.0	116	1	GLHA_CLAGA	GLYCOPROTEIN HORMONES	4.73e-100
26	478	24.0	93	1	GLHA_MURCI	GLYCOPROTEIN HORMONES	1.74e-94
27	476	23.9	97	1	GLHA_RANCA	GLYCOPROTEIN HORMONES	5.90e-94
28	474	23.8	117	1	GLHA_ANGAN	GLYCOPROTEIN HORMONES	1.99e-93
29	448	22.5	114	1	GLH2_ONCKE	GLYCOPROTEIN HORMONES	1.43e-86
30	447	22.4	108	1	GLH1_ONCKE	GLYCOPROTEIN HORMONES	2.62e-86
31	427	21.4	94	1	GLHA_THUOB	GLYCOPROTEIN HORMONES	4.60e-81
32	424	21.3	117	1	GLHA_ACALA	GLYCOPROTEIN HORMONES	2.80e-80
33	377	18.9	125	1	GLHA_FUNHE	GLYCOPROTEIN HORMONES	4.56e-68
34	273	13.7	417	1	WSL1_HUMAN	WSL-1 PROTEIN PRECURSO	8.97e-42
35	231	11.6	435	1	TNRC_HUMAN	LYMPHOTOXIN-BETA RECEP	1.40e-31
36	225	11.3	325	1	VT2_SFVKA	TUMOR NECROSIS FACTOR	3.76e-30
37	221	11.1	326	1	VT2_MYXVL	TUMOR NECROSIS FACTOR	3.33e-29
38	215	10.8	415	1	TNRC_MOUSE	LYMPHOTOXIN-BETA RECEP	8.65e-28
39	214	10.7	349	1	VC22_VARV	PROTEIN C22/B28 HOMOLO	1.49e-27
40	212	10.6	474	1	TNR2_MOUSE	TUMOR NECROSIS FACTOR	4.37e-27
41	207	10.4	425	1	NGFR_RAT	LOW-AFFINITY NERVE GRO	6.44e-26
42	207	10.4	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GRO	6.44e-26
43	204	10.2	260	1	CD27_HUMAN	CD27L RECEPTOR PRECURS	3.21e-25
44	188	9.4	323	1	FASA_BOVIN	FASL RECEPTOR PRECURSO	1.52e-21
45	183	9.2	595	1	CD30_HUMAN	CD30L RECEPTOR PRECURS	2.06e-20

ALIGNMENTS

RESULT 1
ID TNR1_HUMAN STANDARD; PRT; 455 AA.
AC P19438;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
GN TNFR1 OR TNFAR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 90235285.
RA SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL CELL 61:361-370(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90235284.
RA LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA TABUCHI H., LESSLAUER W.;
RL CELL 61:351-359(1990).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE; 91006021.
RA NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA ADERKA D., HOLTMANN H., WALLACH D.;
RL EMBO J. 9:3269-3278(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91090841.
RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL DNA CELL BIOL. 9:705-715(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 91017509.
RA GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92250049.
RA FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;

```
RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RL   CELL 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KHONO H., SPRANG S.R.;
RL   STRUCTURE 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; X55313; G37224; -.
DR   EMBL; M33294; G339745; -.
DR   EMBL; M58286; G339754; -.
DR   EMBL; M63121; G339756; -.
DR   EMBL; M75866; G339750; -.
DR   EMBL; M75864; G339750; JOINED.
DR   EMBL; M75865; G339750; JOINED.
DR   EMBL; M60275; G339760; -.
DR   EMBL; A21522; G579600; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL       1    21
FT   CHAIN       22   455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN       41   291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN      22   211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212   234       POTENTIAL.
FT   DOMAIN     235   455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43   196       4 X TNFR-CYS.
FT   REPEAT      43    82       TNFR-CYS 1.
FT   REPEAT      83   125       TNFR-CYS 2.
FT   REPEAT     126   166       TNFR-CYS 3.
FT   REPEAT     167   196       TNFR-CYS 4.
FT   DOMAIN     356   441       DEATH DOMAIN.
FT   DISULFID    44    58
FT   DISULFID    59    72
FT   DISULFID    62    81
FT   DISULFID    84    99
FT   DISULFID   102   117
FT   DISULFID   105   125
FT   DISULFID   127   143
FT   DISULFID   146   158
FT   DISULFID   149   166
FT   DISULFID   168   179
FT   DISULFID   182   191
FT   DISULFID   185   195
FT   CARBOHYD    54    54       POTENTIAL.
FT   CARBOHYD   145   145       POTENTIAL.
FT   CARBOHYD   151   151       POTENTIAL.
FT   CONFLICT   412   412       MISSING (IN REF. 4).
FT   CONFLICT   443   446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  CE0EA06F CRC32;

  Query Match           56.4%;  Score 1124;  DB 1;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 3.58e-271;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
           |||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    2
ID   TNR1_PIG       STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUTER B., PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; U19994; G1141753; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL       1    21       POTENTIAL.
FT   CHAIN       22   461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN      22   210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   211   233       POTENTIAL.
FT   DOMAIN     234   461       CYTOPLASMIC (POTENTIAL).
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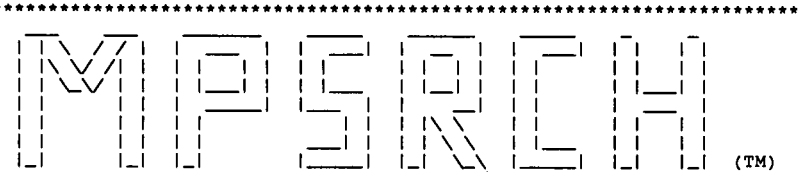

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:48:26 1998; MasPar time 13.91 Seconds
775.210 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 41.143; Variance 64.343; scale 0.639

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	945	47.4	180	4	Q95185	TUMOUR NECROSIS FACTOR	3.15e-213
2	895	44.9	471	4	O19131	TUMOR NECROSIS FACTOR-	6.13e-200
3	454	22.8	108	12	Q90287	GONADOTROPIN ALPHA SUB	6.53e-85
4	453	22.7	107	12	Q90286	GONADOTROPIN ALPHA SUB	1.17e-84
5	451	22.6	119	12	Q91370	GONADOTROPHIN ALPHA 1	3.76e-84
6	446	22.4	114	12	Q91371	GONADOTROPHIN ALPHA 2	6.95e-83
7	433	21.7	117	12	Q91119	GLYCOPROTEIN HORMONES	1.34e-79
8	333	16.7	55	10	Q62589	ALPHA SUBUNIT OF GLYCO	1.06e-54
9	273	13.7	253	2	O00276	LYMPHOCYTE ASSOCIATED	3.29e-40
10	273	13.7	380	2	O00280	LYMPHOCYTE ASSOCIATED	3.29e-40
11	273	13.7	418	2	O00275	LYMPHOCYTE ASSOCIATED	3.29e-40
12	257	12.9	277	2	O14866	SOLUBLE DEATH RECEPTOR	2.00e-36
13	257	12.9	426	2	O14865	DEATH RECEPTOR 3 BETA.	2.00e-36
14	214	10.7	348	11	Q85407	HOMOLOG OF VACCINIA VI	1.76e-26
15	214	10.7	349	11	Q89118	SOMALIA-1977 RIGHT NEA	1.76e-26
16	214	10.7	349	11	Q89098	GARCIA-1966 RIGHT NEAR	1.76e-26
17	210	10.5	355	11	Q85308	SECRETED RECEPTOR BIND	1.42e-25
18	206	10.3	459	10	Q62327	TUMOR NECROSIS FACTOR	1.13e-24
19	187	9.4	267	4	O02764	OX40 PRECURSOR (FRAGME	1.89e-20
20	182	9.1	259	2	O14755	TRAIL RECEPTOR 3.	2.34e-19
21	180	9.0	283	2	Q92956	HERPESVIRUS ENTRY MEDI	6.38e-19
22	180	9.0	299	2	O14798	CYTOTOXIC TRAIL RECEPT	6.38e-19
23	179	9.0	425	2	Q16042	TUMOR NECROSIS FACTOR	1.05e-18
24	178	8.9	324	10	Q63199	FAS ANTIGEN PRECURSOR.	1.73e-18
25	174	8.7	411	2	O15508	P53-REGULATED DNA DAMA	1.27e-17
26	174	8.7	411	2	O15517	CYTOTOXIC TRAIL RECEPT	1.27e-17
27	174	8.7	411	2	O14720	DEATH RECEPTOR 5.	1.27e-17
28	174	8.7	440	2	O15531	APOPTOSIS INDUCING PRO	1.27e-17
29	174	8.7	440	2	O14763	APOPTOSIS INDUCING REC	1.27e-17
30	167	8.4	202	2	Q14405	SOMATOTROPIN PRECURSOR	3.98e-16
31	167	8.4	217	2	Q16631	SOMATOTROPIN PRECURSOR	3.98e-16
32	161	8.1	468	2	O00220	CYTOTOXIC LIGAND TRAIL	7.40e-15
33	160	8.0	202	2	O14643	PLACENTAL GROWTH HORMO	1.20e-14
34	160	8.0	245	2	O14644	PLACENTAL GROWTH HORMO	1.20e-14
35	155	7.8	217	2	Q14407	CHORIONIC SOMATOMAMMOT	1.33e-13
36	156	7.8	372	2	O00279	LYMPHOCYTE ASSOCIATED	8.23e-14
37	154	7.7	199	2	Q14406	CHORIONIC SOMATOMAMMOT	2.14e-13
38	153	7.7	401	2	O00300	OSTEOPROTEGERIN.	3.45e-13
39	153	7.7	625	10	O35305	RANK.	3.45e-13
40	152	7.6	401	10	O08712	OSTEOPROTEGERIN.	5.55e-13
41	150	7.5	274	2	Q13663	CELL SURFACE ANTIGEN O	1.43e-12
42	147	7.4	217	4	Q07367	SOMATOTROPIN 1 PRECURS	5.90e-12
43	148	7.4	401	10	O08727	OSTEOPROTEGERIN.	3.68e-12
44	146	7.3	217	4	Q07369	SOMATOTROPIN 3 PRECURS	9.42e-12
45	143	7.2	212	4	Q07368	SOMATOTROPIN 2 PRECURS	3.82e-11

ALIGNMENTS

RESULT 1
ID Q95185 PRELIMINARY; PRT; 180 AA.

AC Q95185;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN TNFR-1.
OS FELIS SILVESTRIS CATUS (CAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
RN [1]
RP SEQUENCE FROM N.A.
RA DUTHIE S., NASIR L., ECKERSALL P.D.;
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U72344; G1613880; -.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
FT NON_TER 1 1
FT NON_TER 180 180
SQ SEQUENCE 180 AA; 20399 MW; 5452A6B2 CRC32;

Query Match 47.4%; Score 945; DB 4; Length 180;
Best Local Similarity 86.0%; Pred. No. 3.15e-213;
Matches 117; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

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Db     45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
           |||||||||:||||||||||||||||||:||| ||||||||:|:|||||| ||:|||||
Qy     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db    105 KCRKEMYQVEISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQN 164
           |||||| |||||:||| |||||||||||||| ||||  |||:||||||||||::|| | ||
Qy     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db    165 TVCTCHAGFFLRGNEC 180
           |||||||||||| |||
Qy    146 TVCTCHAGFFLRENEC 161
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RESULT 2
ID O19131 PRELIMINARY; PRT; 471 AA.

AC O19131;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

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DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR-RECEPTOR I.
GN   TNF-RI.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AORTA;
RA   LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U90937; G2290398; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
SQ   SEQUENCE   471 AA;  51368 MW;  1D60FF4A CRC32;

  Query Match           44.9%;  Score 895;  DB 4;  Length 471;
  Best Local Similarity  73.2%;  Pred. No. 6.13e-200;
  Matches   104;  Conservative   21;  Mismatches  17;  Indels   0;  Gaps   0;

Db     41 ESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCL 100
          :| |||||| ||||::||||||||||||||||||||:||||| | :|::|| |||||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160
          |||:|| || ||||||:| |||||||||||||| ||:|  |:|:|||||| ||||:::|||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 RQDTICHCHMGFFLKGAKCISC 182
          :|:|:| || ||||:   |:||
Qy    143 KQNTVCTCHAGFFLRENECVSC 164


RESULT    3
ID   Q90287         PRELIMINARY;   PRT;   108 AA.

AC   Q90287;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
RL   SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D86552; G1469838; -.
FT   NON_TER      1      1
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  12129 MW;  B2B1A212 CRC32;

  Query Match           22.8%;  Score 454;  DB 12;  Length 108;
  Best Local Similarity  72.0%;  Pred. No. 6.53e-85;
  Matches    59;  Conservative    7;  Mismatches  15;  Indels   1;  Gaps   1;

Db     28 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKDITSEATCCVAKEV 87
          || || | || :|| |||| |||||||||||||||||||||||| |::|||:||||||
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db     88 KRVLV-DDVKLVNHTDCHCSTC 108
          :|| |    |: ||| ||||||
Qy    230 NRVTVMGGFKVENHTGCHCSTC 251


RESULT    4
ID   Q90286         PRELIMINARY;   PRT;   107 AA.

AC   Q90286;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
RL   SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D86551; G1469836; -.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11959 MW;  880C6840 CRC32;

  Query Match           22.7%;  Score 453;  DB 12;  Length 107;
  Best Local Similarity  72.0%;  Pred. No. 1.17e-84;
  Matches    59;  Conservative    7;  Mismatches  15;  Indels   1;  Gaps   1;

Db     27 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEV 86
          || || | || :|| |||| |||||||||||||||||||||| ||:|||:||||||
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db     87 KRVLV-NDVRLVNHTDCHCSTC 107
          :|| |    :: ||| ||||||
Qy    230 NRVTVMGGFKVENHTGCHCSTC 251


RESULT    5
ID   Q91370         PRELIMINARY;   PRT;   119 AA.

AC   Q91370;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GONADOTROPHIN ALPHA 1 SUBUNIT.
OS   ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94197892.
RA   GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69273; G546258; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ   SEQUENCE   119 AA;  13131 MW;  2EEF28F4 CRC32;

  Query Match           22.6%;  Score 451;  DB 12;  Length 119;
  Best Local Similarity  67.8%;  Pred. No. 3.76e-84;
  Matches    59;  Conservative   11;  Mismatches  16;  Indels   1;  Gaps   1;

Db     34 GCEECKLKENKLFSNPGAPVYQCTGCCFSRAYPTPLQSKKAMLVPKNITSEATCCVAKEG 93
          || || | || :|| |||| || ||||||||||||:|||:||| ||:|||:||||||
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db     94 ERV-VVDNIKLTNHTECWCNTCYHHKS 119
          :|| |:  :|: ||| | |:||| |||
Qy    230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT    6
ID   Q91371         PRELIMINARY;   PRT;   114 AA.

AC   Q91371;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GONADOTROPHIN ALPHA 2 SUBUNIT.
OS   ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE; 94197892.
RA   GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69274; G546260; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ   SEQUENCE   114 AA;  12519 MW;  473D3C83 CRC32;

  Query Match           22.4%;  Score 446;  DB 12;  Length 114;
  Best Local Similarity  71.3%;  Pred. No. 6.95e-83;
  Matches    62;  Conservative    6;  Mismatches  15;  Indels   4;  Gaps   2;

Db     32 GCEECTLKPNTIF--PN--IIQCTGCCFSRAYPTPLRSKQTMLVPKNITSEATCCVAKEG 87
           || ||||  | :|  |   |:|| |||||||||||||| |||| ||:|||:||||||
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db     88 ERVTTKDGFPVTNHTECHCSTCYYHKS 114
           :||| : || | ||| ||||||||||
Qy    230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT    7
ID   Q91119         PRELIMINARY;   PRT;   117 AA.

AC   Q91119;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (GONADOTROPIN ALPHA
DE   CHAIN) (GTH-ALPHA).
OS   MORONE SAXATILIS (STRIPED BASS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   HASSIN S.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENSIS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
DR   EMBL; L35071; G2322657; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    117       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     34     57       BY SIMILARITY.
FT   DISULFID     37     86       BY SIMILARITY.
FT   DISULFID     54    107       BY SIMILARITY.
FT   DISULFID     58    109       BY SIMILARITY.
FT   DISULFID     85    112       BY SIMILARITY.
FT   CARBOHYD     78     78       POTENTIAL.
FT   CARBOHYD    103    103       POTENTIAL.
SQ   SEQUENCE   117 AA;  13066 MW;  CAFB9D0C CRC32;

  Query Match           21.7%;  Score 433;  DB 12;  Length 117;
  Best Local Similarity  65.5%;  Pred. No. 1.34e-79;
  Matches    57;  Conservative   14;  Mismatches  12;  Indels   4;  Gaps   4;

Db     33 GCEECTLRKNSVFSR-DRPVYQCMGCCFSRAYPTPLKAMKTMTIPKNITSEATCCVAKHS 91
           || ||||: |: ||:   |: |||||||||||||||:::||| : ||:|||:|||||| |
Qy    170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK-S 228

Db     92 YE-TEV-AGIKVRNHTDCHCSTCYFHK 116
          |:   | :|:|| ||| |||||||:||
Qy    229 YNRVTVMGGFKVENHTGCHCSTCYYHK 255


RESULT    8
ID   Q62589         PRELIMINARY;   PRT;    55 AA.

AC   Q62589;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   ALPHA SUBUNIT OF GLYCOPROTEIN HORMONES (FRAGMENT).
OS   PHODOPUS SUNGORUS (STRIPED HAIRY-FOOTED HAMSTER) (DJUNGARIAN HAMSTER).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 96198779.
RA   BOCKMANN J., BOCKERS T.M., VENNEMANN B., NIKLOWITZ P., MULLER J.,
RA   WITTKOWSKI W., SABEL B., KREUTZ M.R.;
RL   ENDOCRINOLOGY 137:1804-1813(1996).
DR   EMBL; X90776; E195654; -.
FT   NON_TER       1      1
SQ   SEQUENCE   55 AA;  6047 MW;  E5AAE0F8 CRC32;

  Query Match           16.7%;  Score 333;  DB 10;  Length 55;
  Best Local Similarity  76.4%;  Pred. No. 1.06e-54;
  Matches    42;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db      1 PTPARSKKTMLVPKNITSEATCCVAKAFTKATVMGNARVENHTECHCSTCYYHKS 55
          ||| |||||||| ||:|||:||||||:: : ||||  :||||| ||||||||||
Qy    202 PTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT    9
ID   O00276         PRELIMINARY;   PRT;   253 AA.

AC   O00276;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94503; G2071953; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   253 AA;  26934 MW;  A21C863E CRC32;

  Query Match           13.7%;  Score 273;  DB 2;  Length 253;
  Best Local Similarity  32.4%;  Pred. No. 3.29e-40;
  Matches    60;  Conservative   34;  Mismatches  74;  Indels  17;  Gaps  13;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |      :||  |  | ||   |  | ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
          |  |   :| | |||     |  |  |  : :|| : :|:   || |||:   :     |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 187
          : :    | |  ||: |::|    | |  :::| | || :||: : : ||||: :: | |
Qy    120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG-C 171

Db    188 PERCA 192
          || |:
Qy    172 PE-CT 175
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RESULT   10
ID   O00280         PRELIMINARY;   PRT;   380 AA.

AC   O00280;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94510; G2071967; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   380 AA;  41192 MW;  17C92A14 CRC32;

  Query Match           13.7%;  Score 273;  DB 2;  Length 380;
  Best Local Similarity  32.4%;  Pred. No. 3.29e-40;
  Matches    60;  Conservative   34;  Mismatches  74;  Indels  17;  Gaps  13;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  |  ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
           |  |   :| | |||    |  |  |  : :|| : :|:   || |||:   :     |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 187
          : :    | |  ||: |:::|    | |  :::| | || :||: : : |||| :: | |
Qy    120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG-C 171

Db    188 PERCA 192
          || |:
Qy    172 PE-CT 175


RESULT   11
ID   O00275         PRELIMINARY;   PRT;   418 AA.

AC   O00275;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94502; G2071951; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   418 AA;  45456 MW;  3D04954A CRC32;

  Query Match           13.7%;  Score 273;  DB 2;  Length 418;
  Best Local Similarity  32.4%;  Pred. No. 3.29e-40;
  Matches    60;  Conservative   34;  Mismatches  74;  Indels  17;  Gaps  13;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  |  ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
           |  |   :| | |||    |  |  |  : :|| : :|:   || |||:   :     |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 187
          : :    | |  ||: |:::|    | |  :::| | || :||: : : |||| :: | |
Qy    120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG-C 171

Db    188 PERCA 192
          || |:
Qy    172 PE-CT 175


RESULT   12
ID   O14866         PRELIMINARY;   PRT;   277 AA.

AC   O14866;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   SOLUBLE DEATH RECEPTOR 3 BETA.
GN   DR3.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026071; G2570833; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   277 AA;  29111 MW;  06E165C7 CRC32;

  Query Match           12.9%;  Score 257;  DB 2;  Length 277;
  Best Local Similarity  31.5%;  Pred. No. 2.00e-36;
  Matches    56;  Conservative   34;  Mismatches  73;  Indels  15;  Gaps  11;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  |  ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
           |  |   :| | |||    |  |  |  : :|| : :|:   || |||:   :     |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPPS 185
          : :    | |  ||: |:::|    | |  :::| | || :||: : : |||| ::|:
Qy    120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG 170


RESULT   13
ID   O14865         PRELIMINARY;   PRT;   426 AA.

AC   O14865;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   DEATH RECEPTOR 3 BETA.
GN   DR3.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026070; G2570831; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   426 AA;  45950 MW;  87E00821 CRC32;

  Query Match           12.9%;  Score 257;  DB 2;  Length 426;
  Best Local Similarity  31.5%;  Pred. No. 2.00e-36;
  Matches    56;  Conservative   34;  Mismatches  73;  Indels  15;  Gaps  11;
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Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  |  ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
           |  |   :| | |||    |  |  |  : :|| : :|:   || |||:   :     |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPPS 185
          : :   | |  ||: |::|    | |  :::| | || :||: : : ||||: ::|:
Qy    120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG 170


RESULT  14
ID   Q85407         PRELIMINARY;   PRT;   348 AA.

AC   Q85407;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   HOMOLOG OF VACCINIA VIRUS CDS B28R.
GN   G2R.
OS   VARIOLA VIRUS.
OC   VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC   ORTHOPOXVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BANGLADESH-1975;
RX   MEDLINE; 94088747.
RA   MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
RA   KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
RL   NATURE 366:748-751(1993).
DR   EMBL; L22579; G439102; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   348 AA;  38075 MW;  2A911AF6 CRC32;

  Query Match           10.7%;  Score 214;  DB 11;  Length 348;
  Best Local Similarity  38.5%;  Pred. No. 1.76e-26;
  Matches    30;  Conservative   14;  Mismatches  32;  Indels   2;  Gaps   2;

Db     39 HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 96
          :::||  |  |||    | :   :|:|  | ||:||: :|||  ||||:  | :  |||
Qy     37 NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96

Db     97 RSCNTTHNRICECSPGYY 114
           ||   :: :| |    |
Qy     97 SSCTVDRDTVCGCRKNQY 114


RESULT  15
ID   Q89118         PRELIMINARY;   PRT;   349 AA.

AC   Q89118;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   SOMALIA-1977 RIGHT NEAR-TERMINAL REGION.
OS   VARIOLA VIRUS.
OC   VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC   ORTHOPOXVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SOMALIA-1977;
RA   MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,
RA   TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;
RL   SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U18341; G885855; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   349 AA;  38272 MW;  0FDCC784 CRC32;

  Query Match           10.7%;  Score 214;  DB 11;  Length 349;
  Best Local Similarity  38.5%;  Pred. No. 1.76e-26;
  Matches    30;  Conservative   14;  Mismatches  32;  Indels   2;  Gaps   2;

Db     40 HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 97
          :::||  |  |||    | :   :|:|  | ||:||: :|||  ||||:  | :  |||
Qy     37 NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96

Db     98 RSCNTTHNRICECSPGYY 115
           ||   :: :| |    |
Qy     97 SSCTVDRDTVCGCRKNQY 114


Search completed: Wed May  6 08:49:44 1998
Job time : 78 secs.
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MPSRCH (TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:57:57 1998; MasPar time 1227.99 Seconds
1496.959 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-3
Description: (1-1202) from US08804166.seq
Perfect Score: 1202
N.A. Sequence: 1 CTCGAGATGGCTACAGGTAA.....CCCCGATCCTCCCACAATAA 1202
Comp: GAGCTCTACCGATGTCCATT.....GGGGCTAGGAGGGTGTTATT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl53
1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
13:em_pat
Database: genbank105
14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
26:gb_htg 27:gb_prl 28:gb_pr2

Statistics: Mean 11.143; Variance 5.206; scale 2.140

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	424	35.3	483	25	A29099	Synthetic DNA for TNF-	0.00e+00
2	424	35.3	510	25	A21525	oligonucleotide probe.	0.00e+00
3	424	35.3	600	25	A20257	Synthetic nucleotide s	0.00e+00
4	424	35.3	1331	25	A29103	H.sapiens mRNA for TNF	0.00e+00
5	424	35.3	1368	25	A29098	Synthetic DNA for TNF-	0.00e+00
6	424	35.3	2050	27	HUMTNFRP	Human tumor necrosis f	0.00e+00
7	424	35.3	2062	25	I43805	Sequence 24 from paten	0.00e+00
8	424	35.3	2062	25	A21522	TNF alpha gene.	0.00e+00
9	424	35.3	2087	27	HUMTNFR	Human tumor necrosis f	0.00e+00
10	424	35.3	2111	27	HUMTNFRB	Homo sapiens tumor nec	0.00e+00
11	424	35.3	2111	25	A26412	cDNA for (55kD TNF-BP)	0.00e+00
12	424	35.3	2112	27	HUMTNFRC	Human tumor necrosis f	0.00e+00
13	424	35.3	2161	27	HSTNFR1A	H.sapiens TNF-R mRNA f	0.00e+00
14	424	35.3	2175	25	A43873	Sequence 1 from Patent	0.00e+00
15	424	35.3	2175	25	I64751	Sequence 1 from patent	0.00e+00
16	424	35.3	2176	25	A19907	Synthetic nucleotide s	0.00e+00
17	424	35.3	6889	25	I26928	Sequence 2 from patent	0.00e+00
18	420	34.9	600	25	I43808	Sequence 47 from paten	0.00e+00
19	417	34.7	2061	25	A20255	55kD receptor gene for	0.00e+00
20	414	34.4	539	27	HUMCGB	Human chorionic gonado	0.00e+00
21	381	31.7	504	25	I43813	Sequence 56 from paten	0.00e+00
22	381	31.7	504	25	A20713	Synthetic nucleotide s	0.00e+00
23	379	31.5	501	25	I43786	Sequence 1 from patent	0.00e+00
24	372	30.9	500	25	A20254	Synthetic nucleotide 5	1.79e-296
25	370	30.8	372	25	A20253	Synthetic nucleotide 5	1.14e-294
26	370	30.8	372	25	I43787	Sequence 3 from patent	1.14e-294
27	330	27.5	642	27	BABBCGA	Baboon beta-chorionic	1.27e-258
28	330	27.5	66495	27	HUMGHCSA	Human growth hormone (	1.27e-258
29	308	25.6	1665	27	HSGG02	Human chorionic gonado	7.42e-239
30	306	25.5	468	27	HUMCGBBA3	Human chorionic gonado	4.63e-237
31	306	25.5	475	27	HUMCGBEL03	Human chorionic gonado	4.63e-237
32	306	25.5	1665	27	HSCG01	Human chorionic gonado	4.63e-237
33	303	25.2	1826	25	I02855	Sequence 1 from Patent	2.27e-234
34	302	25.1	581	15	FCU72344	Felis catus tumour nec	1.79e-233
35	302	25.1	1964	27	HUMGH	Human growth hormone (	1.79e-233
36	302	25.1	1964	27	HSGROW2	Human germ line gene f	1.79e-233
37	302	25.1	2771	25	I41411	Sequence 5 from patent	1.79e-233
38	300	25.0	474	25	I43809	Sequence 49 from paten	1.11e-231
39	300	25.0	474	25	A20259	Synthetic nucleotide s	1.11e-231
40	301	25.0	2657	27	HUMGHN	Human growth hormone g	1.41e-232
41	301	25.0	4283	25	I63120	Sequence 3 from patent	1.41e-232
42	293	24.4	2004	15	SSU19994	Sus scrofa p55 TNF rec	2.08e-225
43	283	23.5	426	25	I08477	Sequence 18 from Paten	1.86e-216
44	255	21.2	477	25	A20263	Synthetic nucleotide s	1.84e-191
45	255	21.2	477	25	I43811	Sequence 53 from paten	1.84e-191

ALIGNMENTS

RESULT 1
LOCUS A29099 483 bp DNA PAT 03-JUL-1995

DEFINITION Synthetic DNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION A29099
NID g1248893
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 483)
AUTHORS Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL Patent: EP 0393438-A 49 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES Location/Qualifiers
source 1. .483
/organism="unidentified"
/db_xref="taxon:32644"
source 1. .483
/organism="artificial sequence"
/db_xref="taxon:29278"
BASE COUNT 130 a 124 c 123 g 106 t
ORIGIN

Query Match 35.3%; Score 424; DB 25; Length 483;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     61 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    121 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 180
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                ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    181 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    241 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    301 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    361 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    421 TCCTGT 426
          ||||||
Qy    765 TCCTGT 770


RESULT    2
LOCUS       A21525        510 bp    DNA             PAT       26-JUL-1994

DEFINITION  oligonucleotide probe.
ACCESSION   A21525
NID         g583574
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   .
  JOURNAL   Patent: GB 2246569-A 4 05-FEB-1992;
FEATURES             Location/Qualifiers
     source          1. .510
                     /organism="Artificial sequences"
BASE COUNT      136 a    132 c    133 g    109 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 510;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     34 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 93
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     94 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    154 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 213
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    214 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    274 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    334 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    394 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    454 TCCTGT 459
          ||||||
Qy    765 TCCTGT 770


RESULT    3
LOCUS       A20257        600 bp    DNA             PAT       20-SEP-1995

DEFINITION  Synthetic nucleotide sequence of plasmid p-TNFRecd.
ACCESSION   A20257
NID         g1247896
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   .
  TITLE     MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL   Patent: WO 9207076-A 25 30-APR-1992;
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     source          1. .600
                     /organism="artificial sequence"
                     /db_xref="taxon:29278"
BASE COUNT      148 a    157 c    162 g    133 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 600;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    541 TCCTGT 546
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Qy    765 TCCTGT 770


RESULT    4
LOCUS       A29103       1331 bp    DNA             PAT       03-JUL-1995

DEFINITION  H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29103
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NID         g1247517
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1331)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 53 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1. .1331
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      298 a    407 c    343 g    283 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 1331;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    333 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    393 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    453 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 512
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    513 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    573 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    633 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    693 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    753 TCCTGT 758
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Qy    765 TCCTGT 770


RESULT    5
LOCUS       A29098       1368 bp    DNA             PAT       03-JUL-1995

DEFINITION  Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION   A29098
NID         g1248892
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1368)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 48 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1. .1368
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     source          1. .1368
                     /organism="artificial sequence"
                     /db_xref="taxon:29278"
BASE COUNT      293 a    424 c    375 g    276 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 1368;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    541 TCCTGT 546
          ||||||
Qy    765 TCCTGT 770


RESULT    6
LOCUS       HUMTNFRP     2050 bp    mRNA            PRI       11-OCT-1991

DEFINITION  Human tumor necrosis factor receptor(TNF) mRNA, complete cds.
ACCESSION   M60275 M37764
NID         g339759
KEYWORDS    TNF receptor; transmembrane receptor; tumor necrosis factor
            receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2050)
  AUTHORS   Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.
  TITLE     Cloning of human tumor necrosis factor (TNF) receptor cDNA and
            expression of recombinant soluble TNF-binding protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
  MEDLINE   91017509
COMMENT     Draft entry and computer-readable sequence for [Proc. Natl. Acad.
            Sci. U.S.A. (1990) In press] kindly submitted
            by P.W.Gray, 13-AUG-1990.
FEATURES             Location/Qualifiers
     source          1. .2050
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="placenta"
     sig_peptide     155. .274
                     /gene="TNF receptor"
     CDS             155. .1516
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                     SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
                     GRCLREAQYSMLATWRRRTRREATLELLGRVLRDMDLLGCLEDIEEALCAPPLPPAPS
                     LLR"
     gene            155. .274
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     mat_peptide     275. .1513
                     /product="TNF receptor"
BASE COUNT      429 a    611 c    566 g    444 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 27;  Length 2050;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db     395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy     465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db     455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db     515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db     575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db     635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db     695 TCCTGT 700
           ||||||
Qy     765 TCCTGT 770


RESULT    7
LOCUS       I43805       2062 bp    DNA             PAT       10-JUL-1997

DEFINITION  Sequence 24 from patent US 5633145.
ACCESSION   I43805
NID         g2468903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE     TNF.alpha. receptor-derived binding protein
  JOURNAL   Patent: US 5633145-A 24 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .2062
                     /organism="unknown"
BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db     395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy     465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db     455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db     515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db     575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db     635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db     695 TCCTGT 700
           ||||||
Qy     765 TCCTGT 770


RESULT    8
LOCUS       A21522       2062 bp    RNA             PAT       26-JUL-1994

DEFINITION  TNF alpha gene.
ACCESSION   A21522
NID         g579599
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   .
  JOURNAL   Patent: GB 2246569-A 1 05-FEB-1992;
FEATURES             Location/Qualifiers
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                     /codon_start=1
                     /db_xref="PID:g579600"
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 TCCTGT 700
          ||||||
Qy    765 TCCTGT 770


RESULT    9
LOCUS       HUMTNFR      2087 bp    mRNA            PRI       10-NOV-1993

DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61, 361-370 (1990)
  MEDLINE   90235285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
FEATURES             Location/Qualifiers
     source          1. .2087
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             182. .1549
                     /note="tumor necrosis factor receptor"
                     /codon_start=1
                     /db_xref="PID:g339745"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
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                     PSLLR"
BASE COUNT      433 a    624 c    581 g    449 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 27;  Length 2087;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    302 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 361
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    362 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    422 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 481
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    482 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 541
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    542 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 601
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    602 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 661
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    662 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 721
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    722 TCCTGT 727
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Qy    765 TCCTGT 770


RESULT   10
LOCUS       HUMTNFRB     2111 bp    mRNA            PRI       14-NOV-1990

DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID         g339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cell line HL60, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
  TITLE     Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
  JOURNAL   Cell 61, 351-359 (1990)
  MEDLINE   90235284
FEATURES             Location/Qualifiers
     source          1. .2111
                     /organism="Homo sapiens"
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                     /cell_line="HL60"
     sig_peptide     187. .273
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                     /product="tumor necrosis factor receptor"
     CDS             187. .1554
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                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /db_xref="PID:g339754"
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                     PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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     gene            187. .1554
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BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 27;  Length 2111;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 546
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    547 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 606
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 726
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    727 TCCTGT 732
        ||||||
Qy    765 TCCTGT 770


RESULT   11
LOCUS       A26412       2111 bp    DNA             PAT       26-APR-1995

DEFINITION  cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
            patent EP0417563.
ACCESSION   A26412
NID         g904968
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 24 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .2111
                     /organism="Artificial sequences"
     CDS             187. .1554
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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                     PSLLR"
BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 2111;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 546
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    547 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 606
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 726
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    727 TCCTGT 732
        ||||||
Qy    765 TCCTGT 770


RESULT   12
LOCUS       HUMTNFRC     2112 bp    mRNA            PRI       30-SEP-1991

DEFINITION  Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
            cds.
ACCESSION   M63121 M75861
NID         g339755
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2112)
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  AUTHORS   Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
            Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C. and
            Adolf,G.R.
  TITLE     Molecular cloning and expression of human and rat tumor necrosis
            factor receptor chain (p60) and its soluble derivative, tumor
            necrosis factor-binding protein
  JOURNAL   DNA Cell Biol. 9, 705-715 (1990)
  MEDLINE   91090841
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     source          1. .2112
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /gene="TNF receptor"
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                     /gene="TNF receptor"
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     gene            207. .1574
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     mat_peptide     294. .1571
                     /gene="TNF receptor"
                     /product="tumor necrosis factor receptor"
BASE COUNT      435 a    632 c    589 g    456 t
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  Query Match           35.3%;  Score 424;  DB 27;  Length 2112;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     327 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 386
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Qy     345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     387 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db     447 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 506
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy     465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db     507 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 566
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Qy     525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db     567 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 626
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Qy     585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db     627 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 686
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Qy     645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db     687 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 746
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Qy     705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db     747 TCCTGT 752
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Qy     765 TCCTGT 770
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RESULT   13
LOCUS       HSTNFR1A     2161 bp    RNA             PRI       18-JAN-1993

DEFINITION  H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION   X55313
NID         g37223
KEYWORDS    TNF-R gene; tumor necrosis factor receptor 1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2161)
  AUTHORS   Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
            Aderka,D., Holtmann,H. and Wallach,D.
  TITLE     Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
            for the type I TNF-R, cloned using amino acid sequence data of its
            soluble form, encodes both the cell surface and a soluble form of
            the receptor
  JOURNAL   EMBO J. 9 (10), 3269-3278 (1990)
  MEDLINE   91006021
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     CDS             256. .1623
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                     /codon_start=1
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                     /db_xref="PID:g37224"
                     /db_xref="SWISS-PROT:P19438"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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BASE COUNT      459 a    642 c    604 g    456 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 27;  Length 2161;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db     496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy     465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524
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Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 TCCTGT 801
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Qy    765 TCCTGT 770


RESULT   14
LOCUS       A43873       2175 bp    DNA             PAT       06-MAR-1997

DEFINITION  Sequence 1 from Patent EP0657536.
ACCESSION   A43873
NID         g2299022
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Proteases capable of shedding the soluble TNF-receptor and TNF-R
            derived peptides and antibodies against the proteases inhibiting
            the shedding
  JOURNAL   Patent: EP 0657536-A 1 14-JUN-1995;
            YEDA RES & DEV (IL)
COMMENT     Other publication ZA 9407962 951121
            Other publication JP 7194376 950801
            Other publication AU 7574294 950504
            Other publication CA 2133872 950413.
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                     PSLLR"
BASE COUNT      474 a    641 c    604 g    456 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 2175;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
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Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
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Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

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Qy    765 TCCTGT 770


RESULT   15
LOCUS       I64751       2175 bp    DNA             PAT       26-SEP-1997

DEFINITION  Sequence 1 from patent US 5665859.
ACCESSION   I64751
NID         g2481645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Molecules influencing the shedding of the TNF receptor, their
            preparation and their use
  JOURNAL   Patent: US 5665859-A 1 09-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .2175
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BASE COUNT      474 a    641 c    604 g    456 t
ORIGIN

  Query Match           35.3%;  Score 424;  DB 25;  Length 2175;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
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Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
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Db      736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy      705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db      796 TCCTGT 801
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Search completed: Wed May  6 13:18:35 1998
Job time : 1238 secs.
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MPSRCH (TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:37:52 1998; MasPar time 155.56 Seconds
891.677 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-3
Description: (1-1202) from US08804166.seq
Perfect Score: 1202
N.A. Sequence: 1 CTCGAGATGGCTACAGGTAA.....CCCCGATCCTCCCACAATAA 1202
Comp: GAGCTCTACCGATGTCCATT.....GGGGCTAGGAGGGTGTTATT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.195; Variance 5.326; scale 1.727

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	424	35.3	608	4	Q24441	Encodes truncated TNF	1.67e-282
2	424	35.3	1334	1	Q06282	Plasmid Tumour Necros	1.67e-282
3	424	35.3	1368	8	Q49932	Lambda-derived TNF-R	1.67e-282
4	424	35.3	2062	4	Q24440	Encodes TNF-alpha 55k	1.67e-282
5	424	35.3	2062	3	Q20973	TNF-alpha binding pro	1.67e-282
6	424	35.3	2088	2	Q10883	30kD TNF inhibitor pr	1.67e-282
7	424	35.3	2111	2	Q10955	Encodes human 55kD TN	1.67e-282
8	424	35.3	2141	1	Q06285	Human Tumour Necrosis	1.67e-282
9	424	35.3	2175	15	Q90513	p55 TNF-R gene.	1.67e-282
10	424	35.3	6889	18	T15931	DHFR/intron (WTrasSD)	1.67e-282
11	422	35.1	2170	9	Q50870	p55 Tumour necrosis f	4.91e-281
12	422	35.1	2176	2	Q12215	Type I TNF receptor.	4.91e-281
13	414	34.4	579	3	Q14800	Human chorionic gonad	3.68e-275
14	409	34.0	836	17	T03212	Single chain gonadotr	1.73e-271
15	409	34.0	836	17	T03243	Single chain gonadotr	1.73e-271
16	405	33.7	575	17	T03240	Human CG beta-subunit	1.49e-268
17	381	31.7	504	4	Q24445	Encodes truncated TNF	5.96e-251
18	315	26.2	743	17	T03219	Single chain gonadotr	1.09e-202
19	302	25.1	2771	31	T76770	Rat Fabpl gut-specifi	3.27e-193
20	300	25.0	474	4	Q24442	Encodes truncated TNF	9.37e-192
21	301	25.0	2160	33	T62826	Human growth hormone	1.75e-192
22	294	24.5	336	6	Q41459	Human growth hormone	2.19e-187
23	283	23.5	426	2	N60524	Sequence encoding hum	2.20e-179
24	276	23.0	743	17	T03231	Single chain gonadotr	2.69e-174
25	276	23.0	743	17	T03233	Single chain gonadotr	2.69e-174
26	276	23.0	752	17	T03229	Single chain gonadotr	2.69e-174
27	274	22.8	744	17	T03221	Single chain gonadotr	7.64e-173
28	261	21.7	752	17	T03227	Single chain gonadotr	2.08e-163
29	255	21.2	477	4	Q24444	Encodes truncated TNF	4.65e-159
30	226	18.8	2173	1	Q06284	Rat Tumour Necrosis F	4.31e-138
31	209	17.4	525	1	Q03844	Bovine beta LH subuni	7.56e-126
32	209	17.4	540	1	Q03851	Porcine beta LH subun	7.56e-126
33	206	17.1	2660	4	N30032	Sequence of gene for	1.08e-123
34	184	15.3	496	2	N60523	Sequence encoding dog	6.37e-108
35	179	14.9	611	1	Q03848	Equine beta LH subuni	2.38e-104
36	169	14.1	462	4	Q24443	Encodes truncated TNF	3.19e-97
37	130	10.8	1027	2	Q10878	Partial sequence of c	1.15e-69
38	101	8.4	114	2	N60522	Sequence encoding ami	1.53e-49
39	99	8.2	138	13	Q80819	LH-beta -5 to 41 frag	3.59e-48
c 40	84	7.0	1047	2	Q10572	Human Natriuretic Pep	5.61e-38
41	77	6.4	1047	2	Q10572	Human Natriuretic Pep	2.75e-33
42	72	6.0	114	6	Q34669	DNA encoding hCG beta	5.75e-30
43	71	5.9	651	2	N71239	Sequence encoding hum	2.63e-29
44	71	5.9	700	2	N60678	Sequence encoding pre	2.63e-29
45	71	5.9	3557	2	N60801	Human pro-growth horm	2.63e-29

ALIGNMENTS

RESULT 1
ID Q24441 standard; DNA; 608 BP.
AC Q24441;
DT 05-NOV-1992 (first entry)
DE Encodes truncated TNF-alpha 55kD receptor (197 amino acids).
KW tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningits; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
PN WO9207076-A.
PD 30-APR-1992.
PF 18-OCT-1991; G01826.
PR 18-OCT-1990; GB-022648.
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR WPI; 92-167156/20.
DR P-PSDB; R24080.
PT New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
PS Example; Fig 7; 43pp; English.
CC This sequence encodes the designed TNF-alpha 55kD receptor
CC derivative, as present in pTNFRecd. This was produced as described in
CC Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC the cytoplasmic domain. The derivative could be used in the
CC regulation of TNF-alpha mediated responses by binding and
CC sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC diseases, septic shock, HIV infection, malaria, viral meningitis,
CC graft versus host disease and autoimmune diseases, esp. rheumatoid
CC arthritis.
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ Sequence 608 BP; 148 A; 159 C; 165 G; 136 T;

Query Match 35.3%; Score 424; DB 4; Length 608;
Best Local Similarity 99.8%; Pred. No. 1.67e-282;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    249 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 308
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    309 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 368
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    369 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 428
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    429 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 488
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    489 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 548
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    549 tcctgt 554
Qy    765 TCCTGT 770
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RESULT 2
ID Q06282 standard; DNA; 1334 BP.
AC Q06282;
DT 29-JAN-1991 (first entry)
DE Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW pTNF-BP15; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 213..1325
FT /*tag= a
FT /product=TNF-BP
PN EP-393438-A.
PD 24-OCT-1990.
PF 06-APR-1990; 106624.
PR 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
PA (BOEH) BOEHRINGER INGELHEIMINT.
PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR WPI; 90-321987/43.
DR P-PSDB; R07449.
PT DNA encoding TNF binding protein and TNF- receptor - used in
PT tumour treatment and to understand mechanismsm to TNF action
PS Disclosure; Fig 1(1-3); 51pp; German.
CC pTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC from induced TNF-induced fibrosarcoma cells. A TNF-BP had been
CC isolated from the urine of patients with uraemia and probes/primers
CC were constructed from the determined amino acid sequence.
CC To produce a vector expressing a soluble form of TNF-binding
CC protein, this plasmid was cut with XmmI, amplified by PCR and the
CC amplified DNA cut with BamHI and EcoRI.
CC The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC (BRL) cut with the same enzymes to recover pTNF-BP. This was cut
CC with BamHI and EcoRI, and the recovered fragment inserted into
CC pAD-CMV1 (Q06283) to give the required plasmid pADTNF-BP.
CC See also Q06282-Q06285.
SQ Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T;

Query Match 35.3%; Score 424; DB 1; Length 1334;
Best Local Similarity 99.8%; Pred. No. 1.67e-282;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 632
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    753 tcctgt 758
Qy    765 TCCTGT 770
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RESULT 3
ID Q49932 standard; cDNA to mRNA; 1368 BP.
AC Q49932;
DT 29-APR-1994 (first entry)
DE Lambda-derived TNF-R cDNA.
KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW graft verses host disease; sepsis; inflammation; allergy;
KW autoimmune dysfunction; ss.
OS Homo sapiens.
OS Lambda-gt10-7-ctnfbp.
FH Key Location/Qualifiers
FT CDS 1..1366
FT /*tag= a
FT /product= hTNF-R
FT sig_peptide 1..120
FT /*tag= b
FT mat_peptide 121..1363
FT /*tag= c
PN WO9319777-A.
PD 14-OCT-1993.
PF 26-MAR-1993; U02938.
PR 30-MAR-1992; US-860710.
PA (IMMV) IMMUNEX CORP.
PI Smith CA;
DR WPI; 93-336592/42.
DR P-PSDB; R42059.
PT New fusion protein tumour necrosis factor and human interleukin-1
PT receptor - useful in therapy, diagnosis and assays of e.g.
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS Disclosure; Page 57-59; 85pp; English.
CC The sequences given in Q49931-32 encode human tumour necrosis factor
CC receptor (TNF-R) and the sequences in Q49933-34 encode human
CC interleukin-1 receptor (IL-1R). These sequences were used in the
CC production of a fusion protein which conformed to one of the
CC formulae:
CC TNF-R-linker-TNF-R-linker-IL-1R

```
CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence   1368 BP;    292 A;    424 C;    376 G;    276 T;

  Query Match           35.3%;  Score 424;  DB 8;  Length 1368;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

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Db    181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 240
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
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Db    301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
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Db    361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 420
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    541 tcctgt 546
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Qy    765 TCCTGT 770


RESULT    4
ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-NOV-1992  (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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FT   /*tag=  f
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24000
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Claim 4; Fig 1; 43pp; English.
CC   This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC   library in gt10 was screened with probe Q29236. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in prTNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain. PCR with primers Q29237,8 generated a 300bp
CC   restriction fragment which was cloned into prTNFR, giving pTNFRecd.
CC   DNA sequencing confirmed this contained the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   2062 BP;    429 A;    618 C;    572 G;    443 T;

  Query Match           35.3%;  Score 424;  DB 4;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 tcctgt 700
          ||||||
Qy    765 TCCTGT 770
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RESULT    5
ID   Q20973 standard; DNA; 2062 BP.
AC   Q20973;
DT   11-MAY-1992  (first entry)
DE   TNF-alpha binding protein gene.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             155..1522
FT   /*tag=  a
FT   sig_peptide     155..274
FT   /*tag=  b
FT   mat_peptide     275..1522
FT   /*tag=  c
FT   misc_feature    473..532
FT   /*tag=  d
FT   /note= "homologous to probe Q20974"
FT   misc_feature    242..751
FT   /*tag=  e
FT   /note= "encodes the extracellular domain of human
FT   TNF alpha receptor"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding tumour necrosis factor alpha
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence   2062 BP;    429 A;    616 C;    573 G;    444 T;

  Query Match           35.3%;  Score 424;  DB 3;  Length 2062;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 tcctgt 700
          ||||||
Qy    765 TCCTGT 770


RESULT    6
ID   Q10883 standard; cDNA; 2088 BP.
AC   Q10883;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
KW   Tumour necrosis factor; inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             171..1536
FT   /*tag=  a
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   P-PSDB; R10986.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also Q10878, Q10884 and Q10907.
SQ   Sequence   2088 BP;    439 A;    626 C;    578 G;    445 T;

  Query Match           35.3%;  Score 424;  DB 2;  Length 2088;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    289 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 348
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    349 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    409 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 468
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    469 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    529 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    589 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    649 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    709 tcctgt 714
          ||||||
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Qy    765 TCCTGT 770


RESULT    7
ID   Q10955 standard; cDNA; 2111 BP.
AC   Q10955;
DT   24-MAY-1991  (first entry)
DE   Encodes human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   sig_peptide     187..273
FT   /*tag= a
FT   mat_peptide     274..1551
FT   /*tag= b
FT   /product= 55kD TNF-BP
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   P-PSDB; R11082.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 4; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   2111 BP;    445 A;    628 C;    588 G;    450 T;

  Query Match           35.3%;  Score 424;  DB 2;  Length 2111;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    307 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    367 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    427 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 486
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    487 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    547 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    607 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    667 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    727 tcctgt 732
          ||||||
Qy    765 TCCTGT 770


RESULT    8
ID   Q06285 standard; DNA; 2141 BP.
AC   Q06285;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   lambdaTNF-R2; raTNF-R8; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             213..1577
FT   /*tag= a
FT   /label=huTNF-R
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   P-PSDB; R07451.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).
CC   See also Q06282-Q06285.
SQ   Sequence   2141 BP;    455 A;    633 C;    593 G;    460 T;

  Query Match           35.3%;  Score 424;  DB 1;  Length 2141;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 632
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    753 tcctgt 758
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Qy    765 TCCTGT 770
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RESULT    9
ID   Q90513 standard; DNA; 2175 BP.
AC   Q90513;
DT   19-JAN-1996  (first entry)
DE   p55 TNF-R gene.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT   /*tag= a
FT   /product= p55 TNF-R
FT   misc_signal     2143..2149
FT   /*tag= b
FT   /note= "possible poly-A signal"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
DR   WPI; 95-194342/26.
DR   P-PSDB; R75084.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor  - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment.  The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type.  The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain.  This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain.  The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11.  This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.  The
CC   mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3.  These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence   2175 BP;    474 A;    642 C;    603 G;    456 T;

  Query Match           35.3%;  Score 424;  DB 15;  Length 2175;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 tcctgt 801
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Qy    765 TCCTGT 770


RESULT   10
ID   T15931 standard; DNA; 6889 BP.
AC   T15931;
DT   20-JUN-1996  (first entry)
DE   DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.
KW   Recombinant host cell; dihydrofolate reductase; selectable marker;
KW   DHFR; ras splice donor; dicistronic vector; gene expression;
KW   immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
OS   Synthetic.
PN   WO9604391-A1.
PD   15-FEB-1996.
PF   28-JUL-1995; U09576.
PR   05-AUG-1994; US-286740.
PA   (GETH ) GENENTECH INC.
PI   Crowley CW;
DR   WPI; 96-129407/13.
PT   Improved process for the selection of recombinant host cells
PT   expressing high level of a desired product - uses eukaryotic host
PT   cells contg. a DNA construct comprising a selectable gene
PS   Example 2; Page 36-42; 137pp; English.
CC   A dicistronic vector (T15930) comprises a regulatory region
CC   derived from the cytomegalovirus immediate-early gene, a
CC   selectable dihydrofolate reductase gene positioned within an
CC   intron having a 5' wild-type ras splice donor site, a downstream
CC   sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
CC   tumour necrosis factor, and a poly-A sequence.  Transfection of CHO
CC   DHFR- cells and subsequent methotrexate amplification and growth of
CC   the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC   ug/ml (15-fold higher compared to conventional vector amplified
CC   pools).
SQ   Sequence   6889 BP;    1729 A;    1826 C;    1681 G;    1653 T;

  Query Match           35.3%;  Score 424;  DB 18;  Length 6889;
  Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
  Matches   425;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1725 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 1784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   1785 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 1844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   1845 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 1904
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   1965 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 2084
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 2144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 tcctgt 2150
          ||||||
Qy    765 TCCTGT 770


RESULT   11
ID   Q50870 standard; DNA; 2170 BP.
AC   Q50870;
DT   13-MAY-1994  (first entry)
DE   p55 Tumour necrosis factor receptor coding sequence.
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT   /*tag= a
FT   /product= p55 Tumour necrosis factor receptor.
PN   EP-568925-A.
PD   10-NOV-1993.
PF   29-APR-1993; 106981.
PR   03-MAY-1992; IL-101769.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Brakebusch C,  Wallach D;
DR   WPI; 93-353057/45.
DR   P-PSDB; R42197.
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
PS   Claim 2; Figure 1; 17pp; English.
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor.  This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock.  They can also
CC   be used to treat overdoses of exogenous TNF.
SQ   Sequence   2170 BP;    474 A;    657 C;    584 G;    455 T;

  Query Match           35.1%;  Score 422;  DB 9;  Length 2170;
  Best Local Similarity  99.5%;  Pred. No. 4.91e-281;
  Matches   424;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgcgaccgtgcacctctcctgccaggag 735
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 tcctgt 801
          ||||||
Qy    765 TCCTGT 770


RESULT   12
ID   Q12215 standard; DNA; 2176 BP.
AC   Q12215;
DT   12-SEP-1991  (first entry)
DE   Type I TNF receptor.
KW   Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   terminator      244..246
FT   /*tag= a
FT   /note= "in-frame termination codon"
FT   CDS             256..1620
FT   /*tag= a
FT   /product= type I TNF receptor
FT   sig_peptide     256..318
FT   /*tag= b
FT   mat_peptide     319..1620
FT   /*tag= c
FT   misc_RNA        319..864
FT   /*tag= d
FT   /label= soluble_domain
FT   /note= "may be 2 codons shorter or a few codons
FT   longer"
FT   misc_feature    376..414
FT   /*tag= e
FT   /note= "TBP-I derived sequence"
FT   misc_feature    583..627
FT   /*tag= f
FT   /note= "TBP-I derived sequence"
FT   misc_feature    850..858
FT   /*tag= g
FT   /note= "TBP-I derived sequence"
FT   misc_RNA        889..957
FT   /*tag= h
FT   /label= transmembrane_domain
FT   repeat_unit     385..504
FT   /*tag= i
FT   /number= 1
FT   repeat_unit     505..633
FT   /*tag= j
FT   /number= 2
FT   repeat_unit     634..756
FT   /*tag= k
FT   /number= 3
FT   repeat_unit     757..858
FT   /*tag= l
FT   /number= 4
FT   polyA_signal    2145..2150
FT   /*tag= m
PN   EP-433900-A.
PD   26-JUN-1991.
PF   13-DEC-1990; 124133.
PR   13-DEC-1989; IL-092697.
PR   12-JUL-1990; IL-095064.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI   Aderka D;
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DR   WPI; 91-186774/26.
DR   P-PSDB; R12550.
PT   Recombinant tumour necrosis factor binding protein I - prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PT   acid encoding human type T TNF receptor or soluble domain
PS   Disclosure; Fig 1(D); 30pp; English.
CC   The Tumour Necrosis Factor Binding Protein I is the soluble form of
CC   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA.  The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also Q12212-15.
SQ   Sequence   2176 BP;    475 A;    644 C;    602 G;    455 T;

  Query Match           35.1%;  Score 422;  DB 2;  Length 2176;
  Best Local Similarity  99.5%;  Pred. No. 4.91e-281;
  Matches   424;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgcagtacc 435
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
        |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 675
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 tcctgt 801
        ||||||
Qy    765 TCCTGT 770


RESULT   13
ID   Q14800 standard; DNA; 579 BP.
AC   Q14800;
DT   11-FEB-1992  (first entry)
DE   Human chorionic gonadotropin beta subunit analogue.
KW   Glycoprotein hormone; hCGB'; fertility; immuno-castration;
KW   immuno-contragestive; vaccine; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             26..523
FT   /*tag=  a
FT   mat_peptide     86..520
FT   /*tag=  b
FT   sig_peptide     26..85
FT   /*tag=  c
FT   polyA_site      524..579
FT   /*tag=  d
FT   mutation        229
FT   /*tag=  e
FT   /note="c -> g"
FT   mutation        232
FT   /*tag=  f
FT   /note="c -> g"
PN   WO9116922-A.
PD   14-NOV-1991.
PF   07-MAY-1991; U03162.
PR   08-MAY-1990; US-520703.
PA   (UYNE-) UNIV MED NEW JERSEY.
PI   Campbell RK, Moyle WR;
DR   WPI; 91-353528/48.
DR   P-PSDB; R15043.
PT   New glyco-protein hormone analogues - for inducing fertility as
PT   immuno-castration agents, for suppressing reproductive system
PT   development and as immuno-contragestive vaccines.
PS   Example 3; Fig 4a; 94pp; English.
CC   The sequence is an analogue of hCG beta subunit cDNA contg. two
CC   silent mutations which eliminate restriction sites. It was prepd.
CC   from the plasmid pKMB-hCG-beta, a construct contg. the hCG beta
CC   subunit isolated from human placenta (Fiddes and Goodman) in
CC   plasmid pKMB, a derivative of pUC18 designed to facilitate cloning
CC   of glycoprotein hormones. The sequence was used as the starting
CC   construct for many mutants. (See R15061-R15125 and R15161-R15198).
SQ   Sequence   579 BP;    128 A;    205 C;    151 G;    95 T;

  Query Match           34.4%;  Score 414;  DB 3;  Length 579;
  Best Local Similarity  99.3%;  Pred. No. 3.68e-275;
  Matches   417;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db    104 ccacggtgccgccccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 163
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    783 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 842

Db    164 atcaccgtcaacaccaccatctgtgccggctactgccccaccatgacccgcgtgctgcag 223
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    843 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 902

Db    224 ggggtgctcccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 283
        ||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    903 GGGGTCCTCCCCGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 962

Db    284 atccggctccctggctgcccgcgcggcgtgaaccccgtggtctcctacgccgtggctctc 343
        |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Qy    963 ATCCGGCTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCTGTGGCTCTC 1022

Db    344 agctgtcaatgtgcactctgccgccgcagcaccactgactgcgggggtcccaaggaccac 403
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1023 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1082

Db    404 cccttgacctgtgatgacccccgcttccaggactcctcttcctcaaaggcccctcccccc 463
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1083 CCCTTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCC 1142

Db    464 agccttccaagcccatcccgactcccggggccctcggacaccccgatcctcccacaataa 523
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1143 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGATCCTCCCACAATAA 1202


RESULT   14
ID   T03212 standard; cDNA; 836 BP.
AC   T03212;
DT   26-APR-1996  (first entry)
DE   Single chain gonadotropin analogue 1 coding sequence.
KW   Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW   alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW   inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW   follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             33..830
FT   /*tag=  a
FT   /transl_except= pos:240..242, aa:Arg
FT   sig_peptide     33..92
FT   /*tag=  b
FT   mat_peptide     93..827
```

```
FT   /*tag= c
FT   /label= Analogue_1
FT   /note= "nucleotides 93..527 encode amino acids
FT   1-145 of hCG beta-subunit; nucleotides
FT   528..551 encode a (Gly-Ser)4 linker and
FT   nucleotides 552..827 encode amino acids
FT   1-92 of gonadotropin alpha-subunit"
FT   misc_feature    1..26
FT   /*tag= d
FT   /label= sticky_end
FT   /note= "single-strand overhang. The complementary
FT   strand also has a single-strand overhang at
FT   its 5'-end; the sequence of the overhang is
FT   5'-TCCGGATTAGCTTGAGATGGATCC-3'"
PN   WO9522340-A1.
PD   24-AUG-1995.
PF   17-FEB-1995; U02067.
PR   18-FEB-1994; US-199382.
PA   (SENS-) SENSI-TEST.
PI   Moyle WR;
DR   WPI; 95-302553/39.
DR   P-PSDB; R86247.
PT   Methods for altering fertility in mammals, esp. humans - e.g.
PT   stimulating fertility by reducing the activity and/or levels of
PT   circulating glyco:protein hormones having lutropin activity
PS   Example 12; Fig 6; 102pp; English.
CC   Analogue 1 (human CG-beta(1-145)-linker-human CG-alpha(1-92)) is a
CC   specific example of a single chain gonadotropin having a chorionic
CC   gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-
CC   subunit at the C-terminus, joined by a linker of 1-16 amino acids.
CC   The analogue has luteinising hormone (lutropin) activity and is
CC   useful for inducing ovulation and increasing male fertility.
CC   The sequences coding for analogue 1 were cloned from a human
CC   placental cDNA library using strand overlap extension PCR.
SQ   Sequence   836 BP;    166 A;    282 C;    222 G;    166 T;

  Query Match           34.0%;  Score 409;  DB 17;  Length 836;
  Best Local Similarity  99.0%;  Pred. No. 1.73e-271;
  Matches   413;  Conservative    0;  Mismatches   4;  Indels   0;  Gaps   0;

Db    111 ccacggtgccgccccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    783 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 842

Db    171 atcaccgtcaacaccaccatctgtgccggctactgccccaccatgacccgcgtgctgcag 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    843 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 902

Db    231 ggggtcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 290
          |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    903 GGGGTCCTCCCCGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 962

Db    291 atccggctccctggctgcccgcgcggcgtgaaccccgtggtctcctacgccgtggctctc 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy    963 ATCCGGCTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCTGTGGCTCTC 1022

Db    351 agctgtcaatgtgcactctgccgccgcagcaccactgactgcgggggtcccaaggaccac 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1023 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1082

Db    411 cccttgacctgtgatgaccccccgcttccaggactcctcttcctcaaaggcccctcccccc 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1083 CCCTTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCC 1142

Db    471 agccttccaagcccatcccgactcccgggggccctcggacaccccgatcctccccaa 527
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy   1143 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGATCCTCCCACAA 1199


RESULT   15
ID   T03243 standard; cDNA; 836 BP.
AC   T03243;
DT   08-MAY-1996  (first entry)
DE   Single chain gonadotropin analogue 1a coding sequence.
KW   Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW   alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW   inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW   follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             33..830
FT   /*tag= a
FT   /transl_except= pos:240..242, aa:Arg
FT   sig_peptide     33..92
FT   /*tag= b
FT   mat_peptide     93..827
FT   /*tag= c
FT   /label= Analogue_1a
FT   /note= "nucleotides 93..527 encode amino acids
FT   1-145 of hCG beta-subunit; nucleotides
FT   528..551 encode a (Gly-Ser)4 linker and
FT   nucleotides 552..827 encode amino acids
FT   1-92 of gonadotropin alpha-subunit lacking
FT   the glycosylation sites at amino acid
FT   positions 52 and 78"
FT   Misc_difference 705..707
FT   /*tag= d
FT   /note= "wild-type Asn 52 codon has been changed to a
FT   Gln codon to remove a glycosylation site"
FT   Misc_difference 783..785
FT   /*tag= e
FT   /note= "wild-type Asn 78 codon has been changed to a
FT   Gln codon to remove a glycosylation site"
FT   misc_feature    1..26
FT   /*tag= f
FT   /label= sticky_end
FT   /note= "single-strand overhang. The complementary
FT   strand also has a single-strand overhang at
FT   its 5'-end; the sequence of the overhang is
FT   5'-TCCGGATTAGCTTGAGATGGATCC-3'"
PN   WO9522340-A1.
PD   24-AUG-1995.
PF   17-FEB-1995; U02067.
PR   18-FEB-1994; US-199382.
PA   (SENS-) SENSI-TEST.
PI   Moyle WR;
DR   WPI; 95-302553/39.
DR   P-PSDB; R86259.
PT   Methods for altering fertility in mammals, esp. humans - e.g.
PT   stimulating fertility by reducing the activity and/or levels of
PT   circulating glyco:protein hormones having lutropin activity
PS   Example 23; Fig 18; 102pp; English.
CC   Analogue 1a (human CG-beta(1-145)-linker-human CG-alpha(1-92)[N53Q,
CC   N78Q]) is a specific example of a single chain gonadotropin having
CC   a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a
CC   CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino
CC   acids. The analogue 1a was derived from analogue 1 by removing the
CC   two glycosylation sites from the alpha-subunit. The analogue has
CC   anti-luteinising hormone (lutropin) activity and can be used for
CC   facilitating ovulation, terminating pregnancy and reducing androgen
CC   secretion. The present sequence codes for analogue 1a.
SQ   Sequence   836 BP;    166 A;    282 C;    222 G;    166 T;

  Query Match           34.0%;  Score 409;  DB 17;  Length 836;
  Best Local Similarity  99.0%;  Pred. No. 1.73e-271;
  Matches   413;  Conservative    0;  Mismatches   4;  Indels   0;  Gaps   0;

Db    111 ccacggtgccgccccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    783 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 842

Db    171 atcaccgtcaacaccaccatctgtgccggctactgccccaccatgacccgcgtgctgcag 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    843 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 902

Db    231 ggggtcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 290
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        |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     903 GGGGTCCTCCCCGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 962

Db     291 atccggctccctggctgcccgcgcggcgtgaaccccgtggtctcctacgccgtggctctc 350
        |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy     963 ATCCGGCTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCTGTGGCTCTC 1022

Db     351 agctgtcaatgtgcactctgccgccgcagcaccactgactgcgggggtcccaaggaccac 410
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1023 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1082

Db     411 cccttgacctgtgatgacccccgcttccaggactcctcttcctcaaaggcccctcccccc 470
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1083 CCCTTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCC 1142

Db     471 agccttccaagcccatcccgactcccggggccctcggacaccccgatcctcccccaa 527
        |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    1143 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGATCCTCCCACAA 1199
```

Search completed: Wed May 6 13:40:33 1998
Job time : 161 secs.

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:18:57 1998; MasPar time 1103.82 Seconds
1323.848 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-3
Description: (1-1202) from US08804166.seq
Perfect Score: 1202
N.A. Sequence: 1 CTCGAGATGGCTACAGGTAA.....CCCCGATCCTCCCACAATAA 1202
Comp: GAGCTCTACCGATGTCCATT.....GGGGCTAGGAGGGTGTTATT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est8 8:em_gss 9:em_est13
Database: genbank-est
10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13
25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.212; Variance 2.135; scale 5.252

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c 1	391	32.5	601	13	N32759	yw91b05.s1 Homo sapien	0.00e+00
c 2	384	31.9	537	13	N30276	yw69d04.s1 Homo sapien	0.00e+00
c 3	382	31.8	593	13	N29730	yw78h03.s1 Homo sapien	0.00e+00
c 4	381	31.7	564	13	N32604	yw95d03.s1 Homo sapien	0.00e+00
c 5	379	31.5	442	13	N32233	yw81f08.s1 Homo sapien	0.00e+00
c 6	379	31.5	473	13	N27302	yw71f12.s1 Homo sapien	0.00e+00
c 7	379	31.5	548	13	N30036	yw80b11.s1 Homo sapien	0.00e+00
c 8	377	31.4	566	13	N30831	yw70b04.s1 Homo sapien	0.00e+00
c 9	373	31.0	563	13	N31955	yw89a07.s1 Homo sapien	0.00e+00
c 10	371	30.9	473	25	AA400910	zt71h09.s1 Soares test	0.00e+00
c 11	372	30.9	479	13	N30684	yw77h04.s1 Homo sapien	0.00e+00
c 12	365	30.4	446	13	N31616	yw84a02.s1 Homo sapien	0.00e+00
c 13	363	30.2	526	28	AA644163	af62d08.s1 Soares NhHM	0.00e+00
c 14	354	29.5	400	25	AA232905	zr46c04.s1 Soares NhHM	0.00e+00
c 15	350	29.1	531	16	W71989	zd66b03.s1 Soares feta	0.00e+00
c 16	345	28.7	419	16	H95374	yw60b03.s1 Soares plac	0.00e+00
c 17	331	27.5	403	13	N26397	yw76g11.s1 Homo sapien	0.00e+00
c 18	325	27.0	441	13	N30741	yw74b04.s1 Homo sapien	0.00e+00
c 19	322	26.8	422	11	R23214	yh28a03.s1 Homo sapien	0.00e+00
c 20	319	26.5	515	13	N30608	yw72c07.s1 Homo sapien	0.00e+00
c 21	317	26.4	404	13	N30833	yw70b08.s1 Homo sapien	0.00e+00
c 22	311	25.9	386	13	N30822	yw65h07.s1 Homo sapien	0.00e+00
c 23	309	25.7	367	11	R68815	yi43c05.s1 Homo sapien	0.00e+00
c 24	301	25.0	329	12	H12587	yj12g11.s1 Homo sapien	0.00e+00
c 25	299	24.9	367	16	H94446	yw55f02.s1 Soares plac	0.00e+00
c 26	298	24.8	380	13	N30290	yw69f05.s1 Homo sapien	0.00e+00
c 27	294	24.5	352	13	H87464	yw17e05.s1 Homo sapien	0.00e+00
28	290	24.1	526	25	AA393716	zt71h09.r1 Soares test	0.00e+00
c 29	288	24.0	386	16	H94451	yw55g08.s1 Soares plac	0.00e+00
c 30	289	24.0	427	13	N27111	yw75h12.s1 Homo sapien	0.00e+00
c 31	283	23.5	319	13	H87631	yw17e12.s1 Homo sapien	0.00e+00
c 32	278	23.1	329	13	H87156	yw15b04.s1 Homo sapien	0.00e+00
c 33	276	23.0	311	10	T47334	yb10e11.s1 Homo sapien	0.00e+00
c 34	269	22.4	284	13	H93656	yw55a11.s1 Homo sapien	0.00e+00
c 35	267	22.2	303	13	H86993	yw15b10.s1 Homo sapien	0.00e+00
c 36	257	21.4	291	10	T90191	yd38g09.s1 Homo sapien	0.00e+00
c 37	249	20.7	266	13	H93668	yw55c12.s1 Homo sapien	0.00e+00
38	241	20.0	251	19	AA330413	EST34462 Embryo, 6 wee	0.00e+00
39	238	19.8	519	23	C18044	Human placenta cDNA 5'	0.00e+00
40	237	19.7	278	10	T49170	yb09g02.r1 Homo sapien	0.00e+00
c 41	233	19.4	248	16	H95381	yw60d07.s1 Soares plac	0.00e+00
42	228	19.0	341	12	T29543	EST83815 Homo sapiens	0.00e+00
c 43	222	18.5	244	16	H94107	yw58h09.s1 Soares plac	0.00e+00
c 44	217	18.1	255	11	R63352	yi07h10.s1 Homo sapien	0.00e+00
45	214	17.8	275	10	T47316	yb10c02.r1 Homo sapien	0.00e+00

ALIGNMENTS

RESULT 1
LOCUS N32759 601 bp mRNA EST 10-JAN-1996

DEFINITION yw91b05.s1 Homo sapiens cDNA clone 259569 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION N32759
NID g1153158
KEYWORDS EST.
SOURCE human clone=259569 primer=m13 -40 forward library=Soares placenta 8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 601)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

```
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 387
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES                Location/Qualifiers
     source             1. .601
                        /organism="Homo sapiens"
                        /clone="259569"
     mRNA               <1. .>601
BASE COUNT      112 a    154 c    219 g    110 t      6 others
ORIGIN

  Query Match           32.5%;  Score 391;  DB 13;  Length 601;
  Best Local Similarity  97.1%;  Pred. No. 0.00e+00;
  Matches   408;  Conservative    0;  Mismatches  11;  Indels   1;  Gaps   1;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
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Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGCAGCCAAGGGAGCCGGAT 255
           ||||||||| |||||||||||||||||||||||||||||    | ||||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCCC 315
           |||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     316 TTGCAGCACGCGGGTCATGGTGGGGCAGTAGCGGGCACAGATGGTGGTGTTGACGGTGAT 375
           ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 843

Db     376 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTGG 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     842 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTGG 783


RESULT    2
LOCUS       N30276        537 bp    mRNA            EST       05-JAN-1996

DEFINITION  yw69d04.s1 Homo sapiens cDNA clone 257479 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30276
NID         g1148796
KEYWORDS    EST.
SOURCE      human clone=257479 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 537)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 313
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES                Location/Qualifiers
     source             1. .537
                        /organism="Homo sapiens"
                        /clone="257479"
     mRNA               <1. .>537
BASE COUNT       98 a    145 c    201 g     90 t      3 others
ORIGIN

  Query Match           31.9%;  Score 384;  DB 13;  Length 537;
  Best Local Similarity  97.0%;  Pred. No. 0.00e+00;
  Matches   415;  Conservative    0;  Mismatches   9;  Indels   4;  Gaps   4;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     196 GAGAGCCACGGCGTTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGA 254
           ||||||||| |||| ||||||||||||||||||||||||||| |||||||||||||||
Cp    1022 GAGAGCCACAGCGT-AGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGA 964

Db     255 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCC 314
           |||||||||||||||||||||||||||||||||||||||||||||| || | |||||
Cp     963 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCC 904

Db     315 CCCTGCAGCACGCGGGTCATGGTGGGGCAGTAACCGGCACAGATGGTGGTGTTGACGGTG 374
           || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Cp     903 CC-TGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTG 845

Db     375 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCANCGT 434
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Cp     844 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGT 785

Db     435 GGCNAAGC 442
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Cp     784 GGACCAGC 777


RESULT    3
LOCUS       N29730        593 bp    mRNA            EST       05-JAN-1996

DEFINITION  yw78h03.s1 Homo sapiens cDNA clone 258389 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N29730
NID         g1148250
KEYWORDS    EST.
SOURCE      human clone=258389 primer=m13 -40 forward library=Soares placenta
```

```
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 368
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
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BASE COUNT      109 a    151 c    216 g    111 t      6 others
ORIGIN

  Query Match           31.8%;  Score 382;  DB 13;  Length 593;
  Best Local Similarity  96.7%;  Pred. No. 0.00e+00;
  Matches   414;  Conservative    0;  Mismatches  10;  Indels   4;  Gaps   4;

Db      18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      78 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     138 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 196
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Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGNGG-CAGCCAGGGAGCCGGAT 255
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Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGCAAGACCACC 315
           |||||||||||||||||||||||||||||||||||||||||||||||  ||  | ||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     316 CTGCAGCACGCGGGTCATGGTTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 375
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp     902 CTGCAGCACGCGGGTCATGGT-GGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 844

Db     376 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCANGGTTGGCATTGATGGGGCGGCACCGT 435
           |||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||
Cp     843 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGT-GGCATTGATGGGGCGGCACCGT 785

Db     436 GGCCAAGC 443
           || | |||
Cp     784 GGACCAGC 777


RESULT    4
LOCUS       N32604        564 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw95d03.s1 Homo sapiens cDNA clone 259973 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32604
NID         g1153003
KEYWORDS    EST.
SOURCE      human clone=259973 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 364
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .564
                     /organism="Homo sapiens"
                     /clone="259973"
     mRNA            <1. .>564
BASE COUNT      103 a    148 c    206 g     99 t      8 others
ORIGIN

  Query Match           31.7%;  Score 381;  DB 13;  Length 564;
  Best Local Similarity  96.5%;  Pred. No. 0.00e+00;
  Matches   410;  Conservative    0;  Mismatches  12;  Indels   3;  Gaps   3;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 76
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
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Cp   1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db    196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGCAGCCAAGGGAGCCGGAT 255
          ||||||||| |||||||||||||||||||||||||||||||     | ||||||||||||
Cp   1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db    256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCCC 315
          |||||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Cp    962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db    316 CTTGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGA 374
          || |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Cp    902 CT-GCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 844

Db    375 TGCACACGGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    843 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 784

Db    435 GCCNA 439
          | | |
Cp    783 GACCA 779


RESULT    5
LOCUS       N32233        442 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw81f08.s1 Homo sapiens cDNA clone 258663 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32233
NID         g1152632
KEYWORDS    EST.
SOURCE      human clone=258663 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 364
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .442
                      /organism="Homo sapiens"
                      /clone="258663"
     mRNA             <1. .>442
BASE COUNT       85 a    110 c    174 g     68 t      5 others

ORIGIN

  Query Match           31.5%;  Score 379;  DB 13;  Length 442;
  Best Local Similarity  94.6%;  Pred. No. 0.00e+00;
  Matches   402;  Conservative    0;  Mismatches  22;  Indels   1;  Gaps   1;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACCCCGCAAGTCAGTTGGTGCTGCGGCGGCAGAGTGCACATTGACAGC 196
           |||||||||||||||||   ||||||| ||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCGCAGTCAGT-GGTGCTGCGGCGGCAGAGTGCACATTGACAGC 1024

Db     197 TGAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCNCGGCAGCCANGGGAGCCGGA 256
           |||||||||| |||||||||||||||||||||||||||||| |||    |  ||||||||||
Cp    1023 TGAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGA 964

Db     257 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGNCAAGACCAC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||   ||  | |
Cp     963 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCC 904

Db     317 CCTGCAGCACGCGGGTCATGGTGGGGCAGTAACCGGCACAGATGGTGGTGTTGACGGTNA 376
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |
Cp     903 CCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 844

Db     377 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCANCGTG 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Cp     843 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 784

Db     437 GCCCA 441
           | |||
Cp     783 GACCA 779


RESULT    6
LOCUS       N27302        473 bp    mRNA            EST       29-DEC-1995

DEFINITION  yw71f12.s1 Homo sapiens cDNA clone 257711 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N27302
NID         g1141650
KEYWORDS    EST.
SOURCE      human clone=257711 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
```

```
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 225
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .473
                      /organism="Homo sapiens"
                      /clone="257711"
     mRNA             <1. .>473
BASE COUNT       87 a    122 c    182 g     76 t      6 others
ORIGIN

  Query Match           31.5%;  Score 379;  DB 13;  Length 473;
  Best Local Similarity  95.5%;  Pred. No. 0.00e+00;
  Matches   402;  Conservative    0;  Mismatches  17;  Indels   2;  Gaps   2;

Db      18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 77
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      78 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     138 GTGGTCCTTGGGACCCCGCCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 197
           ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     198 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGANCCGGAT 256
           |||||||| |||||||||||||||||||||||||||||||| |||||||||| ||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     257 GGACTCGAANCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGACAAGACCACC 316
           |||||||| ||||||||||||||||||||||||||||||||||||   ||  | ||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     317 TTGCAGCACGCGGGTCATGGTGGGGCAGTANCCGGGCACAGATGGTGGTGTTNACGGTGA 376
           ||||||||||||||||||||||||||||| |||| ||||||||||||||| |||||||
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGG-CACAGATGGTGGTGTTGACGGTGA 844

Db     377 TGCACACGGGGCAGCCCNCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTN 436
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp     843 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 784

Db     437 G 437
           |
Cp     783 G 783


RESULT    7
LOCUS       N30036        548 bp    mRNA            EST       05-JAN-1996

DEFINITION  yw80b11.s1 Homo sapiens cDNA clone 258525 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30036
NID         g1148556
KEYWORDS    EST.
SOURCE      human clone=258525 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 548)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 333
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .548
                      /organism="Homo sapiens"
                      /clone="258525"
     mRNA             <1. .>548
BASE COUNT       99 a    143 c    206 g     93 t      7 others
ORIGIN

  Query Match           31.5%;  Score 379;  DB 13;  Length 548;
  Best Local Similarity  96.9%;  Pred. No. 0.00e+00;
  Matches   410;  Conservative    0;  Mismatches   9;  Indels   4;  Gaps   4;

Db      18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      78 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     138 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 196
           |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGCAAGCCATGGGAGCCGGA 256
           |||||||| |||||||||||||||||||||||||||||  ||||| ||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCA-GGGAGCCGGA 964

Db     257 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCN 316
           |||||||||||||||||||||||||||||||||||||||||||||||||| || | ||||
Cp     963 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCC 904

Db     317 CCTTGCAAGCACGCGGGTCATGGTGGGGCAGTAGCGGGCACAGATGGTGGTGTTGACGGT 376
           ||| ||| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Cp     903 CCT-GCA-GCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGT 846

Db     377 GATGNACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 436
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     845 GATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 786

Db     437 TGG 439
           |||
Cp     785 TGG 783


RESULT    8
LOCUS       N30831        566 bp    mRNA            EST       05-JAN-1996
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DEFINITION  yw70b04.s1 Homo sapiens cDNA clone 257551 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30831
NID         g1149351
KEYWORDS    EST.
SOURCE      human clone=257551 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 566)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 400
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .566
                     /organism="Homo sapiens"
                     /clone="257551"
     mRNA            <1. .>566
BASE COUNT      103 a    148 c    209 g    100 t      6 others
ORIGIN

  Query Match           31.4%;  Score 377;  DB 13;  Length 566;
  Best Local Similarity  96.4%;  Pred. No. 0.00e+00;
  Matches   407;  Conservative    0;  Mismatches  12;  Indels   3;  Gaps   3;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 76
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGG-CCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     196 GAGAGCCACGGCTTAGGAGACCACGGGGTTCACGCCGCGCGGCAAGCCANGGGAGCCGGA 255
           ||||||||| || |||||||||||||||||||||||||||  ||||| ||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCA-GGGAGCCGGA 964

Db     256 TGGACTCGAAGCGCAAATCGCGGGTAGTTGCACACCACCTGAGGCAGGGCGGCCAGACCC 315
           ||||||||||||||| ||||||| |||||||||||||||||||||||  ||  ||
Cp     963 TGGACTCGAAGCGCACATCGCGG-TAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACC 905

Db     316 CCCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCGGTCACAGATGGTGGTGTTGACGGTG 375
           |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Cp     904 CCCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTG 845

Db     376 ATGCACACGGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGT 435
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     844 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGT 785

Db     436 GG 437
           ||
Cp     784 GG 783


RESULT    9
LOCUS       N31955        563 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw89a07.s1 Homo sapiens cDNA clone 259380 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N31955
NID         g1152354
KEYWORDS    EST.
SOURCE      human clone=259380 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 335
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Homo sapiens"
                     /clone="259380"
     mRNA            <1. .>563
BASE COUNT      101 a    148 c    208 g    103 t      3 others
ORIGIN

  Query Match           31.0%;  Score 373;  DB 13;  Length 563;
  Best Local Similarity  97.0%;  Pred. No. 0.00e+00;
  Matches   416;  Conservative    0;  Mismatches   7;  Indels   6;  Gaps   6;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143
```

```
Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTTGGTGCTGCGGCGGCAGAGTGCACATTGACAGC 195
           |||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGT-GGTGCTGCGGCGGCAGAGTGCACATTGACAGC 1024

Db     196 TGAGAGCCACGGCGTTAGGAGACCACGGGGTTCACGCCGCGCGGCAAGCCANGGGAGCCG 255
           ||||||||| |||| |||||||||||||||||||||||||  ||||| ||||||||
Cp    1023 TGAGAGCCACAGCGT-AGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCA-GGGAGCCG 966

Db     256 GATGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGCAAG-AC 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||  || ||
Cp     965 GATGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGAC 906

Db     315 CCC-TGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGT 373
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     905 CCCCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGT 846

Db     374 GATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     845 GATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 786

Db     434 TGGCCAAGC 442
           ||| | |||
Cp     785 TGGACCAGC 777
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RESULT 10
LOCUS AA400910 473 bp mRNA EST 12-AUG-1997

DEFINITION zt71h09.s1 Soares testis NHT Homo sapiens cDNA clone 727841 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION AA400910
NID g2054783
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 640 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 392.
FEATURES Location/Qualifiers
source 1. .473
/organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="727841"
/clone_lib="Soares testis NHT"
/sex="male"
/lab_host="DH10B"
mRNA complement(<1. .>473)
/db_xref="GDB:5924752"
BASE COUNT 84 a 120 c 190 g 78 t 1 others
ORIGIN

Query Match 30.9%; Score 371; DB 25; Length 473;
Best Local Similarity 97.6%; Pred. No. 0.00e+00;
Matches 405; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

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Db      20 TTATTGTGGGAGGATCGGGGTGTCTGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 79
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      80 GGGGGGAGGGGCCTTTGAGGAAGAGGAGGCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 139
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     140 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 198
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     199 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGAT 257
           ||||||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     258 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGNCAG-ACCCC 316
           |||||||||||||||||||||||||||||||||||||||||||||||||||  || |||||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     317 -TGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGAT 374
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 843

Db     375 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCAC 429
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     842 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCAC 788
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RESULT 11
LOCUS N30684 479 bp mRNA EST 05-JAN-1996

DEFINITION yw77h04.s1 Homo sapiens cDNA clone 258295 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION N30684
NID g1149204
KEYWORDS EST.
SOURCE human clone=258295 primer=m13 -40 forward library=Soares placenta 8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

```
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 333
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .479
                     /organism="Homo sapiens"
                     /clone="258295"
     mRNA            <1. .>479
BASE COUNT       86 a    122 c    184 g     79 t      8 others
ORIGIN

  Query Match           30.9%;  Score 372;  DB 13;  Length 479;
  Best Local Similarity  95.5%;  Pred. No. 0.00e+00;
  Matches   401;  Conservative    0;  Mismatches  16;  Indels   3;  Gaps   3;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     196 GAGAGCCACGGCNTAGGAGACCACGGGGTTCACGCCGCGCGGCAGCCANGGGAGCCGGAT 255
           ||||||||| || |||||||||||||||||||||||||||||    |  ||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGC-AGACCCCC 314
           |||||||||||||||||||||||||||||||||||||||||||||||||  ||  ||||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     315 TTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTNACGGTGAT 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 843

Db     375 GCACACGGGGCAGCCCTCCTTCTCCACAGCCANGGGTGGNATTGATGGGGCGGCACNTTG 434
           |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||  ||
Cp     842 GCACACGGGGCAGCCCTCCTTCTCCACAGCCA-GGGTGGCATTGATGGGGCGGCACCGTG 784


RESULT   12
LOCUS       N31616         446 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw84a02.s1 Homo sapiens cDNA clone 258890 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N31616
NID         g1152015
KEYWORDS    EST.
SOURCE      human clone=258890 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 446)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 329
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .446
                     /organism="Homo sapiens"
                     /clone="258890"
     mRNA            <1. .>446
BASE COUNT       82 a    108 c    170 g     71 t      15 others
ORIGIN

  Query Match           30.4%;  Score 365;  DB 13;  Length 446;
  Best Local Similarity  94.1%;  Pred. No. 0.00e+00;
  Matches   396;  Conservative    0;  Mismatches  21;  Indels   4;  Gaps   4;

Db      17 TTANTGTGGGANGATNGGGGTTTNCGANGGCCCCGGGANTNNNNATGGACTTGGNAGGCT 76
           ||| |||||||| ||| ||||| | ||| ||||||||||| |    |||| ||||| |||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGGGGCCTTTNAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTNACAGCT 195
           |||||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGAT 254
           |||||||| |||||||||||||||||||||||||||||||||| |||||||||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     255 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAG-ACCCC 313
           |||||||||||||||||||||||||||||||||||||||||||||||||| || || |||||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     314 TTGCAGCACGCGGGTCATGGTGGGGCAGTAACCGGCACAGATGGTGGTGTTGACGGTGAT 373
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 843

Db     374 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTTGATGGNGCGGCACCGTG 433
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||
Cp     842 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATT-GATGGGGCGGCACCGTG 784

Db     434 G 434
           |
Cp     783 G 783
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```
RESULT   13
LOCUS       AA644163      526 bp    mRNA            EST       27-OCT-1997

DEFINITION  af62d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 1046607 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.
ACCESSION   AA644163
NID         g2569381
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 335.
FEATURES              Location/Qualifiers
     source           1. .526
                      /organism="Homo sapiens"
                      /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; Equal amounts of plasmid DNA from three
                      normalized libraries (melanocyte 2NbHM, pregnant uterus
                      NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                      were made in vitro. Following HAP purification, this DNA
                      was used as tracer in a subtractive hybridization
                      reaction. The driver was PCR-amplified cDNAs from pools of
                      5,000 clones made from the same 3 libraries. The pools
                      consisted of I.M.A.G.E. clones 260232-265223,
                      340488-345479, and 484488-489479."
                      /db_xref="taxon:9606"
                      /clone="1046607"
                      /clone_lib="Soares NhHMPu S1"
                      /tissue_type="Pooled human melanocyte, fetal heart, and
                      pregnant uterus"
                      /lab_host="DH10B"
BASE COUNT      100 a    140 c    201 g     85 t
ORIGIN

  Query Match           30.2%;  Score 363;  DB 28;  Length 526;
  Best Local Similarity  96.7%;  Pred. No. 0.00e+00;
  Matches   407;  Conservative    0;  Mismatches   8;  Indels   6;  Gaps   6;

Db      16 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 75
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      76 GGCAGGAGGGGCCTTTAAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 135
           ||  ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     136 GTGGTCCTTGGGACCCCGACAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGAT 254
           ||||||||| |||||||||||||||||||||||||||||||| |||||||||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     255 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGC-AGGACCCC 313
           ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     314 -TGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGAT 371
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 843

Db     372 GGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGG-ACCGTG 430
           | ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Cp     842 G-CACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 784

Db     431 G 431
           |
Cp     783 G 783


RESULT   14
LOCUS       AA232905      400 bp    mRNA            EST       06-AUG-1997

DEFINITION  zr46c04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666438 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.
ACCESSION   AA232905
NID         g1855917
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 834   Std Error: 0.00
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 361.
FEATURES              Location/Qualifiers
     source           1. .400
                      /organism="Homo sapiens"
                      /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; Equal amounts of plasmid DNA from three
                      normalized libraries (melanocyte 2NbHM, pregnant uterus
                      NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                      were made in vitro. Following HAP purification, this DNA
                      was used as tracer in a subtractive hybridization
                      reaction. The driver was PCR-amplified cDNAs from pools of
                      5,000 clones made from the same 3 libraries. The pools
                      consisted of I.M.A.G.E. clones 260232-265223,
                      340488-345479, and 484488-489479."
                      /db_xref="taxon:9606"
                      /clone="666438"
                      /clone_lib="Soares NhHMPu S1"
                      /tissue_type="Pooled human melanocyte, fetal heart, and
                      pregnant uterus"
                      /lab_host="DH10B"
```

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     mRNA            complement(<1. .>400)
                     /db_xref="GDB:5428470"
BASE COUNT       74 a     98 c    165 g     63 t
ORIGIN

  Query Match           29.5%;  Score 354;  DB 25;  Length 400;
  Best Local Similarity  97.2%;  Pred. No. 0.00e+00;
  Matches   375;  Conservative    0;  Mismatches   9;  Indels   2;  Gaps   2;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      77 GGGGGGAGTGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     137 GTGGTCCTTGGGACACCCGCAGTCAGTGGTGCTGCGGCGGCAGGAGGCACATTGACAGCT 196
           |||||||||||||| |||||||||||||||||||||||||||||   ||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 256
           ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     257 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGTCAG-AGCCC 315
           |||||||||||||||||||||||||||||||||||||||||||||||||||  || | |||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     316 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGAT 374
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 843

Db     375 GCACACGGGGCAGCCCTCCTTCTCCA 400
           |||||||||||||||||||||||||||
Cp     842 GCACACGGGGCAGCCCTCCTTCTCCA 817


RESULT   15
LOCUS       W71989        531 bp    mRNA            EST       17-OCT-1996

DEFINITION  zd66b03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
            345581 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN
            PRECURSOR (HUMAN);.
ACCESSION   W71989
NID         g1382299
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 957   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 346.
FEATURES             Location/Qualifiers
     source          1. .531
                     /organism="Homo sapiens"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
                     /db_xref="taxon:9606"
                     /clone="345581"
                     /clone_lib="Soares fetal heart NbHH19W"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
     mRNA            complement(<1. .>531)
BASE COUNT      102 a    125 c    193 g     93 t     18 others
ORIGIN

  Query Match           29.1%;  Score 350;  DB 16;  Length 531;
  Best Local Similarity  93.1%;  Pred. No. 0.00e+00;
  Matches   391;  Conservative    0;  Mismatches  25;  Indels   4;  Gaps   4;

Db      18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 77
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db      78 NNNGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1083

Db     138 GTGGTCNTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 196
           |||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1023

Db     197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGCAGCCANGGGAGCCGGAT 256
           ||||||||| ||||||||||||||||||||||||||||||    |  ||||||||||||
Cp    1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 963

Db     257 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGCAAGACCCCC 316
           |||||||||||||||||||||||||||||||||||||||||||||||||||  ||  ||||
Cp     962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGGGAGGACCCC 903

Db     317 TTGCAGCACGCGGGTCATGGTGGGGCAGTAACCGGCACAGATNGTGGTGTTTGACGGTTG 376
           ||||||||||||||||||||||||||||| |||||||||| |||||||| |||||| |
Cp     902 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTT-GACGGT-G 845

Db     377 ATGCANACGGGGCAGCC-TCCTTCTCCACAGCCAAGGTGGCATTGATGGGGGNGGAACGT 435
           ||||| |||||||||||| |||||||||||||||| |||||||||||||||  | | |||
Cp     844 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGT 785


Search completed: Wed May  6 13:37:32 1998
Job time : 1115 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:56:17 1998; MasPar time 9.51 Seconds
482.526 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 32.496; Variance 135.826; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	2341	100.0	307	26	W33358	TBP(20-161)/hCG-beta	9.21e-224
2	2022	86.4	336	26	W33360	TBP(20-190)/hCG-beta	4.77e-191
3	1321	56.4	256	26	W33357	TBP(20-161)/hCG-alpha	1.84e-119
4	1289	55.1	285	26	W33359	TBP(20-190)/hCG-alpha	3.29e-116
5	1124	48.0	161	5	R27496	Native 30 kD TNF inhi	1.82e-99
6	1124	48.0	199	4	R24080	Truncated TNF-alpha 5	1.82e-99
7	1124	48.0	309	13	R70108	TNF-R-GBPH fusion pro	1.82e-99
8	1124	48.0	371	2	R07449	Tumour Necrosis Facto	1.82e-99
9	1124	48.0	451	13	R70107	TNF-R-GBP 130 fusion	1.82e-99
10	1124	48.0	455	8	R42059	Lambda derived TNF-R.	1.82e-99
11	1124	48.0	455	2	R10986	30kD TNF inhibitor pr	1.82e-99
12	1124	48.0	455	4	R20787	TNF-alpha binding pro	1.82e-99
13	1124	48.0	455	14	R75084	p55 TNF-R.	1.82e-99
14	1124	48.0	455	2	R07451	Human Tumour Necrosis	1.82e-99
15	1124	48.0	455	2	R11082	Human 55kD TNF-bindin	1.82e-99
16	1124	48.0	455	4	R24000	TNF-alpha 55kD recept	1.82e-99
17	1124	48.0	547	13	R70104	TNF-R-GBPH fusion pro	1.82e-99
18	1124	48.0	884	13	R70109	TNF-R-GBP 130 fusion	1.82e-99
19	1124	48.0	900	13	R70103	TNF-R-GBP 130 fusion	1.82e-99
20	1124	48.0	1245	13	R70106	TNF-R-Pl. vivax Duffy	1.82e-99
21	1124	48.0	1604	13	R70105	TNF-R-EBA 175 fusion	1.82e-99
22	1118	47.8	433	8	R51032	Mutant p55 tumour nec	7.38e-99
23	1118	47.8	443	8	R51033	Mutant p55 tumour nec	7.38e-99
24	1118	47.8	455	8	R51034	Mutant p55 tumour nec	7.38e-99
25	1118	47.8	455	8	R42197	p55 Tumour necrosis f	7.38e-99
26	1110	47.4	455	3	R12550	Type I TNF receptor.	4.76e-98
27	1030	44.0	165	3	R15043	Human chorionic gonad	5.90e-90
28	1025	43.8	145	6	R30999	Human chorionic gonad	1.89e-89
29	1022	43.7	145	3	R15174	hCG histidine substit	3.80e-89
30	1021	43.6	145	3	R15171	hCG methionine substi	4.79e-89
31	1021	43.6	145	3	R15120	hCG/hLH chimera, A5.	4.79e-89
32	1020	43.6	145	25	W31200	Human chorionic gonad	6.04e-89
33	1020	43.6	145	3	R15117	hCG/hLH chimera, A3a.	6.04e-89
34	1020	43.6	145	3	R15169	hCG methionine substi	6.04e-89
35	1021	43.6	265	15	R86247	Single chain gonadotr	4.79e-89
36	1021	43.6	265	15	R86259	Partially deglycosyla	4.79e-89
37	1018	43.5	145	3	R15173	hCG histidine substit	9.63e-89
38	1015	43.4	145	24	W27681	Chorionic gonadotroph	1.93e-88
39	1015	43.4	145	3	R15177	hCG histidine substit	1.93e-88
40	1016	43.4	181	15	R86258	Human CG beta-subunit	1.53e-88
41	1014	43.3	145	24	W27688	Chorionic gonadotroph	2.44e-88
42	1013	43.3	145	3	R15103	hCG/bLH chimera, D7.	3.08e-88
43	1013	43.3	145	3	R15170	hCG methionine substi	3.08e-88
44	1013	43.3	145	24	W27687	Chorionic gonadotroph	3.08e-88
45	1013	43.3	145	24	W27682	Chorionic gonadotroph	3.08e-88

ALIGNMENTS

RESULT 1
ID W33358 standard; Protein; 307 AA.
AC W33358;
DT 19-MAR-1998 (first entry)
DE TBP(20-161)/hCG-beta fusion protein.
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW beta subunit; hCG-beta.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 279..1202
FT /*tag= a
PN WO9730161-A1.
PD 21-AUG-1997.
PF 20-FEB-1997; U02315.
PR 20-FEB-1996; US-011936.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PI Campbell RK, Chappel SC, Jameson BA;
DR WPI; 97-425036/39.
DR N-PSDB; T94008.
PT Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation
PS Example; Pages 34-35; 60pp; English.
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein hormone capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC (hCG-beta) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed.
SQ Sequence 307 AA;

Query Match 100.0%; Score 2341; DB 26; Length 307;
Best Local Similarity 100.0%; Pred. No. 9.21e-224;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

```
Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscagagprcrpinatlav 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCAGAGPRCRPINATLAV 180

Db    181 ekegcpvcitvntticagycptmtrvlqgvlpalpqvvcnyrdvrfesirlpgcprgvnp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 EKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNP 240

Db    241 vvsyavalscqcalcrrsttdcggpkdhpltcddprfqdsssskapppslpspsrlpgps 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 VVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPS 300

Db    301 dtpilpq 307
          |||||||
Qy    301 DTPILPQ 307


RESULT    2
ID   W33360 standard; Protein; 336 AA.
AC   W33360;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94022.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 39-40; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   336 AA;

  Query Match           86.4%;  Score 2022;  DB 26;  Length 336;
  Best Local Similarity  91.4%;  Pred. No. 4.77e-191;
  Matches   307;  Conservative    0;  Mismatches   0;  Indels  29;  Gaps   1;

Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscsnckkslectklclpq 180
          ||||||||||||||||||||||||||||||||||||||||||
Qy    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSC---------------- 164

Db    181 ienvkgtedsgttagagprcrpinatlavekegcpvcitvntticagycptmtrvlqgvl 240
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    165 ------------AGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVL 211

Db    241 palpqvvcnyrdvrfesirlpgcprgvnpvvsyavalscqcalcrrsttdcggpkdhplt 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    212 PALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLT 271

Db    301 cddprfqdsssskapppslpspsrlpgpsdtpilpq 336
          |||||||||||||||||||||||||||||||||||||
Qy    272 CDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 307


RESULT    3
ID   W33357 standard; Protein; 256 AA.
AC   W33357;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94007.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 32-33; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   256 AA;

  Query Match           56.4%;  Score 1321;  DB 26;  Length 256;
  Best Local Similarity  98.8%;  Pred. No. 1.84e-119;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscagaapgc 171
          |||||||||||||||||||||||||||||||||||||||||||||||:| |
Qy    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCAGAGPRC 171


RESULT    4
ID   W33359 standard; Protein; 285 AA.
AC   W33359;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
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PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94021.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 37-38; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   285 AA;

  Query Match           55.1%;  Score 1289;  DB 26;  Length 285;
  Best Local Similarity  98.8%;  Pred. No. 3.29e-116;
  Matches   163;  Conservative    2;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfnctlclngtvhlscqekqntvctchagfflrenecvscs 165
          ||||||||:||||||||||||||||||||||||||||||||||||:
Qy    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165


RESULT    5
ID   R27496 standard; protein; 161 AA.
AC   R27496;
DT   09-MAR-1993  (first entry)
DE   Native 30 kD TNF inhibitor.
KW   Tumour necrosis factor; ethylene glycol; pharmokinetic;
KW   adult respiratory distress syndrome; rheumatoid arthritis;
KW   septic shock; pulmonary fibrosis; spacer.
OS   Homo sapiens.
PN   WO9216221-A.
PD   01-OCT-1992.
PF   13-MAR-1992; U02122.
PR   15-MAR-1991; US-669862.
PR   17-JAN-1992; US-822296.
PA   (SYND ) SYNERGEN INC.
PI   Armes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;
DR   WPI; 92-348933/42.
PT   New ethylene glycolated polypeptide(s) with improved
PT   pharmacokinetic properties - for treating e.g. TNF and IL-1
PT   mediated diseases, e.g. adult respiratory distress syndrome,
PT   rheumatoid arthritis, septic shock etc.
PS   Claim 54; Fig 2; 100pp; English.
CC   The sequence shows a native 30 kD TNF inhibitor which may be
CC   modified to contain at least one non-native cysteine residue, pref.
CC   at positions 1, 14, 105, 111 and/or 165.  The non-native cysteine is
CC   joined to a non-peptidic polymer, pref. monomethoxy PEG via
CC   thio-ether bonds.  Two such TNF inhibitor mols. may be linked via
CC   this non-peptidic spacer.  The modified polypeptides show improved
CC   pharmokinetic properties, i.e. increased mol. wt. hence reduced
CC   clearance rate following s.c. or systemic administration, increased
CC   sol. of native TNF inhibitors, and reduced antigenicity.  The
CC   polypeptides may be used for treatment of TNF mediated diseases such
CC   as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
CC   arthritis,inflammatory bowel disease and septic shock.  The same
CC   method may be applied to the interleukin-1 receptor antagonist
CC   IL-1ra.           See also R27495.
SQ   Sequence   161 AA;

  Query Match           48.0%;  Score 1124;  DB 5;  Length 161;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     61 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    121 kqntvctchagfflrenecvscs 143
          |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    6
ID   R24080 standard; Protein; 199 AA.
AC   R24080;
DT   05-NOV-1992  (first entry)
DE   Truncated TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   N-PSDB; Q24441.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence is a truncated TNF-alpha receptor derivative, as encoded
CC   in pTNFRecd. This was produced as described in Q24440.
CC   This derivative lacks the 81 carboxyl terminal residues of the
CC   cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   199 AA;

  Query Match           48.0%;  Score 1124;  DB 4;  Length 199;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
          |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    7
ID   R70108 standard; Protein; 309 AA.
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AC   R70108;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
FH   Key             Location/Qualifiers
FT   misc_difference 230..269
FT                   /label= repeat_region
FT                   /note= "can be repeated n times, where n is a real
FT                   number"
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 54-55; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The
CC   use of cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   309 AA;

  Query Match           48.0%;  Score 1124;  DB 13;  Length 309;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscs 162
          |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    8
ID   R07449 standard; protein; 371 AA.
AC   R07449;
DT   29-JAN-1991  (first entry)
DE   Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06282.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of
CC   e.g. COS7 cells.  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   371 AA;

  Query Match           48.0%;  Score 1124;  DB 2;  Length 371;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
          |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    9
ID   R70107 standard; Protein; 451 AA.
AC   R70107;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 53-54; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
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CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence   451 AA;

  Query Match           48.0%;  Score 1124;  DB 13;  Length 451;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscs 162
           |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   10
ID   R42059 standard; Protein; 455 AA.
AC   R42059;
DT   29-APR-1994  (first entry)
DE   Lambda derived TNF-R.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction.
OS   Homo sapiens.
OS   Lambda-gt10-7ctnfbp.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "Signal peptide"
FT   protein         41..455
FT                   /note= "Mature hTNF-R"
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   N-PSDB; Q49932.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.
CC   The sequences given in R42058-59 repressent human tumour necrosis
CC   factor receptor (TNF-R) and the sequences in R42060-61 represent
CC   human interleukin-1 receptor (IL-1R).  These sequences were used in
CC   the production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence   455 AA;

  Query Match           48.0%;  Score 1124;  DB 8;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   11
ID   R10986 standard; Protein; 455 AA.
AC   R10986;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor.
KW   Tumour necrosis factor; inhibitor.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cleavage_site   40..41
FT                   note=" cleavage gives active protein "
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   N-PSDB; Q10883.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC   from which the sequence was deduced was isolated from a cDNA
CC   library prepd. from RNA form U937 cells treated with PMA/PHA.
CC   The whole gene can be inserted into expression vectors for prepn.
CC   of TNF inhibitor for use in the treatment of inflammatory and
CC   degenerative diseases.  The active protein is claimed (Claim 8).
CC   See also R10984 and R11001.
SQ   Sequence   455 AA;

  Query Match           48.0%;  Score 1124;  DB 2;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
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Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   12
ID   R20787 standard; Protein; 455 AA.
AC   R20787;
DT   11-MAY-1992  (first entry)
DE   TNF-alpha binding protein.
```

```
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "signal peptide"
FT   peptide         41..455
FT                   /note= "mature peptide"
FT   domain          30..199
FT                   /note= "extracellular domain"
FT   domain          212..234
FT                   /note= "transmembrane domain"
FT   modified_site   145..147
FT                   /note= "potential N-glycosylation site"
FT   modified_site   151..153
FT                   /note= "potential N-glycosylation site"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   N-PSDB; Q20973.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
CC   can therefore be used therapeutically to treat disorders such as
CC   cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC   arthritis.
SQ   Sequence   455 AA;

  Query Match           48.0%;  Score 1124;  DB 4;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   13
ID   R75084 standard; Protein; 455 AA.
AC   R75084;
DT   19-JAN-1996  (first entry)
DE   p55 TNF-R.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         41..53
FT                   /note= "N terminus of soluble p55 TNF-R"
FT   modified_site   54..56
FT                   /note= "glycosylation site"
FT   modified_site   145..147
FT                   /note= "glycosylation site"
FT   modified_site   161..163
FT                   /note= "glycosylation site"
FT   peptide         193..210
FT                   /note= "peptide used in creation of chimeras"
FT   region          198..210
FT                   /note= "spacer region"
FT   misc_difference 201
FT                   /note= "major C terminus for soluble p55 TNF-R"
FT   misc_difference 202
FT                   /note= "essential for shedding reaction"
FT   misc_difference 203
FT                   /note= "minor C terminus for soluble p55 TNF-R"
FT   region          212..234
FT                   /note= "transmembrane region"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
DR   WPI; 95-194342/26.
DR   N-PSDB; Q90513.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor  - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R).
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment.  The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type.  The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain.  This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain.  The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11.  This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.
CC   The mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3.  These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence   455 AA;

  Query Match           48.0%;  Score 1124;  DB 14;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
           |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   14
ID   R07451 standard; protein; 455 AA.
AC   R07451;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
```

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OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06285.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   455 AA;

  Query Match           48.0%;  Score 1124;  DB 2;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
        |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   15
ID   R11082 standard; Protein; 455 AA.
AC   R11082;
DT   24-MAY-1991  (first entry)
DE   Human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   modified_site   54
FT                   /label= putative N-glycosylation site
FT   modified_site   145
FT                   /label= putative N-glycosylation site
FT   modified_site   151
FT                   /label= putative N-glycosylation site
FT   modified_site   270
FT                   /label= putative N-glycosylation site
FT   region          212..230
FT                   /label= transmembrane region
FT   peptide         1..28
FT                   /label= signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   455 AA;

  Query Match           48.0%;  Score 1124;  DB 2;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
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Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscs 183
        |||||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


Search completed: Wed May  6 08:57:56 1998
Job time : 99 secs.
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SMITH-WATERMAN (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:55:24 1998; MasPar time 13.64 Seconds
821.959 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 42.076; Variance 82.446; scale 0.510

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	48.0	158	5	1EXTB	tumor necrosis factor	2.76e-207
2	1124	48.0	455	1	GQHUT1	tumor necrosis factor	2.76e-207
3	1118	47.8	160	5	1EXTA	tumor necrosis factor	5.28e-206
4	1114	47.6	142	5	1NCFB	tumor necrosis factor	3.78e-205
5	1105	47.2	139	5	1TNRR	tumor necrosis factor	3.17e-203
6	1098	46.9	140	5	1NCFA	tumor necrosis factor	9.90e-202
7	1030	44.0	145	2	I37412	beta-gonadotropin - h	3.16e-187
8	1030	44.0	165	1	KTHUB	choriogonadotropin be	3.16e-187
9	1024	43.7	145	2	I37231	beta-gonadotropin - h	6.00e-186
10	955	40.8	461	2	JC4302	tumor necrosis factor	2.83e-171
11	857	36.6	165	1	KTBAB	choriogonadotropin be	1.63e-150
12	841	35.9	454	2	I57826	tumor necrosis factor	3.90e-147
13	841	35.9	454	1	GQMST1	tumor necrosis factor	3.90e-147
14	809	34.6	461	1	GQRTT1	tumor necrosis factor	2.19e-140
15	803	34.3	110	5	1XULB	chorionic gonadotropi	4.02e-139
16	803	34.3	110	5	1HCNB	Human chorionic gonad	4.02e-139
17	803	34.3	110	5	1HRPB	chorionic gonadotropi	4.02e-139
18	740	31.6	121	2	I37994	beta-LH - human (frag	6.96e-126
19	709	30.3	115	1	UTHUB	lutropin beta chain -	2.16e-119
20	614	26.2	141	1	UTBOB	lutropin beta chain p	1.30e-99
21	614	26.2	141	2	I46949	luteinizing hormone b	1.30e-99
22	613	26.2	169	1	KTHOB	choriogonadotropin be	2.10e-99
23	596	25.5	119	2	A61465	lutropin beta chain -	6.93e-96
24	598	25.5	141	1	UTPGB	lutropin beta chain p	2.67e-96
25	597	25.5	141	1	UTRTB	lutropin beta chain p	4.31e-96
26	595	25.4	118	2	PN0139	lutropin beta chain -	1.12e-95
27	594	25.4	141	1	UTSHB	lutropin beta chain p	1.80e-95
28	587	25.1	138	2	S00512	lutropin beta chain p	5.02e-94
29	585	25.0	118	2	PN0141	lutropin beta chain -	1.30e-93
30	582	24.9	141	2	JC4527	luteinizing hormone b	5.41e-93
31	430	18.4	144	1	UTCAB	gonadotropin beta cha	5.53e-62
32	427	18.2	141	2	B60626	gonadotropin beta cha	2.22e-61
33	426	18.2	146	2	S16763	gonadotropin beta cha	3.52e-61
34	420	17.9	119	2	S09344	gonadotropin II beta	5.64e-60
35	416	17.8	142	2	C36179	gonadotropin II beta	3.57e-59
36	411	17.6	142	2	I51232	gonadotropin II beta	3.58e-58
37	407	17.4	113	2	S07092	gonadotropin beta cha	2.26e-57
38	405	17.3	112	2	S21196	lutropin beta chain -	5.68e-57
39	403	17.2	140	2	A48166	gonadotropin II beta	1.42e-56
40	398	17.0	142	2	A25800	gonadotropin beta cha	1.42e-55
41	388	16.6	142	2	I50143	gonadotropin II beta	1.39e-53
42	366	15.6	158	2	A61091	lutropin beta chain p	3.18e-49
43	361	15.4	147	2	I50994	gonadotropin II beta	3.09e-48
44	357	15.2	166	2	I51242	luteinizing hormone b	1.89e-47
45	350	15.0	159	2	I51373	luteinizing hormone b	4.51e-46

ALIGNMENTS

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RESULT    1
ENTRY           1EXTB       #type complete

TITLE           tumor necrosis factor receptor extracellular domain, chain B
PDB_TITLE       extracellular domain of the 55kda tumor necrosis factor
                  receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM        #formal_name Homo sapiens #common_name man
  #note         expressed in Escherichia coli, the construct contains
                  residues 12 to 172 of the mature sequence of the entire
                  receptor. residue 11 is mutated to met as a result of the
                  expression system
REFERENCE       A65560
  #authors      Naismith, J.H.; Sprang, S.R.
  #submission   submitted to the Brookhaven Protein Data Bank, July 1996
  #cross-references PDB:1EXT
REFERENCE       TN026251
  #authors      Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
  #journal      J. Biol. Chem. (1995) 270:13303
  #title        Crystallographic evidence for dimerization of unliganded
                  tumor necrosis factor receptor.
REFERENCE       TN026252
  #authors      Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                  K.; Naismith, J.H.; Sprang, S.R.
  #journal      J. Mol. Biol. (1994) 239:332
  #title        Two crystal forms of the extracellular domain of type i tumor
                  necrosis factor receptor.
REFERENCE       A40737
  #authors      Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
  #journal      Cell (1993) 73:431-445
  #title        Crystal structure of the soluble human 55 kd TNF
                  receptor-human TNFbeta complex: implications for TNF
                  receptor activation.
COMMENT     Resolution: 1.85 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS        binding protein; cytokine; signalling protein
FEATURE
  68-70             #region helix (right hand 3-10)\
  143-145           #region helix (right hand 3-10)\
  9-11,19-21        #region beta sheet\
  133-136,139-142   #region beta sheet\
  27-31,41-44       #region beta sheet\
  73-76,85-87       #region beta sheet\
  92-98,101-106     #region beta sheet\
  113-117,126-129   #region beta sheet\
  5-19              #disulfide_bonds\
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   20-33              #disulfide_bonds\
   23-42              #disulfide_bonds\
   45-60              #disulfide_bonds\
   63-78              #disulfide_bonds\
   66-86              #disulfide_bonds\
   88-104             #disulfide_bonds\
   107-119            #disulfide_bonds\
   110-127            #disulfide_bonds\
   129-140            #disulfide_bonds\
   143-156            #disulfide_bonds\
   146-152            #disulfide_bonds
SUMMARY          #length 158  #molecular-weight 17827  #checksum 5022

  Query Match           48.0%;  Score 1124;  DB 5;  Length 158;
  Best Local Similarity  99.3%;  Pred. No. 2.76e-207;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
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Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENECVSCS 144
          |||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    2
ENTRY             GQHUT1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAMES
CONTAINS          tumor necrosis factor alpha inhibitor; tumor necrosis factor
                    binding protein 1 (TNF blocking factor)
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    24-Oct-1997
ACCESSIONS        A38208; A34899; A34900; A36555; C36555; A38281; S12057;
                    JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE         A38208
   #authors       Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
   #journal       Genomics (1992) 13:219-224
   #title         Structure of the human TNF receptor 1 (p60) gene (TNRF1) and
                    localization to chromosome 12p13.
   #accession     A38208
      ##molecule_type DNA
      ##residues      1-455 ##label FUC
      ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
                          PID:g339750
REFERENCE         A34899
   #authors       Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
                    M.; Tabuchi, H.; Lesslauer, W.
   #journal       Cell (1990) 61:351-359
   #title         Molecular cloning and expression of the human 55 kd tumor
                    necrosis factor receptor.
   #cross-references MUID:90235284
   #accession     A34899
      ##molecule_type mRNA
      ##residues      1-455 ##label LOE
      ##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
      ##experimental_source placenta
      ##note          part of this sequence, including the amino end of the
                       mature protein, confirmed by protein sequencing
REFERENCE         A34900
   #authors       Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
                    Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
                    H.; Kohr, W.J.; Goeddel, D.V.
   #journal       Cell (1990) 61:361-370
   #title         Molecular cloning and expression of a receptor for human
                    tumor necrosis factor.
   #cross-references MUID:90235285
   #accession     A34900
      ##molecule_type mRNA
      ##residues      1-455 ##label SCH
      ##cross-references GB:M33294; NID:g339744; PID:g339745
REFERENCE         A36555
   #authors       Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                    Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                    Stratowa, C.; Adolf, G.R.
   #journal       DNA Cell Biol. (1990) 9:705-715
   #title         Molecular cloning and expression of human and rat tumor
                    necrosis factor receptor chain (p60) and its soluble
                    derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
   #accession     A36555
      ##molecule_type mRNA
      ##residues      1-455 ##label HIM
      ##cross-references GB:M63121; NID:g339755; PID:g339756
   #accession     C36555
      ##molecule_type protein
      ##residues      30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
                       107-128;162-167,'X',169-201 ##label HI2
      ##note          the purified protein, called tumor necrosis factor
                       binding protein, is a soluble derivative of the
                       receptor
REFERENCE         A38281
   #authors       Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
                    M.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
   #title         Cloning of human tumor necrosis factor (TNF) receptor cDNA
                    and expression of recombinant soluble TNF-binding protein.
   #cross-references MUID:91017509
   #accession     A38281
      ##molecule_type mRNA
      ##residues      1-455 ##label GRA
      ##cross-references GB:M37764
      ##note          the authors translated the codon TGG for residue 371 as
                       Thr, AAG for residue 372 as Leu, and GAC for residue
                       427 as Asn
REFERENCE         S12057
   #authors       Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
                    R.; Aderka, D.; Holtmann, H.; Wallach, D.
   #journal       EMBO J. (1990) 9:3269-3278
   #title         Soluble forms of tumor necrosis factor receptors (TNF-Rs).
                    The cDNA for the type I TNF-R, cloned using amino acid
                    sequence data of its soluble form, encodes both the cell
                    surface and a soluble form of the receptor.
   #cross-references MUID:91006021
   #accession     S12057
      ##molecule_type mRNA
      ##residues      1-455 ##label NOP
      ##cross-references EMBL:X55313; NID:g37223; PID:g37224
      ##note          parts of soluble TNF binding protein 1, including its
                       amino and carboxyl ends, were confirmed by protein
                       sequencing
REFERENCE         JT0758
   #authors       Kemper, O.; Wallach, D.
   #journal       Gene (1993) 134:209-216
   #title         Cloning and partial characterization of the promoter for the
                    human p55 tumor necrosis factor (TNF) receptor.
   #accession     JT0758
      ##molecule_type DNA
      ##residues      1-13 ##label KEM
REFERENCE         A60231
   #authors       Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
                    J.M.
   #journal       Eur. J. Immunol. (1990) 20:1167-1174
   #title         Tumor necrosis factor inhibitor: purification, NH-2-terminal
                    amino acid sequence and evidence for anti-inflammatory and
                    immunomodulatory activities.
   #cross-references MUID:90292116
   #accession     A60231
      ##molecule_type protein
      ##residues      41-43,'X',45-53,'X',55-57 ##label SEC
```

```
REFERENCE       A38258
  #authors      Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
                  J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
                  R.S.; Granger, G.A.
  #journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
  #title        Purification and characterization of an inhibitor (soluble
                  tumor necrosis factor receptor) for tumor necrosis factor
                  and lymphotoxin obtained from the serum ultrafiltrates of
                  human cancer patients.
  #cross-references MUID:91062364
  #accession    A38258
    ##molecule_type protein
    ##residues      41-60 ##label GAT
    ##experimental_source cancer patient serum
REFERENCE       A60594
  #authors      Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
                  Grubb, A.; Adolf, G.
  #journal      Eur. J. Haematol. (1989) 42:270-275
  #title        Isolation and characterization of a tumor necrosis factor
                  binding protein from urine.
  #accession    A60594
    ##molecule_type protein
    ##residues      41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
    ##experimental_source renal failure patient urine
REFERENCE       A35010
  #authors      Engelmann, H.; Novick, D.; Wallach, D.
  #journal      J. Biol. Chem. (1990) 265:1531-1536
  #title        Two tumor necrosis factor-binding proteins purified from
                  human urine. Evidence for immunological cross-reactivity
                  with cell surface tumor necrosis factor receptors.
  #cross-references MUID:90110215
  #accession    A35010
    ##molecule_type protein
    ##residues      41-45 ##label ENG
    ##experimental_source normal urine
REFERENCE       JC2404
  #authors      Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
  #journal      Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
  #title        Amino acid sequence of natural tumor necrosis factor alpha
                  inhibitor purified from human urine.
  #accession    JC2404
    ##molecule_type protein
    ##residues      41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
                     ##label KAJ
    ##experimental_source urine
COMMENT     This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
GENETICS
  #gene         GDB:TNFR1
    ##cross-references GDB:125913; OMIM:191190
  #map_position 12p13.2-12p13.2
  #introns      13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                  receptor repeat homology
KEYWORDS        duplication; glycoprotein; receptor; transmembrane protein
FEATURE
  1-21              #domain signal sequence #status predicted #label SIG\
  22-455            #product tumor necrosis factor receptor type 1 #status
                      predicted #label MAT\
  30-211            #domain extracellular #status predicted #label EXT\
  41-201            #product TNF binding protein 1 (tumor necrosis factor
                      alpha inhibitor) #status experimental #label TBP1\
  44-82             #domain NGF receptor repeat homology #label NG1\
  84-126            #domain NGF receptor repeat homology #label NG2\
  127-167           #domain NGF receptor repeat homology #label NG3\
  168-196           #domain NGF receptor repeat homology #label NG4\
  212-234           #domain transmembrane #status predicted #label MEM\
  235-455           #domain intracellular #status predicted #label INT\
  54,145,151        #binding_site carbohydrate (Asn) (covalent) #status
                      predicted
SUMMARY         #length 455  #molecular-weight 50494  #checksum 153

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  Best Local Similarity  99.3%;  Pred. No. 2.76e-207;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCTCHAGFFLRENECVSCS 183
           |||||||||||||||||||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    3
ENTRY           1EXTA      #type complete

TITLE           tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE       extracellular domain of the 55kda tumor necrosis factor
                  receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM        #formal_name Homo sapiens #common_name man
  #note         expressed in Escherichia coli, the construct contains
                  residues 12 to 172 of the mature sequence of the entire
                  receptor. residue 11 is mutated to met as a result of the
                  expression system
REFERENCE       A65560
  #authors      Naismith, J.H.; Sprang, S.R.
  #submission   submitted to the Brookhaven Protein Data Bank, July 1996
  #cross-references PDB:1EXT
REFERENCE       TN026248
  #authors      Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
  #journal      J. Biol. Chem. (1995) 270:13303
  #title        Crystallographic evidence for dimerization of unliganded
                  tumor necrosis factor receptor.
REFERENCE       TN026249
  #authors      Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                  K.; Naismith, J.H.; Sprang, S.R.
  #journal      J. Mol. Biol. (1994) 239:332
  #title        Two crystal forms of the extracellular domain of type i tumor
                  necrosis factor receptor.
REFERENCE       A40737
  #authors      Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
  #journal      Cell (1993) 73:431-445
  #title        Crystal structure of the soluble human 55 kd TNF
                  receptor-human TNFbeta complex: implications for TNF
                  receptor activation.
COMMENT     Resolution: 1.85 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS        binding protein; cytokine; signalling protein
FEATURE
  66-68             #region helix (right hand 3-10)\
  141-143           #region helix (right hand 3-10)\
  151-154           #region helix (right hand alpha)\
  7-9,17-19         #region beta sheet\
  131-134,137-140   #region beta sheet\
  25-29,39-42       #region beta sheet\
  71-74,83-85       #region beta sheet\
  90-96,99-104      #region beta sheet\
  111-115,124-127   #region beta sheet\
  3-17              #disulfide_bonds\
  18-31             #disulfide_bonds\
  21-40             #disulfide_bonds\
  43-58             #disulfide_bonds\
  61-76             #disulfide_bonds\
  64-84             #disulfide_bonds\
  86-102            #disulfide_bonds\
  105-117           #disulfide_bonds\
  108-125           #disulfide_bonds\
  127-138           #disulfide_bonds\
```

```
   141-154            #disulfide_bonds\
   144-150            #disulfide_bonds
SUMMARY           #length 160  #molecular-weight 18065  #checksum 2297

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  Best Local Similarity  99.3%;  Pred. No. 5.28e-206;
  Matches   141;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     24 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 83

Db     61 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     84 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 143

Db    121 QNTVCTCHAGFFLRENECVSCS 142
          ||||||||||||||||||||:
Qy    144 QNTVCTCHAGFFLRENECVSCA 165


RESULT    4
ENTRY             1NCFB      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain B - hu
ALTERNATE_NAMES   stnfrl; type i receptor
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029041
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   2-16               #disulfide_bonds\
   17-30              #disulfide_bonds\
   20-39              #disulfide_bonds\
   42-57              #disulfide_bonds\
   60-75              #disulfide_bonds\
   63-83              #disulfide_bonds\
   85-101             #disulfide_bonds\
   104-116            #disulfide_bonds\
   107-124            #disulfide_bonds\
   126-137            #disulfide_bonds
SUMMARY           #length 142  #molecular-weight 16046  #checksum 1225

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  Best Local Similarity  99.3%;  Pred. No. 3.78e-205;
  Matches   140;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db     61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db    121 NTVCTCHAGFFLRENECVSCS 141
          ||||||||||||||||||||:
Qy    145 NTVCTCHAGFFLRENECVSCA 165


RESULT    5
ENTRY             1TNRR      #type complete

TITLE             tumor necrosis factor receptor type 1 (P55 extracellular
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          recombinant form expressed in Baculovirus SF9
REFERENCE         A52442
   #authors       Banner, D.W.
   #submission    submitted to the Brookhaven Protein Data Bank, May 1994
   #cross-references PDB:1TNR
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
REFERENCE         TN034093
   #authors       D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
                    Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
                    Lesslauer, W.
   #journal       J. Mol. Biol. (1993) 229:555
   #title         Crystallization and preliminary analysis of tnf-beta and a
                    tnf-beta-55 kd tnf receptor complex.
COMMENT     Resolution: 2.85 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS          Complex(lymphokineRECEPTOR)
FEATURE
   1-15               #disulfide_bonds\
   16-29              #disulfide_bonds\
   19-38              #disulfide_bonds\
   41-56              #disulfide_bonds\
   59-74              #disulfide_bonds\
   62-82              #disulfide_bonds\
   84-100             #disulfide_bonds\
   103-115            #disulfide_bonds\
   106-123            #disulfide_bonds\
   125-136            #disulfide_bonds
SUMMARY           #length 139  #molecular-weight 15746  #checksum 5235

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  Best Local Similarity 100.0%;  Pred. No. 3.17e-203;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db     61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db    121 TVCTCHAGFFLRENECVSC 139
          |||||||||||||||||||
Qy    146 TVCTCHAGFFLRENECVSC 164


RESULT    6
ENTRY             1NCFA      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain A - hu
ALTERNATE_NAMES   stnfrl; type i receptor
```

```
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029039
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   5-19                #disulfide_bonds\
   20-33               #disulfide_bonds\
   23-42               #disulfide_bonds\
   45-60               #disulfide_bonds\
   63-78               #disulfide_bonds\
   66-86               #disulfide_bonds\
   88-104              #disulfide_bonds\
   107-119             #disulfide_bonds\
   110-127             #disulfide_bonds\
   129-140             #disulfide_bonds
SUMMARY           #length 140  #molecular-weight 15889  #checksum 6622

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  Best Local Similarity 100.0%;  Pred. No. 9.90e-202;
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Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENEC 140
          ||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENEC 161


RESULT    7
ENTRY             I37412      #type fragment

TITLE             beta-gonadotropin - human (fragment)ORGANISM         #formal_name Homo
DATE              21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
                    09-May-1997
ACCESSIONS        I37412
REFERENCE         I37231
   #authors       Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
   #journal       Nature (1984) 307:37-40
   #title         Evolution of the genes for the beta subunits of human
                    chorionic gonadotropin and luteinizing hormone.
   #cross-references MUID:84093590
   #accession     I37412
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-145 ##label RES
      ##cross-references EMBL:X00265; NID:g31719
GENETICS
   #introns       41/3
CLASSIFICATION    #superfamily pituitary glycoprotein hormone beta chain
SUMMARY           #length 145  #checksum 2358

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  Best Local Similarity 100.0%;  Pred. No. 3.16e-187;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    127 SLPSPSRLPGPSDTPILPQ 145
          |||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    8
ENTRY             KTHUB       #type complete

TITLE             choriogonadotropin beta chain precursor - humanALTERNATE_NAMES  chor
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change
                    20-Mar-1998
ACCESSIONS        A93230; I69972; I55224; I55250; I70007; I70008; A92303;
                    A92181; A92142; PC1016; A61097; B56873; A01502
REFERENCE         A93230
   #authors       Fiddes, J.C.; Goodman, H.M.
   #journal       Nature (1980) 286:684-687
   #title         The cDNA for the beta-subunit of human chorionic gonadotropin
                    suggests evolution of a gene by readthrough into the
                    3'-untranslated region.
   #cross-references MUID:81012134
   #accession     A93230
      ##molecule_type mRNA
      ##residues       1-165 ##label FID
      ##cross-references GB:J00117; GB:M38559; GB:M54963; NID:g180436;
                          PID:g180437
REFERENCE         I55224
   #authors       Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, H.;
                    Boothby, M.R.; Boime, I.
   #journal       J. Biol. Chem. (1983) 258:11492-11499
   #title         The beta subunit of human chorionic gonadotropin is encoded
                    by multiple genes.
   #cross-references MUID:84008141
   #accession     I69972
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-165 ##label POL
      ##cross-references GB:K03189; NID:g180450; PID:g180453
      ##note           clone CG-beta-e
   #accession     I55224
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-23,'M',25-136,'A',138-165 ##label PO2
      ##cross-references GB:K03183; NID:g180442; PID:g180444
      ##note           clone CG-beta-a
REFERENCE         I55250
   #authors       Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
   #journal       J. Biol. Chem. (1986) 261:5907-5916
   #title         A map of the hCG beta-LH beta gene cluster.
   #cross-references MUID:86195987
   #accession     I55250
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-5 ##label PO3
      ##cross-references GB:M13504; NID:g180419; PID:g463088
      ##note           CG-beta-3 gene
   #accession     I70007
```

```
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-5 ##label PO4
      ##cross-references GB:M13505; NID:g180429; PID:g463089
      ##note          CG-beta-6 gene
   #accession     I70008
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-5 ##label RE5
      ##cross-references GB:M13503; NID:g180432; PID:g463090
      ##note          CG-beta-7 gene
REFERENCE         A92303
   #authors       Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
   #journal       J. Biol. Chem. (1981) 256:1816-1823
   #title         The amino acid sequences of the prepeptides contained in the
                   alpha and beta subunits of human choriogonadotropin.
   #cross-references MUID:81117268
   #accession     A92303
      ##molecule_type protein
      ##residues      1-20 ##label BIR
      ##note          the identity of the residue at position 19 could not be
                       determined
REFERENCE         A92181
   #authors       Morgan, F.J.; Birken, S.; Canfield, R.E.
   #journal       J. Biol. Chem. (1975) 250:5247-5258
   #title         The amino acid sequence of human chorionic gonadotropin. The
                   alpha subunit and beta subunit.
   #cross-references MUID:75211304
   #accession     A92181
      ##molecule_type protein
      ##residues      21-165 ##label MOR
REFERENCE         A92142
   #authors       Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
   #journal       J. Biol. Chem. (1973) 248:6810-6827
   #cross-references MUID:74011267
   #accession     A92142
      ##molecule_type protein
      ##residues      21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
                       ##label CAR
REFERENCE         PC1016
   #authors       Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.;
                   Wang, Y.
   #journal       Chinese Biochem. J. (1990) 6:558-562
   #title         The immunological characteristics of the enzymatic fragments
                   of human chorionic gonadotropin beta-subunit.
   #accession     PC1016
      ##molecule_type protein
      ##residues      21-165 ##label SHI
      ##note          article in Chinese with English abstract
REFERENCE         A61097
   #authors       Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.;
                   Agosto, G.M.; Krichevsky, A.; Vaitukaitis, J.L.; Canfield,
                   R.E.
   #journal       Endocrinology (1988) 123:572-583
   #title         Structure of the human chorionic gonadotropin beta-subunit
                   fragment from pregnancy urine.
   #accession     A61097
      ##molecule_type protein
      ##residues      26-32,'X',34-49,'X',51-60;75-112 ##label BI2
      ##note          this material from pregancy urine lacks sialic acid in
                       its carbohydrate and has been processed further from
                       the mature form into two chains linked by disulfide
                       bonds
REFERENCE         A56873
   #authors       Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
   #journal       Br. J. Cancer (1993) 67:686-692
   #title         Characterisation of UGP and its relationship with beta-core
                   fragment.
   #cross-references MUID:93229246
   #accession     B56873
      ##molecule_type protein
      ##residues      26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',
                       78-91,'G',93-102 ##label KAR
      ##experimental_source urine
      ##note          sequence modified after extraction from NCBI backbone
      ##note          this material was designated urinary gonadotrophin
                       peptide (peak 2)
REFERENCE         A44674
   #authors       Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                   J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                   N.W.
   #journal       Nature (1994) 369:455-461
   #title         Crystal structure of human chorionic gonadotropin.
   #contents      annotation; X-ray crystallography, 3.0 angstroms; correction
                   of disulfide bonds
GENETICS
   #gene          GDB:CGB
      ##cross-references GDB:119055; OMIM:118860
   #map_position 19q13.3-19q13.3
   #introns       5/3; 61/3
   #note          the choriogonadotropin beta chain locus contains six genes
                   (or pseudogenes)
CLASSIFICATION    #superfamily pituitary glycoprotein hormone beta chain
KEYWORDS          glycoprotein; hormone; pituitary
FEATURE
   1-20               #domain signal sequence #status experimental #label SIG\
   21-165             #product choriogonadotropin beta chain #status
                       experimental #label MAT\
   29-77,43-92,46-130,
   54-108,58-110,
   113-120            #disulfide_bonds #status experimental\
   33,50              #binding_site carbohydrate (Asn) (covalent) #status
                       experimental\
   138,150            #binding_site carbohydrate (Ser) (covalent) #status
                       predicted\
   141,147,152,158    #binding_site carbohydrate (Ser) (covalent) #status
                       experimental
SUMMARY           #length 165  #molecular-weight 17739  #checksum 6523

  Query Match           44.0%;  Score 1030;  DB 1;  Length 165;
  Best Local Similarity 100.0%;  Pred. No. 3.16e-187;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     27 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 146
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    147 SLPSPSRLPGPSDTPILPQ 165
        ||||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    9
ENTRY             I37231     #type fragment

TITLE             beta-gonadotropin - human (fragment)ORGANISM         #formal_name Ho
DATE              21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
                    09-May-1997
ACCESSIONS        I37231
REFERENCE         I37231
   #authors       Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
   #journal       Nature (1984) 307:37-40
   #title         Evolution of the genes for the beta subunits of human
                   chorionic gonadotropin and luteinizing hormone.
   #cross-references MUID:84093590
   #accession     I37231
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-145 ##label RES
      ##cross-references EMBL:X00266; NID:g29907
GENETICS
   #introns       41/3
```

```
CLASSIFICATION   #superfamily pituitary glycoprotein hormone beta chain
SUMMARY          #length 145  #checksum 2349

  Query Match           43.7%;  Score 1024;  DB 2;  Length 145;
  Best Local Similarity  99.3%;  Pred. No. 6.00e-186;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP 126
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    127 SLPSPSRLPGPSDTPILPQ 145
          |||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT   10
ENTRY            JC4302      #type complete

TITLE            tumor necrosis factor receptor p55 - pigORGANISM          #formal_name S
DATE             29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                   12-Dec-1997
ACCESSIONS       JC4302; PC4093
REFERENCE        JC4302
   #authors      Suter, B.; Pauli, U.
   #journal      Gene (1995) 163:263-266
   #title        Cloning of the cDNA encoding the porcine p55 tumor necrosis
                   factor receptor.
   #accession    JC4302
      ##molecule_type mRNA
      ##residues      1-461 ##label SUT
      ##cross-references GB:U19994; NID:g1141752; PID:g1141753
   #accession    PC4093
      ##molecule_type protein
      ##residues      1-7 ##label SU2
      ##experimental_source kidney cell line 15
GENETICS
   #gene         tnfr
CLASSIFICATION   #superfamily tumor necrosis factor receptor type 1; NGF
                   receptor repeat homology
KEYWORDS         glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
   1-29               #domain signal sequence #status predicted #label SIG\
   30-461             #product tumor necrosis factor receptor p55 #status
                        predicted #label MAT\
   44-194             #domain extracellular cysteine rich #status predicted
                        #label EXT\
   44-82              #domain NGF receptor repeat homology #label NG1\
   211-231            #domain transmembrane #status predicted #label TMM\
   361-447            #domain signal transduction #status predicted #label
                        SIT\
   54,145,151         #binding_site carbohydrate (Asn) (covalent) #status
                        predicted
SUMMARY          #length 461  #molecular-weight 50696  #checksum 8079

  Query Match           40.8%;  Score 955;  DB 2;  Length 461;
  Best Local Similarity  80.3%;  Pred. No. 2.83e-171;
  Matches   114;  Conservative   16;  Mismatches  12;  Indels   0;  Gaps   0;

Db     41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|:|||||| |||| |||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |||||| ||:|||||:|||||||||||||||| |||| ||||:||||| ||||:|:| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQDTICNCHSGFFLRDKECVSC 182
          ||:|:| ||:|||||::|||||
Qy    143 KQNTVCTCHAGFFLRENECVSC 164


RESULT   11
ENTRY            KTBAB       #type complete

TITLE            choriogonadotropin beta chain precursor - olive baboonORGANISM
                   #common_name olive baboon
DATE             31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
                   03-May-1996
ACCESSIONS       A25808
REFERENCE        A25808
   #authors      Crawford, R.J.; Tregear, G.W.; Niall, H.D.
   #journal      Gene (1986) 46:161-169
   #title        The nucleotide sequences of baboon chorionic gonadotropin
                   beta-subunit genes have diverged from the human.
   #cross-references MUID:87106851
   #accession    A25808
      ##molecule_type mRNA
      ##residues      1-165 ##label CRA
COMMENT          There are at least five copies of CG-related genes and at least two
                   of these are expressed in the baboon placenta.
CLASSIFICATION   #superfamily pituitary glycoprotein hormone beta chain
KEYWORDS         glycoprotein; hormone; placenta; pregnancy maintenance
FEATURE
   1-20               #domain signal sequence #status predicted #label SIG\
   21-165             #product choriogonadotropin beta chain #status predicted
                        #label CGB\
   29-77,43-92,46-130,
   54-108,58-110,
   113-120            #disulfide_bonds #status predicted\
   33,50              #binding_site carbohydrate (Asn) (covalent) #status
                        predicted\
   140,147,152        #binding_site carbohydrate (Ser) (covalent) #status
                        predicted
SUMMARY          #length 165  #molecular-weight 17592  #checksum 4960

  Query Match           36.6%;  Score 857;  DB 1;  Length 165;
  Best Local Similarity  81.3%;  Pred. No. 1.63e-150;
  Matches   113;  Conservative   14;  Mismatches  12;  Indels   0;  Gaps   0;

Db     27 PLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES 86
          | ||||||||| |||:||||:|||||||||||||| ||||:|||::||||||||:|||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSSKDPPP 146
          ||||||| ||:|:|| :|||||:|||||||||:|||||||||||||| :| ||||| |||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    147 SPPSPSRLLEPAGTPFLPQ 165
          | ||||||  |: ||:|||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT   12
ENTRY            I57826      #type complete

TITLE            tumor necrosis factor receptor - mouseORGANISM          #formal_name
DATE             02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                   23-May-1997
ACCESSIONS       I57826
REFERENCE        I57826
   #authors      Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
                   Steinmetz, M.
   #journal      Mol. Immunol. (1993) 30:165-176
   #title        Genomic organization and promoter function of the murine
                   tumor necrosis factor receptor beta gene.
   #cross-references MUID:93156721
   #accession    I57826
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-454 ##label RES
      ##cross-references GB:M76656; NID:g202100; PID:g202102
```

```
GENETICS
   #gene          TNFR-2
   #introns       13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          cytokine receptor
SUMMARY           #length 454  #molecular-weight 50030  #checksum 4267

  Query Match             35.9%;  Score 841;  DB 2;  Length 454;
  Best Local Similarity  70.6%;  Pred. No. 3.90e-147;
  Matches   101;  Conservative   23;  Mismatches  19;  Indels   0;  Gaps   0;

Db      41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
           ||:||||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 TQNTVCNCHAGFFLRESECVPCS 183
           ||||| |||||||||:|||:|:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   13
ENTRY             GQMST1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    05-Sep-1997
ACCESSIONS        A38634; B40254; S16677; S19021; I54532
REFERENCE         A38634
   #authors       Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
                    G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
   #title         Cloning and expression of cDNAs for two distinct murine tumor
                    necrosis factor receptors demonstrate one receptor is
                    species specific.
   #cross-references MUID:91187885
   #accession     A38634
      ##molecule_type mRNA
      ##residues       1-454 ##label LEW
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         A40254
   #authors       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
                    C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
   #journal       Mol. Cell. Biol. (1991) 11:3020-3026
   #title         Molecular cloning and expression of the type 1 and type 2
                    murine receptors for tumor necrosis factor.
   #cross-references MUID:91246168
   #accession     B40254
      ##molecule_type mRNA
      ##residues       1-454 ##label GO2
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         S16677
   #authors       Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis,
                    A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
   #journal       Eur. J. Immunol. (1991) 21:1649-1656
   #title         Cloning, expression and cross-linking analysis of the murine
                    p55 tumor necrosis factor receptor.
   #cross-references MUID:91285014
   #accession     S16677
      ##molecule_type mRNA
      ##residues       1-454 ##label BAR
      ##cross-references EMBL:X59238; NID:g53578; PID:g53579
REFERENCE         S19021
   #authors       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
   #journal       Immunogenetics (1991) 34:338-340
   #title         Molecular cloning and expression of the mouse Tnf receptor
                    type b.
   #cross-references MUID:92039815
   #accession     S19021
      ##molecule_type mRNA
      ##residues       1-454 ##label ROT
      ##cross-references EMBL:X57796; NID:g54848; PID:g54849
REFERENCE         I54532
   #authors       Bebo, B.F.
   #journal       Immunogenetics (1994) 39:450-451
   #title         Nucleotide sequence of the TNF type I receptor from a mouse
                    endothelioma cell line.
   #cross-references MUID:94245292
   #accession     I54532
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-454 ##label RES
      ##cross-references GB:L26349; NID:g430732; PID:g430733
COMMENT      This protein is one of two distantly related receptors for both
               TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                 #domain signal sequence #status predicted #label SIG\
   30-454               #product tumor necrosis factor receptor type 1 #status
                          predicted #label MAT\
   30-212               #domain extracellular #status predicted #label EXT\
   44-82                #domain NGF receptor repeat homology #label NG1\
   84-126               #domain NGF receptor repeat homology #label NG2\
   127-167              #domain NGF receptor repeat homology #label NG3\
   168-204              #domain NGF receptor repeat homology #label NG4\
   213-235              #domain transmembrane #status predicted #label MEM\
   236-454              #domain intracellular #status predicted #label INT\
   54,151,202           #binding_site carbohydrate (Asn) (covalent) #status
                          predicted
SUMMARY           #length 454  #molecular-weight 50129  #checksum 4839

  Query Match             35.9%;  Score 841;  DB 1;  Length 454;
  Best Local Similarity  70.6%;  Pred. No. 3.90e-147;
  Matches   101;  Conservative   23;  Mismatches  19;  Indels   0;  Gaps   0;

Db      41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
           ||:||||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 TQNTVCNCHAGFFLRESECVPCS 183
           ||||| |||||||||:|||:|:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   14
ENTRY             GQRTT1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
                    05-Sep-1997
ACCESSIONS        B36555
REFERENCE         A36555
   #authors       Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                    Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                    Stratowa, C.; Adolf, G.R.
   #journal       DNA Cell Biol. (1990) 9:705-715
   #title         Molecular cloning and expression of human and rat tumor
                    necrosis factor receptor chain (p60) and its soluble
                    derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
   #accession     B36555
      ##molecule_type mRNA
      ##residues       1-461 ##label HIM
      ##cross-references GB:M63122; NID:g207361; PID:g207362
```

```
COMMENT     This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                #domain signal sequence #status predicted #label SIG\
   30-461              #product tumor necrosis factor receptor type 1 #status
                         predicted #label MAT\
   30-211              #domain extracellular #status predicted #label EXT\
   30-201              #product tumor necrosis factor binding protein #status
                         predicted #label TBP\
   44-82               #domain NGF receptor repeat homology #label NG1\
   84-126              #domain NGF receptor repeat homology #label NG2\
   127-167             #domain NGF receptor repeat homology #label NG3\
   168-204             #domain NGF receptor repeat homology #label NG4\
   212-234             #domain transmembrane #status predicted #label MEM\
   235-461             #domain intracellular #status predicted #label INT\
   54,151,201          #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
SUMMARY           #length 461  #molecular-weight 50969  #checksum 1617

  Query Match           34.6%;  Score 809;  DB 1;  Length 461;
  Best Local Similarity  68.5%;  Pred. No. 2.19e-140;
  Matches    98;  Conservative   21;  Mismatches  24;  Indels   0;  Gaps   0;

Db      41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
           |::|||||| || ||||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  ||||| |||||:|  | ||||||:|||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCNCHAGFFLSGNECTPCS 183
           |||||| ||||||| ||| :|:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT   15
ENTRY             1XULB      #type complete

TITLE             chorionic gonadotropin, chain B - humanPDB_TITLE       theoretical mod
                    receptor complexed with human chorionic gonadotropin
ORGANISM          #formal_name Homo sapiens #common_name man
REFERENCE         A66957
   #authors       Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                    Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #submission    submitted to the Brookhaven Protein Data Bank, December 1996
   #cross-references PDB:1XUL
REFERENCE         TN032625
   #authors       Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                    Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #journal       Structure (London) (1996) 3:1341
   #title         Structural predictions for the ligand-binding region of
                    glycoprotein hormone receptors and the nature of
                    hormone-receptor interactions structure.
REFERENCE         TN032626
   #authors       Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                    Hendrickson, W.A.
   #journal       Structure (London) (1994) 2:545
   #title         Structure of human chorionic gonadotropin at 2.6 a resolution
                    from mad analysis of the selenomethionyl protein.
COMMENT     Resolution: not applicable
COMMENT     Determination: theoretical model
KEYWORDS          complex; glycoprotein hormone receptor glycoprotein; hormone;
                    phosphorylation; receptor
FEATURE
   97-101,26-39,9-17  #region beta sheet\
   54-59,86-91        #region beta sheet\
   61-67,78-84        #region beta sheet\
   8-56               #disulfide_bonds\
   22-71              #disulfide_bonds\
   25-109             #disulfide_bonds\
   33-87              #disulfide_bonds\
   37-89              #disulfide_bonds\
   92-99              #disulfide_bonds
SUMMARY           #length 110  #molecular-weight 11906  #checksum 6414

  Query Match           34.3%;  Score 803;  DB 5;  Length 110;
  Best Local Similarity 100.0%;  Pred. No. 4.02e-139;
  Matches   105;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       6 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 65
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db      66 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 110
           |||||||||||||||||||||||||||||||||||||||||||||
Qy     229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 273


Search completed: Wed May  6 08:55:58 1998
Job time : 34 secs.
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:53:11 1998; MasPar time 9.09 Seconds
846.789 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 43.895; Variance 73.304; scale 0.599

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	48.0	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	2.90e-242
2	1030	44.0	165	1	CGHB_HUMAN	CHORIOGONADOTROPIN BET	8.92e-219
3	955	40.8	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	4.23e-200
4	857	36.6	165	1	CGHB_PAPAN	CHORIOGONADOTROPIN BET	8.42e-176
5	841	35.9	454	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	7.59e-172
6	809	34.6	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	5.98e-164
7	740	31.6	141	1	LSHB_HUMAN	LUTROPIN BETA CHAIN PR	5.55e-147
8	709	30.3	164	1	CGHB_CALJA	CHORIOGONADOTROPIN BET	2.18e-139
9	630	26.9	169	1	LSHB_EQUAS	LUTROPIN/CHORIOGONADOT	3.88e-120
10	614	26.2	141	1	LSHB_BOVIN	LUTROPIN BETA CHAIN PR	2.94e-116
11	613	26.2	169	1	LSHB_HORSE	LUTROPIN/CHORIOGONADOT	5.13e-116
12	602	25.7	141	1	LSHB_SHEEP	LUTROPIN BETA CHAIN PR	2.36e-113
13	598	25.5	141	1	LSHB_PIG	LUTROPIN BETA CHAIN PR	2.19e-112
14	597	25.5	141	1	LSHB_RAT	LUTROPIN BETA CHAIN PR	3.82e-112
15	595	25.4	118	1	LSHB_BALAC	LUTROPIN BETA CHAIN (L	1.16e-111
16	587	25.1	138	1	LSHB_CANFA	LUTROPIN BETA CHAIN PR	9.94e-110
17	585	25.0	118	1	LSHB_PHYCA	LUTROPIN BETA CHAIN (L	3.02e-109
18	542	23.2	105	1	LSHB_MOUSE	LUTROPIN BETA CHAIN PR	6.71e-99
19	430	18.4	144	1	GTHB_CYPCA	GONADOTROPIN BETA CHAI	2.64e-72
20	427	18.2	141	1	GTHB_HYPMO	GONADOTROPIN BETA CHAI	1.33e-71
21	426	18.2	146	1	GTHB_CTEID	GONADOTROPIN BETA CHAI	2.29e-71
22	416	17.8	142	1	GTH2_ONCKE	GONADOTROPIN BETA-II C	5.02e-69
23	411	17.6	138	1	GTHB_CLAGA	GONADOTROPIN BETA CHAI	7.39e-68
24	411	17.6	142	1	GTH2_ONCMA	GONADOTROPIN BETA-II C	7.39e-68
25	407	17.4	113	1	GTHB_MURCI	GONADOTROPIN BETA CHAI	6.34e-67
26	405	17.3	112	1	LSHB_RANCA	LUTROPIN BETA CHAIN (L	1.85e-66
27	403	17.2	140	1	GTH2_ANGAN	GONADOTROPIN BETA-II C	5.42e-66
28	398	17.0	142	1	GTHB_ONCTS	GONADOTROPIN BETA CHAI	7.91e-65
29	388	16.6	142	1	GTH2_CORAU	GONADOTROPIN BETA-II C	1.66e-62
30	371	15.8	128	1	LSHB_STRCA	LUTROPIN BETA CHAIN (L	1.42e-58
31	355	15.2	115	1	GTH2_THUOB	GONADOTROPIN BETA-II C	6.78e-55
32	357	15.2	166	1	LSHB_COTJA	LUTROPIN BETA CHAIN PR	2.76e-55
33	350	15.0	159	1	LSHB_MELGA	LUTROPIN BETA CHAIN PR	9.48e-54
34	328	14.0	138	1	TSHB_CANFA	THYROTROPIN BETA CHAIN	9.76e-49
35	320	13.7	138	1	TSHB_MOUSE	THYROTROPIN BETA CHAIN	6.31e-47
36	319	13.6	136	1	GTH2_FUNHE	GONADOTROPIN BETA-II C	1.06e-46
37	318	13.6	138	1	TSHB_PIG	THYROTROPIN BETA CHAIN	1.79e-46
38	318	13.6	138	1	TSHB_RAT	THYROTROPIN BETA CHAIN	1.79e-46
39	317	13.5	138	1	TSHB_BOVIN	THYROTROPIN BETA CHAIN	3.00e-46
40	316	13.5	138	1	TSHB_HUMAN	THYROTROPIN BETA CHAIN	5.05e-46
41	305	13.0	130	1	FSHB_MOUSE	FOLLITROPIN BETA CHAIN	1.50e-43
42	303	12.9	130	1	FSHB_RAT	FOLLITROPIN BETA CHAIN	4.22e-43
43	297	12.7	118	1	FSHB_HORSE	FOLLITROPIN BETA CHAIN	9.28e-42
44	289	12.3	129	1	FSHB_SHEEP	FOLLITROPIN BETA CHAIN	5.63e-40
45	281	12.0	129	1	FSHB_HUMAN	FOLLITROPIN BETA CHAIN	3.35e-38

ALIGNMENTS

RESULT 1
ID TNR1_HUMAN STANDARD; PRT; 455 AA.
AC P19438;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
GN TNFR1 OR TNFAR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 90235285.
RA SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL CELL 61:361-370(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90235284.
RA LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA TABUCHI H., LESSLAUER W.;
RL CELL 61:351-359(1990).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE; 91006021.
RA NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA ADERKA D., HOLTMANN H., WALLACH D.;
RL EMBO J. 9:3269-3278(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91090841.
RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL DNA CELL BIOL. 9:705-715(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 91017509.
RA GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92250049.
RA FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;

```
RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RL   CELL 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KHONO H., SPRANG S.R.;
RL   STRUCTURE 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; X55313; G37224; -.
DR   EMBL; M33294; G339745; -.
DR   EMBL; M58286; G339754; -.
DR   EMBL; M63121; G339756; -.
DR   EMBL; M75866; G339750; -.
DR   EMBL; M75864; G339750; JOINED.
DR   EMBL; M75865; G339750; JOINED.
DR   EMBL; M60275; G339760; -.
DR   EMBL; A21522; G579600; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL       1     21
FT   CHAIN       22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN       41    291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN      22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212    234       POTENTIAL.
FT   DOMAIN     235    455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43    196       4 X TNFR-CYS.
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     356    441       DEATH DOMAIN.
FT   DISULFID    44     58
FT   DISULFID    59     72
FT   DISULFID    62     81
FT   DISULFID    84     99
FT   DISULFID   102    117
FT   DISULFID   105    125
FT   DISULFID   127    143
FT   DISULFID   146    158
FT   DISULFID   149    166
FT   DISULFID   168    179
FT   DISULFID   182    191
FT   DISULFID   185    195
FT   CARBOHYD    54     54       POTENTIAL.
FT   CARBOHYD   145    145       POTENTIAL.
FT   CARBOHYD   151    151       POTENTIAL.
FT   CONFLICT   412    412       MISSING (IN REF. 4).
FT   CONFLICT   443    446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  CE0EA06F CRC32;

  Query Match           48.0%;  Score 1124;  DB 1;  Length 455;
  Best Local Similarity  99.3%;  Pred. No. 2.90e-242;
  Matches   142;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCS 183
           |||||||||||||||||||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    2
ID   CGHB_HUMAN     STANDARD;      PRT;   165 AA.
AC   P01233;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81012134.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 286:684-687(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
RN   [4]
RP   SEQUENCE OF 1-20.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 21-165.
RX   MEDLINE; 75211304.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [6]
RP   PRELIMINARY SEQUENCE OF 21-165.
RX   MEDLINE; 74011267.
RA   CARLSEN R.B., BAHL O.P., SWAMINATHAN N.;
RL   J. BIOL. CHEM. 248:6810-6827(1973).
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RN   [7]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE; 86195987.
RA   POLICASTRO P.F., DANIELS-MCQUEEN S., CARLE G., BOIME I.;
RL   J. BIOL. CHEM. 261:5907-5916(1986).
RN   [8]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81215630.
RA   MISE T., BAHL O.P.;
RL   J. BIOL. CHEM. 256:6587-6592(1981).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE; 90094415.
RA   SACCUZO BEEBE J., MOUNTJOY K., KRZESICKI R.F., PERINI F.,
RA   RUDDON R.W.;
RL   J. BIOL. CHEM. 265:312-317(1990).
RN   [10]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 92314469.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   GLYCOBIOLOGY 1:393-404(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
DR   EMBL; J00117; G180437; -.
DR   EMBL; M13504; G463088; -.
DR   EMBL; M13505; G463089; -.
DR   EMBL; M13503; G463090; -.
DR   EMBL; K03189; G180453; -.
DR   EMBL; K03187; G180453; JOINED.
DR   EMBL; K03188; G180453; JOINED.
DR   PIR; A01502; KTHUB.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   MIM; 118860; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT   SIGNAL        1     20
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77
FT   DISULFID     43     92
FT   DISULFID     46    130
FT   DISULFID     54    108
FT   DISULFID     58    110
FT   DISULFID    113    120
FT   CARBOHYD     33     33
FT   CARBOHYD     50     50
FT   CARBOHYD    141    141
FT   CARBOHYD    147    147
FT   CARBOHYD    152    152
FT   CARBOHYD    158    158
FT   VARIANT     137    137       D -> A (IN GENE 6).
SQ   SEQUENCE   165 AA;  17739 MW;  FF1D4802 CRC32;

  Query Match           44.0%;  Score 1030;  DB 1;  Length 165;
  Best Local Similarity 100.0%;  Pred. No. 8.92e-219;
  Matches  139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     27 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    147 SLPSPSRLPGPSDTPILPQ 165
           |||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    3
ID   TNR1_PIG       STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUTER B., PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; U19994; G1141753; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    233       POTENTIAL.
FT   DOMAIN      234    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      362    447       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD     86     86       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
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FT   CARBOHYD    151    151       POTENTIAL.
SQ   SEQUENCE   461 AA;  50696 MW;  8E2C350A CRC32;

  Query Match           40.8%;  Score 955;  DB 1;  Length 461;
  Best Local Similarity  80.3%;  Pred. No. 4.23e-200;
  Matches   114;  Conservative   16;  Mismatches  12;  Indels   0;  Gaps   0;

Db     41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|:|||||| |||| |||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |||||| ||:|||||:|||||||||||||||| |||| ||||:||||| ||||:|:| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQDTICNCHSGFFLRDKECVSC 182
          ||:|:| ||:|||||::|||||
Qy    143 KQNTVCTCHAGFFLRENECVSC 164


RESULT    4
ID   CGHB_PAPAN     STANDARD;      PRT;   165 AA.
AC   P07434;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   PAPIO ANUBIS (OLIVE BABOON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87106851.
RA   CRAWFORD R.J., TREGEAR G.W., NIALL H.D.;
RL   GENE 46:161-169(1986).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES AND AT LEAST
CC       TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
DR   EMBL; M14966; G176573; -.
DR   PIR; A25808; KTBAB.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       BY SIMILARITY.
FT   CARBOHYD     50     50       BY SIMILARITY.
FT   CARBOHYD    141    141       BY SIMILARITY.
FT   CARBOHYD    147    147       BY SIMILARITY.
FT   CARBOHYD    152    152       BY SIMILARITY.
SQ   SEQUENCE   165 AA;  17592 MW;  78987D30 CRC32;

  Query Match           36.6%;  Score 857;  DB 1;  Length 165;
  Best Local Similarity  81.3%;  Pred. No. 8.42e-176;
  Matches   113;  Conservative   14;  Mismatches  12;  Indels   0;  Gaps   0;

Db     27 PLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES 86
          | ||||||||| |||:||||:|||||||||||||| ||||:|||::||||||||:|||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSSKDPPP 146
          ||||||| ||:|:|| :|||||:|||||||:|||||||||||||| :| ||||| |||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    147 SPPSPSRLLEPAGTPFLPQ 165
          | |||||| |: ||:|||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    5
ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL   MOL. CELL. BIOL. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL   EUR. J. IMMUNOL. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL   IMMUNOGENETICS 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RL   IMMUNOGENETICS 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL   MOL. IMMUNOL. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M60468; G199826; -.
DR   EMBL; M59377; G202097; -.
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DR   EMBL; X59238; G53579; -.
DR   EMBL; X57796; G54849; -.
DR   EMBL; L26349; G430733; -.
DR   EMBL; M76656; G202102; -.
DR   EMBL; M88067; G202102; JOINED.
DR   EMBL; M76655; G202102; JOINED.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1TNR.
DR   MGD; MGI:98781; TNFR1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235       POTENTIAL.
FT   DOMAIN      236    454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      356    441       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    202    202       POTENTIAL.
FT   CONFLICT    394    394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  4B6EEC09 CRC32;

  Query Match           35.9%;  Score 841;  DB 1;  Length 454;
  Best Local Similarity  70.6%;  Pred. No. 7.59e-172;
  Matches   101;  Conservative   23;  Mismatches  19;  Indels   0;  Gaps   0;

Db      41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
           ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 TQNTVCNCHAGFFLRESECVPCS 183
           ||||| |||||||||:|||:|:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165


RESULT    6
ID   TNR1_RAT       STANDARD;      PRT;   461 AA.
AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M63122; G207362; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      363    448       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    201    201       POTENTIAL.
SQ   SEQUENCE   461 AA;  50969 MW;  82F68B08 CRC32;

  Query Match           34.6%;  Score 809;  DB 1;  Length 461;
  Best Local Similarity  68.5%;  Pred. No. 5.98e-164;
  Matches    98;  Conservative   21;  Mismatches  24;  Indels   0;  Gaps   0;

Db      41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
           |::|||||| || |||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  ||||| |||||:|  | ||||||:|||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCNCHAGFFLSGNECTPCS 183
           |||||| |||||||  ||| :|:
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165
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RESULT    7
ID   LSHB_HUMAN     STANDARD;      PRT;   141 AA.
AC   P01229;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [2]
RP   SEQUENCE OF 21-141.
RX   MEDLINE; 76062547.
RA   SAIRAM M.R., LI C.H.;
RL   BIOCHIM. BIOPHYS. ACTA 412:70-81(1975).
RN   [3]
RP   PRELIMINARY SEQUENCE OF 21-141.
RX   MEDLINE; 73090987.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 36:618-621(1973).
RN   [4]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 73221227.
RA   CLOSSET J., HENNEN G., LEQUIN R.M.;
RL   FEBS LETT. 29:97-100(1973).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91122088.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [6]
RP   STRUCTURE BY NMR OF 58-77.
RX   MEDLINE; 92357029.
RA   KEUTMANN H.T., HUA Q.-X., WEISS M.A.;
RL   MOL. ENDOCRINOL. 6:904-913(1992).
RN   [7]
RP   VARIANT ARG-74.
RX   MEDLINE; 92085985.
RA   WEISS J., AXELROD L., WHITCOMB R.W., HARRIS P.E., CROWLEY W.F.,
RA   JAMESON J.L.;
RL   NEW ENGL. J. MED. 326:179-183(1992).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PITUITARY.
CC   -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC       CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
DR   EMBL; X00264; E28368; -.
DR   EMBL; S71273; E91454; -.
DR   PIR; A01497; UTHUB.
DR   HSSP; P01233; 1HCN.
DR   MIM; 152780; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; PSEUDOHERMAPHRODITISM;
KW   DISEASE MUTATION.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50
FT   VARIANT      74     74       Q -> R (IN HYPOGONADISM; LACK OF
FT                                RECEPTOR-BINDING).
FT   CONFLICT     39     39       E -> Q (IN REF. 2).
FT   CONFLICT     76     76       MISSING (IN REF. 2).
FT   CONFLICT    132    135       HPQL -> PQH (IN REF. 2).
SQ   SEQUENCE   141 AA;  15345 MW;  A2457F6F CRC32;

  Query Match           31.6%;  Score 740;  DB 1;  Length 141;
  Best Local Similarity  84.4%;  Pred. No. 5.55e-147;
  Matches    92;  Conservative   12;  Mismatches   5;  Indels   0;  Gaps   0;

Db     27 PWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRDVRFES 86
          |:|:|||| |||||||||||||||||||||||| |||||:|||:|||||| ||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQL 135
          ||||||||||:|||||::|||||:|: |||||:|||||||||||||| |::
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 277


RESULT    8
ID   CGHB_CALJA     STANDARD;      PRT;   164 AA.
AC   P51500;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   CALLITHRIX JACCHUS (COMMON MARMOSET).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 96115012.
RA   SIMULA A.P., AMATO F., FAAST R., LOPATA A., BERKA J., NORMAN R.J.;
RL   BIOL. REPROD. 53:380-389(1995).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
DR   EMBL; U04447; G606607; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    164       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50       BY SIMILARITY.
FT   CARBOHYD    146    146       BY SIMILARITY.
FT   CARBOHYD    151    151       BY SIMILARITY.
SQ   SEQUENCE   164 AA;  17712 MW;  E36A4DB3 CRC32;

  Query Match           30.3%;  Score 709;  DB 1;  Length 164;
  Best Local Similarity  64.7%;  Pred. No. 2.18e-139;
  Matches    90;  Conservative   25;  Mismatches  23;  Indels   1;  Gaps   1;

Db     27 PLCRPVNAILAAEKEGCPVCVAFNTTICAGYCSSMVRVLQTILPPLPQSVCNYHELRFTS 86
          | |||:|| || |||||||:: ||||||||||::| |||| :||:||| ||||:::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 VRLPGCRPGVDPVVSMPVALSCRCGLCRRSYSDCGSLRNEPLGCDYSTFQDSSS-KDPPR 145
          :||||| ||:|||| :|||||:|:||||| :|||: :: || || : |||||| | ||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288
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Db    146 NLTSPSQLLEPADPPLVPQ 164
          :| |||:|  |:| |::||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    9
ID   LSHB_EQUAS     STANDARD;      PRT;   169 AA.
AC   P19794;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS ASINUS (DONKEY).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CHOPINEAU M., COMBARNOUS Y., ALLEN W.R., STEWART F.;
RL   SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90262634.
RA   LEIGH S.E.A., STEWART F.;
RL   J. MOL. ENDOCRINOL. 4:143-150(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X80116; G510971; -.
DR   EMBL; X53669; E27544; ALT_SEQ.
DR   PIR; S15676; S15676.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       PROBABLE.
SQ   SEQUENCE   169 AA;  17943 MW;  9D4B5421 CRC32;

  Query Match           26.9%;  Score 630;  DB 1;  Length 169;
  Best Local Similarity  63.4%;  Pred. No. 3.88e-120;
  Matches    85;  Conservative   21;  Mismatches  23;  Indels   5;  Gaps   4;

Db     27 PLCRPINATLAAEKEACPICITFTTSICAGYCRSMVRVMPAALPPIPQPVCTYRELRFGS 86
          | |||||||| |||:||:|||  |:|||||| :| ||: : ||::|| || ||::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACA-P--QTSSSCKDPPS 143
          ||||||| ||:|:||::|||||:|: ||  |||||||:||||:|  |  | ||| | ||:
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    144 QPLTSTSTPTPGAS 157
          :| | |   ||:|
Qy    289 -SLPSPS-RLPGPS 300


RESULT   10
ID   LSHB_BOVIN     STANDARD;      PRT;   141 AA.
AC   P04651;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85207729.
RA   VIRGIN J.B., SILVER B.J., THOMASON A.R., NILSON J.H.;
RL   J. BIOL. CHEM. 260:7072-7077(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85182575.
RA   MAURER R.A.;
RL   J. BIOL. CHEM. 260:4684-4687(1985).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 74075724.
RA   MAGHUIN-ROGISTER G., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; M10077; G163301; -.
DR   EMBL; M11506; G163299; -.
DR   PIR; A01499; UTBOB.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33
FT   CONFLICT      1      2       MISSING (IN REF. 2).
FT   CONFLICT     74     74       Q -> E (IN REF. 3).
FT   CONFLICT    112    112       P -> S (IN REF. 2).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
FT   CONFLICT    126    126       Q -> E (IN REF. 3).
SQ   SEQUENCE   141 AA;  15202 MW;  82879D1F CRC32;

  Query Match           26.2%;  Score 614;  DB 1;  Length 141;
  Best Local Similarity  64.9%;  Pred. No. 2.94e-116;
  Matches    72;  Conservative   22;  Mismatches  17;  Indels   0;  Gaps   0;

Db     27 PLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELRFAS 86
          | |:|||||||| |||:|||||  |:|||||||:| |||  :||::|| || |:::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 VRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137
          :|||||| ||:|:||::|||||:|: || |:|||||: :||:|| | : |
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 279


RESULT   11
ID   LSHB_HORSE     STANDARD;      PRT;   169 AA.
AC   P08751; P01234;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS CABALLUS (HORSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE; 92357035.
RA   SHERMAN G.B., WOLFE M.W., FARMERIE T.A., CLAY C.M.,
RA   THREADGILL D.S., SHARP D.C., NILSON J.H.;
RL   MOL. ENDOCRINOL. 6:951-959(1992).
RN   [2]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250476.
RA   BOUSFIELD G.R., LIU W.-K., SUGINO H., WARD D.N.;
RL   J. BIOL. CHEM. 262:8610-8620(1987).
RN   [3]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250475.
RA   SUGINO H., BOUSFIELD G.R., MOORE W.T. JR., WARD D.N.;
RL   J. BIOL. CHEM. 262:8603-8609(1987).
RN   [4]
RP   CHORIOGONADOTROPIN, PARTIAL SEQUENCE.
RA   WARD D.N., MOORE W.T. JR., BURLEIGH B.D.;
RL   J. PROTEIN CHEM. 1:263-280(1982).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 90235854.
RA   DAMM J.B.L., HARD K., KAMERLING J.P., VAN DEDEM G.W.K.,
RA   VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 189:175-183(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- PTM: AT LEAST FOUR O-GLYCOSYLATION SITES ARE PRESENT.
DR   EMBL; S41704; G252741; -.
DR   PIR; A01503; KTHOB.
DR   PIR; A29304; A29304.
DR   PIR; A29305; A29305.
DR   PIR; A41917; A41917.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       GLYCAN SHOWING A REMARKABLY STRUCTURAL
FT                                HETEROGENEITY.
SQ   SEQUENCE   169 AA;  17865 MW;  9AB1CAA3 CRC32;

  Query Match           26.2%;  Score 613;  DB 1;  Length 169;
  Best Local Similarity  62.7%;  Pred. No. 5.13e-116;
  Matches    84;  Conservative   22;  Mismatches  23;  Indels   5;  Gaps   4;

Db     27 PLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAIPQPVCTYRELRFAS 86
          | ||||||||| |||:||:||| |:||||||:| ||: : |||:|| || ||::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTDCGVFRDQPLACA-P--QASSSSKDPPS 143
          ||||||| ||:|:||::|||||:|: |:  ||||| :|:||:|  |  | ||||| ||:
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    144 QPLTSTSTPTPGAS 157
           :| | |   ||:|
Qy    289 -SLPSPS-RLPGPS 300


RESULT   12
ID   LSHB_SHEEP     STANDARD;      PRT;   141 AA.
AC   P01231;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   OVIS ARIES (SHEEP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93351742.
RA   BROWN P., MCNEILLY J.R., WALLACE R.M., MCNEILLY A.S., CLARK A.J.;
RL   MOL. CELL. ENDOCRINOL. 93:157-165(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 90245669.
RA   D'ANGELO-BERNARD G., MOUMNI M., JUTISZ M., COUNIS R.;
RL   NUCLEIC ACIDS RES. 18:2175-2175(1990).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 72211145.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., HOLCOMB G.N., WARD D.N.;
RL   J. BIOL. CHEM. 247:4365-4381(1972).
RN   [4]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 73190035.
RA   SAIRAM M.R., SAMY T.S.A., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:572-586(1972).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91006170.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; S64695; G408241; -.
DR   EMBL; X52488; G1320; -.
DR   PIR; A01500; UTSHB.
DR   PIR; S09232; S09232.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   MOD_RES      21     21       BLOCKED.
FT   CARBOHYD     33     33
FT   VARIANT     138    141       MISSING (IN SOME MOLECULES).
FT   CONFLICT     30     30       Q -> E (IN REF. 4).
FT   CONFLICT     59     59       L -> P (IN REF. 1).
FT   CONFLICT     63     63       R -> Q (IN REF. 2).
FT   CONFLICT     71     72       PM -> PPM (IN REF. 4).
FT   CONFLICT     81     81       E -> Q (IN REF. 4).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3 AND 4).
FT   CONFLICT    126    126       Q -> E (IN REF. 3 AND 4).
SQ   SEQUENCE   141 AA;  15184 MW;  BA2C0204 CRC32;

  Query Match           25.7%;  Score 602;  DB 1;  Length 141;
  Best Local Similarity  64.0%;  Pred. No. 2.36e-113;
  Matches    71;  Conservative   22;  Mismatches  18;  Indels   0;  Gaps   0;

Db     27 PLCQPINATLAAEKEACPVCITFTTSICAGYCLSMKRVLPVILPPMPQRVCTYHELRFAS 86
          | |:||||||| |||:|||||  |:|||||| :| |||  :|||::|| || |:::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
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Db     87 VRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137
          :|||||| ||:|:|||::|||||:|: || |:||||||: :||:|| | : |
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 279


RESULT   13
ID   LSHB_PIG       STANDARD;      PRT;   141 AA.
AC   P01232;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91063934.
RA   EZASHI T., HIRAI T., KATO T., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 5:137-146(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89306142.
RA   KATO Y., HIRAI T.;
RL   MOL. CELL. ENDOCRINOL. 62:47-53(1989).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 74075724.
RA   MAGHUIN-ROGISTER G., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; D00579; G217694; -.
DR   PIR; A30322; UTPGB.
DR   PIR; A48170; A48170.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33
FT   MOD_RES      21     21       BLOCKED.
FT   VARIANT      30     30       R -> Z.
FT   CONFLICT     40     40       N -> D (IN REF. 3).
FT   CONFLICT     62     62       V -> R (IN REF. 3).
FT   CONFLICT     83     83       S -> I (IN REF. 3).
FT   CONFLICT     87     87       I -> S (IN REF. 3).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
SQ   SEQUENCE   141 AA;  14889 MW;  DA2EF539 CRC32;

  Query Match           25.5%;  Score 598;  DB 1;  Length 141;
  Best Local Similarity  66.4%;  Pred. No. 2.19e-112;
  Matches    71;  Conservative   19;  Mismatches  17;  Indels    0;  Gaps    0;

Db     27 PLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELSFAS 86
          | ||||||||| |:|:|||||  |:|||||||:| ||| : ||::|| || ||:: | |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDRP 133
          ||||||| ||:| ||::|||||:|: || |::|||||: :||:|| |
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 275


RESULT   14
ID   LSHB_RAT       STANDARD;      PRT;   141 AA.
AC   P01230;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE; 83273673.
RA   CHIN W.W., GODINE J.E., KLEIN D.R., CHANG A.S., TAN L.K.,
RA   HABENER J.F.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 80:4649-4653(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85080043.
RA   JAMESON L., CHIN W.W., HOLLENBERG A.N., CHANG A.S., HABENER J.F.;
RL   J. BIOL. CHEM. 259:15474-15480(1984).
RN   [3]
RP   SEQUENCE OF 4-141 FROM N.A.
RC   STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   ZOOL. SCI. 7:877-885(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01542; G758262; -.
DR   EMBL; J00749; G205176; -.
DR   EMBL; D00576; G220808; -.
DR   PIR; A01498; UTRTB.
DR   PIR; S42527; S42527.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       PROBABLE.
SQ   SEQUENCE   141 AA;  15177 MW;  6E0C19BA CRC32;

  Query Match           25.5%;  Score 597;  DB 1;  Length 141;
  Best Local Similarity  64.2%;  Pred. No. 3.82e-112;
  Matches    70;  Conservative   23;  Mismatches  16;  Indels    0;  Gaps    0;

Db     27 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELRFAS 86
          | |||:||||| |:| ||||||  |:|||||||:| ||| : ||::|| || ||::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLPHL 135
          :|||||| ||:|:||::|||||:|: || |::|||||: :|:||| |::
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 277


RESULT   15
ID   LSHB_BALAC     STANDARD;      PRT;   118 AA.
AC   P33088;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
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DE   LUTROPIN BETA CHAIN (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.
RA   KARASEV V.S., PANKOV Y.A.;
RL   BIOKHIMIIA 50:1972-1986(1985).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; PN0139; PN0139.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; FALSE_NEG.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID      9     57       BY SIMILARITY.
FT   DISULFID     23     72       BY SIMILARITY.
FT   DISULFID     26    110       BY SIMILARITY.
FT   DISULFID     34     88       BY SIMILARITY.
FT   DISULFID     38     90       BY SIMILARITY.
FT   DISULFID     93    100       BY SIMILARITY.
FT   CARBOHYD     13     13
SQ   SEQUENCE   118 AA;  12414 MW;  DE251ECF CRC32;

  Query Match           25.4%;  Score 595;  DB 1;  Length 118;
  Best Local Similarity  60.6%;  Pred. No. 1.16e-111;
  Matches    66;  Conservative   25;  Mismatches  17;  Indels   1;  Gaps   1;

Db       7 PLCRPINATLAAZBZACPVCITFTTSICAGYCPSMVRVLPAALPPVPZPVCTYRZLRFAS 66
           | |||||||||  ::::||||||   |:|||||||:| ||| : ||::|: || ||::|| |
Qy     169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db      67 IRLPGCPPGVBPMVSFPVALSCHCGPCRLSSSBCGPGRAZPLACBRSPR 115
           ||||||| ||:|:||::|||||:|: || |:::|| : :||:|:  ||
Qy     229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD-DPR 276


Search completed: Wed May  6 08:53:30 1998
Job time : 19 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:53:48 1998; MasPar time 15.81 Seconds
817.861 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 42.863; Variance 77.650; scale 0.552

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1024	43.7	145	2	Q13991	BETA-GONADOTROPIN.	1.26e-200
2	1024	43.7	165	2	Q14000	CHORIONIC GONADOTROPIN	1.26e-200
3	945	40.4	180	4	Q95185	TUMOUR NECROSIS FACTOR	1.78e-182
4	895	38.2	471	4	O19131	TUMOR NECROSIS FACTOR-	5.05e-171
5	596	25.5	135	4	O19102	LUTEINIZING HORMONE BE	2.46e-103
6	595	25.4	139	10	Q62778	TESTICULAR LUTEINIZING	4.12e-103
7	582	24.9	141	10	Q60844	LUTEINIZING HORMONE BE	3.27e-100
8	430	18.4	140	12	Q98849	GONADOTROPIN II BETA S	9.70e-67
9	391	16.7	80	10	Q63013	TESTICULAR LUTEINIZING	2.54e-58
10	361	15.4	147	12	Q91121	GONADOTROPIN II BETA S	6.54e-52
11	353	15.1	137	12	Q90225	GONADOTROPIN BETA-SUBU	3.27e-50
12	321	13.7	130	12	O13050	GONADOTROPIN I BETA SU	1.80e-43
13	314	13.4	138	4	P79357	THYROTROPIN BETA CHAIN	5.23e-42
14	312	13.3	130	12	Q98848	GONADOTROPIN I BETA SU	1.37e-41
15	311	13.3	138	2	Q16163	THYROID-STIMULATING HO	2.21e-41
16	310	13.2	138	4	Q28376	THYROTROPIN BETA CHAIN	3.57e-41
17	301	12.9	150	12	O13051	THYROTROPIN BETA SUBUN	2.64e-39
18	294	12.6	147	12	O13052	THYROTROPIN BETA SUBUN	7.41e-38
19	289	12.3	150	12	O13049	THYROTROPIN BETA SUBUN	7.96e-37
20	271	11.6	101	10	Q62590	BETA-THYROTROPIN (FRAG	3.87e-33
21	253	10.8	277	2	O14866	SOLUBLE DEATH RECEPTOR	1.71e-29
22	253	10.8	426	2	O14865	DEATH RECEPTOR 3 BETA.	1.71e-29
23	248	10.6	253	2	O00276	LYMPHOCYTE ASSOCIATED	1.72e-28
24	248	10.6	380	2	O00280	LYMPHOCYTE ASSOCIATED	1.72e-28
25	248	10.6	418	2	O00275	LYMPHOCYTE ASSOCIATED	1.72e-28
26	214	9.1	348	11	Q85407	HOMOLOG OF VACCINIA VI	8.90e-22
27	214	9.1	349	11	Q89098	GARCIA-1966 RIGHT NEAR	8.90e-22
28	214	9.1	349	11	Q89118	SOMALIA-1977 RIGHT NEA	8.90e-22
29	210	9.0	87	2	Q15962	THYROTROPIN BETA SUBUN	5.30e-21
30	210	9.0	355	11	Q85308	SECRETED RECEPTOR BIND	5.30e-21
31	205	8.8	61	10	Q63012	TESTICULAR LUTEINIZING	4.88e-20
32	206	8.8	459	10	Q62327	TUMOR NECROSIS FACTOR	3.13e-20
33	187	8.0	267	4	O02764	OX40 PRECURSOR (FRAGME	1.29e-16
34	182	7.8	259	2	O14755	TRAIL RECEPTOR 3.	1.11e-15
35	180	7.7	283	2	Q92956	HERPESVIRUS ENTRY MEDI	2.61e-15
36	180	7.7	299	2	O14798	CYTOTOXIC TRAIL RECEPT	2.61e-15
37	178	7.6	324	10	Q63199	FAS ANTIGEN PRECURSOR.	6.13e-15
38	179	7.6	425	2	Q16042	TUMOR NECROSIS FACTOR	4.00e-15
39	167	7.1	202	2	Q14405	SOMATOTROPIN PRECURSOR	6.39e-13
40	167	7.1	217	2	Q16631	SOMATOTROPIN PRECURSOR	6.39e-13
41	163	7.0	411	2	O14720	DEATH RECEPTOR 5.	3.38e-12
42	163	7.0	411	2	O15508	P53-REGULATED DNA DAMA	3.38e-12
43	163	7.0	411	2	O15517	CYTOTOXIC TRAIL RECEPT	3.38e-12
44	163	7.0	440	2	O15531	APOPTOSIS INDUCING PRO	3.38e-12
45	163	7.0	440	2	O14763	APOPTOSIS INDUCING REC	3.38e-12

ALIGNMENTS

RESULT 1
ID Q13991 PRELIMINARY; PRT; 145 AA.

AC Q13991;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE BETA-GONADOTROPIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84093590.
RA TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL NATURE 307:37-40(1984).
DR EMBL; X00266; E27486; -.
KW SIGNAL.
SQ SEQUENCE 145 AA; 15488 MW; AC321C60 CRC32;

Query Match 43.7%; Score 1024; DB 2; Length 145;
Best Local Similarity 99.3%; Pred. No. 1.26e-200;
Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP 126
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307
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RESULT 2
ID Q14000 PRELIMINARY; PRT; 165 AA.

AC Q14000;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

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DE   CHORIONIC GONADOTROPIN BETA SUBUNIT.
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
DR   EMBL; K03183; G180444; -.
DR   EMBL; K00092; G180444; JOINED.
DR   EMBL; K03182; G180444; JOINED.
SQ   SEQUENCE   165 AA;  17729 MW;  B1CAA0B1 CRC32;

  Query Match           43.7%;  Score 1024;  DB 2;  Length 165;
  Best Local Similarity  99.3%;  Pred. No. 1.26e-200;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     27 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP 146
        ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db    147 SLPSPSRLPGPSDTPILPQ 165
          ||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307


RESULT    3
ID   Q95185         PRELIMINARY;   PRT;   180 AA.

AC   Q95185;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN   TNFR-1.
OS   FELIS SILVESTRIS CATUS (CAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CARNIVORA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   DUTHIE S., NASIR L., ECKERSALL P.D.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72344; G1613880; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
FT   NON_TER       1      1
FT   NON_TER     180    180
SQ   SEQUENCE   180 AA;  20399 MW;  5452A6B2 CRC32;

  Query Match           40.4%;  Score 945;  DB 4;  Length 180;
  Best Local Similarity  86.0%;  Pred. No. 1.78e-182;
  Matches   117;  Conservative    9;  Mismatches  10;  Indels   0;  Gaps   0;

Db     45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
          ||||||||||:||||||||||||||||||||:||| |||||||:|:|||||| ||:|||||
Qy     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db    105 KCRKEMYQVEISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQN 164
          |||||| |||||:||| |||||||||||| ||||  |||:|||||||||::|| | ||
Qy     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db    165 TVCTCHAGFFLRGNEC 180
          |||||||||||| |||
Qy    146 TVCTCHAGFFLRENEC 161


RESULT    4
ID   O19131         PRELIMINARY;   PRT;   471 AA.

AC   O19131;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR-RECEPTOR I.
GN   TNF-RI.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AORTA;
RA   LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U90937; G2290398; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
SQ   SEQUENCE   471 AA;  51368 MW;  1D60FF4A CRC32;

  Query Match           38.2%;  Score 895;  DB 4;  Length 471;
  Best Local Similarity  73.2%;  Pred. No. 5.05e-171;
  Matches   104;  Conservative   21;  Mismatches  17;  Indels   0;  Gaps   0;

Db     41 ESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCL 100
          :| |||||| ||||::|||||||||||||||||||:||||| | :|::|| |||||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160
          |||:|| || |||||:| ||||||||||||||| ||:|  |:|:||||| ||||:::|||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 RQDTICHCHMGFFLKGAKCISC 182
          :|:|:| || ||||:   |:||
Qy    143 KQNTVCTCHAGFFLRENECVSC 164


RESULT    5
ID   O19102         PRELIMINARY;   PRT;   135 AA.

AC   O19102;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LUTEINIZING HORMONE BETA SUBUNIT (FRAGMENT).
OS   CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED RHINOCEROS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 97449288.
RA   SHERMAN G.B., LUND L.A., BUNICK D., WINN R.J.;
RL   GENE 195:131-139(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   SHERMAN G.B., LUND L.A.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72659; G2462779; -.
FT   NON_TER       1      1
SQ   SEQUENCE   135 AA;  14212 MW;  F4F196D2 CRC32;

  Query Match           25.5%;  Score 596;  DB 4;  Length 135;
  Best Local Similarity  66.4%;  Pred. No. 2.46e-103;
  Matches    71;  Conservative   20;  Mismatches  16;  Indels   0;  Gaps   0;

Db     21 PLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPAPQPVCTYHELRFAS 80
          | |||||||| |:|:|||||  |:|||||||:| ||| : ||: || || |:::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     81 IRLPGCPPGVDPMVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDRP 127
          ||||||| ||:|:|||::|||||:|: || |::|||||: :|||:|| |
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Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 275


RESULT    6
ID   Q62778         PRELIMINARY;   PRT;   139 AA.

AC   Q62778;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   TESTICULAR LUTEINIZING HORMONE BETA-SUBUNIT.
GN   TLHB1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAQUE DAWLEY;
RX   MEDLINE; 95283549.
RA   ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR   EMBL; U25653; G915217; -.
SQ   SEQUENCE   139 AA;  14880 MW;  5B2E7DBF CRC32;

  Query Match           25.4%;  Score 595;  DB 10;  Length 139;
  Best Local Similarity  63.3%;  Pred. No. 4.12e-103;
  Matches    69;  Conservative   24;  Mismatches  16;  Indels   0;  Gaps   0;

Db     25 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRILPAALPPVPQPVCTYRELRFAS 84
          | |||:||||| |:| ||||||  |:||||||:| |:| : ||::|| || ||::|| |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     85 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLPHL 133
          :|||||| ||:|:||::|||||:|: || |::|||||: :|:||| |::
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 277


RESULT    7
ID   Q60844         PRELIMINARY;   PRT;   141 AA.

AC   Q60844;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LUTEINIZING HORMONE BETA (LUTENIZING HORMONE BETA-SUBUNIT).
GN   LHB.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129 SVEV;
RA   KAPUR V., MATZUK M.M.;
RL   SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U25145; G930345; -.
DR   MGD; MGI:96782; LHB.
SQ   SEQUENCE   141 AA;  15028 MW;  BE50AB2B CRC32;

  Query Match           24.9%;  Score 582;  DB 10;  Length 141;
  Best Local Similarity  62.4%;  Pred. No. 3.27e-100;
  Matches    68;  Conservative   24;  Mismatches  17;  Indels   0;  Gaps   0;

Db     27 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELAFAS 86
          | |||:||||| |:| ||||||  |:||||||:| ||| : ||::|| || ||:: | |
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMACDLPHL 135
          :|||||| ||:|:||::|||||:|: || |::|||||: :|::|| |::
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 277


RESULT    8
ID   Q98849         PRELIMINARY;   PRT;   140 AA.

AC   Q98849;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D88024; G1644243; -.
KW   SIGNAL.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    140       GONADOTROPIN II BETA SUBUNIT.
SQ   SEQUENCE   140 AA;  15533 MW;  7205FD03 CRC32;

  Query Match           18.4%;  Score 430;  DB 12;  Length 140;
  Best Local Similarity  50.0%;  Pred. No. 9.70e-67;
  Matches    54;  Conservative   22;  Mismatches  32;  Indels   0;  Gaps   0;

Db     27 PPCEPVNETVAVEKEGCPKCLVLQTTICSGHCLTKEPVYKSPFSTVYQHVCTYRDVRYET 86
          | | |:| |:|||||||| |: : ||||:| | |:  |  : :::: | || |||||:|:
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     87 VRLPDCPPGVDPHITYPVALSCDCSLCTMDTSDCTIESLQPDFCMSQR 134
          :||| || ||:| ::|:|||||:|:||   |:||     :|  |  .|
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 276


RESULT    9
ID   Q63013         PRELIMINARY;   PRT;    80 AA.

AC   Q63013;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   TESTICULAR LUTEINIZING HORMONE BETA SUBUNIT.
GN   TLHB3.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAQUE DAWLEY;
RX   MEDLINE; 95283549.
RA   ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR   EMBL; U25803; G904026; -.
SQ   SEQUENCE   80 AA;  8515 MW;  74FA772D CRC32;

  Query Match           16.7%;  Score 391;  DB 10;  Length 80;
  Best Local Similarity  60.0%;  Pred. No. 2.54e-58;
  Matches    45;  Conservative   18;  Mismatches  11;  Indels   1;  Gaps   1;

Db      1 MVRVLPAALPPVPQPVCTYRE-RFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDC 59
          | ||| : ||::|| || ||: || |:|||||| ||:|:||::|||||:|: || |::||
Qy    203 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262

Db     60 GGPRTQPMTCDLPHL 74
          |||: :|:||| |::
Qy    263 GGPKDHPLTCDDPRF 277


RESULT   10
ID   Q91121         PRELIMINARY;   PRT;   147 AA.

AC   Q91121;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
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DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS   MORONE SAXATILIS (STRIPED BASS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
DR   EMBL; L35096; G598255; -.
KW   SIGNAL.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33    147       GONADOTROPIN II BETA SUBUNIT.
SQ   SEQUENCE   147 AA;  16398 MW;  292F2F62 CRC32;

  Query Match           15.4%;  Score 361;  DB 12;  Length 147;
  Best Local Similarity  44.5%;  Pred. No. 6.54e-52;
  Matches    49;  Conservative   24;  Mismatches  36;  Indels   1;  Gaps   1;

Db     36 PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVIKIPFSNVYQHVCTYRDLHYKT 95
           | |: || |:::|||||| |  |:||||:| | |:  |:   :: : | || |||::: :
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     96 FELPDCPPGVDPTVTYPVAQSCHCGRCAMDTSDCTFESLQPNFCMNDIPF 145
           : || || ||:| |:|:|| ||:|: |   |:||     :|  | :|  |
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC-DDPRF 277


RESULT   11
ID   Q90225         PRELIMINARY;   PRT;   137 AA.

AC   Q90225;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN BETA-SUBUNIT.
OS   ACANTHOPAGRUS LATUS.
OC   EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES;
OC   ACTINOPTERYGII; PERCIFORMES; PERCOIDEI; SPARIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   TSAI H.J., YANG L.T.;
RL   SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; L11722; G437308; -.
SQ   SEQUENCE   137 AA;  15330 MW;  F87577B5 CRC32;

  Query Match           15.1%;  Score 353;  DB 12;  Length 137;
  Best Local Similarity  44.5%;  Pred. No. 3.27e-50;
  Matches    49;  Conservative   22;  Mismatches  36;  Indels   3;  Gaps   3;

Db     28 PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVMKTRY-VYQHV-CTYRDLHYKT 85
           | |: || |:::|||||| |  |:||||:| | |:  |:        :| | |||::: :
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     86 FELPDCPLGVDPTVTYPVAVSCNCGLCAMDTSDCTFESLQPNFCMNDIPF 135
           : || || ||:| |:|:||:|| |:||   |:||     :|  | :|  |
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC-DDPRF 277


RESULT   12
ID   O13050         PRELIMINARY;   PRT;   130 AA.

AC   O13050;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CYPRINUS CARPIO (COMMON CARP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., IWASAKI M., KONDO H., YOSHIURA Y., WATABE S.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB003583; D1020895; -.
KW   SIGNAL.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    130       GONADOTROPIN I BETA SUBUNIT.
SQ   SEQUENCE   130 AA;  14393 MW;  3D37E6B1 CRC32;

  Query Match           13.7%;  Score 321;  DB 12;  Length 130;
  Best Local Similarity  41.3%;  Pred. No. 1.80e-43;
  Matches    43;  Conservative   24;  Mismatches  35;  Indels   2;  Gaps   2;

Db     26 CRLTNISITVESEECGSCITIDTTACAGLCKTQESVYRSPL-MLSYQNTCNFREWTYETY 84
           ||  | :::|| | |  |||::|| ||| | |   | :: |  |: |  ||:|:  :|:
Qy    171 CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI 229

Db     85 EFKGCPARADSVFTYPVALSCECSKCNSDITDCGALSQQTLSCN 128
            : |||   ::| :|:|||||:|: |    ||||:  :: |:|:
Qy    230 RLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 273


RESULT   13
ID   P79357         PRELIMINARY;   PRT;   138 AA.

AC   P79357;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE   THYROTROPIN BETA CHAIN.
OS   LAMA GLAMA (LLAMA).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RA   KANIA S.A., FRANK L.A., ODOM T.F.;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U89294; G1872550; -.
SQ   SEQUENCE   138 AA;  15571 MW;  332E4E82 CRC32;

  Query Match           13.4%;  Score 314;  DB 4;  Length 138;
  Best Local Similarity  45.7%;  Pred. No. 5.23e-42;
  Matches    48;  Conservative   22;  Mismatches  29;  Indels   6;  Gaps   4;

Db     13 LACGQAMSFCIPTEYMMHVERKECAYCLTINTTICAGYC--MTRDFNGKLFLPKFALSQD 70
           ::|: | : | | :  : ||:  |: |:|:|||||||||  ||| : | : ||  ||:|
Qy    162 VSCAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQG-V-LP--ALPQV 217

Db     71 VCTYRDFMYKTVEIPGCPHHVTPYFSYPVAVSCKCGKCDTDYSDC 115
           || |||  : :: :|||||: | |  ||:||:|| |: |    :||
Qy    218 VCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262


RESULT   14
ID   Q98848         PRELIMINARY;   PRT;   130 AA.

AC   Q98848;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D88023; G1644241; -.
KW   SIGNAL.
FT   SIGNAL        1     18       POTENTIAL.
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FT   CHAIN        19    130       GONADOTROPIN I BETA SUBUNIT.
SQ   SEQUENCE   130 AA;  14422 MW;  3C222BFD CRC32;

  Query Match           13.3%;  Score 312;  DB 12;  Length 130;
  Best Local Similarity  40.4%;  Pred. No. 1.37e-41;
  Matches    42;  Conservative   23;  Mismatches  37;  Indels   2;  Gaps   2;

Db      26 CRLTNISITVESEECGSCITIDTTACAGLCKTQESVYRSPL-MLSYQNTCNFREWTYETY 84
           ||  | :::|| | |  |||::|| ||| | |   | :: |  |: |  ||:|:  :|:
Qy     171 CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI 229

Db      85 EFKGCPARADSIFTYPVALSCECSKCNSDITDCGVLSQQTLGCN 128
             : |||   ::: :|:|||||:|: |    ||||   :: | |:
Qy     230 RLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 273


RESULT   15
ID   Q16163         PRELIMINARY;   PRT;   138 AA.

AC   Q16163;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   THYROID-STIMULATING HORMONE BETA SUBUNIT (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94254248.
RA   MIYOSHI I., KASAI N., HAYASHIZAKI Y.;
RL   NIPPON RINSHO 52:940-947(1994).
DR   EMBL; S70587; G546849; -.
FT   NON_TER     138    138
SQ   SEQUENCE   138 AA;  15627 MW;  0539646F CRC32;

  Query Match           13.3%;  Score 311;  DB 2;  Length 138;
  Best Local Similarity  45.7%;  Pred. No. 2.21e-41;
  Matches    48;  Conservative   22;  Mismatches  29;  Indels   6;  Gaps   4;

Db      13 LACGQAMSFCIPTEYTMHIERRECAYCLTINTTMCAGYC-MTRDINGKLFLPKYALSQD 70
           ::|: | : | | : |: :|:  |: |:|:|||:|||||  ||| : | : ||  ||:|
Qy     162 VSCAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQG-V-LP--ALPQV 217

Db      71 VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCNTDYSDC 115
           || |||  : :: :|||| | |  ||:||||| |: |    :||
Qy     218 VCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262


Search completed: Wed May  6 08:55:06 1998
Job time : 78 secs.
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MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:          Wed May  6 13:40:53 1998;  MasPar time 1173.41 Seconds
                                            1494.904 Million cell updates/sec
Tabular output not generated.

Title:           >US-08-804-166-5
Description:     (1-1147) from US08804166.seq
Perfect Score:   1147
N.A. Sequence:         1 TCGAGATGGCTACAGGTAAG.....AATCTTAAGGATCCCTCGAG 1147
     Comp:               AGCTCTACCGATGTCCATTC.....TTAGAATTCCTAGGGAGCTC

Scoring table:   TABLE default
                 Gap 6

Nmatch   STD :   Dbase 0;  Query 0

Searched:        436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        embl53
                   1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
                   7:em_huml 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
                   13:em_pat
Database:        genbank105
                   14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
                   20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
                   26:gb_htg 27:gb_prl 28:gb_pr2

Statistics:      Mean 11.072;  Variance 4.877;  scale 2.270

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	506	44.1	1331	25	A29103	H.sapiens mRNA for TNF	0.00e+00
2	506	44.1	1368	25	A29098	Synthetic DNA for TNF-	0.00e+00
3	506	44.1	2050	27	HUMTNFRP	Human tumor necrosis f	0.00e+00
4	506	44.1	2062	25	A21522	TNF alpha gene.	0.00e+00
5	506	44.1	2062	25	I43805	Sequence 24 from paten	0.00e+00
6	506	44.1	2087	27	HUMTNFR	Human tumor necrosis f	0.00e+00
7	506	44.1	2111	27	HUMTNFRB	Homo sapiens tumor nec	0.00e+00
8	506	44.1	2111	25	A26412	cDNA for (55kD TNF-BP)	0.00e+00
9	506	44.1	2112	27	HUMTNFRC	Human tumor necrosis f	0.00e+00
10	506	44.1	2161	27	HSTNFR1A	H.sapiens TNF-R mRNA f	0.00e+00
11	506	44.1	2175	25	I64751	Sequence 1 from patent	0.00e+00
12	506	44.1	2175	25	A43873	Sequence 1 from Patent	0.00e+00
13	506	44.1	2176	25	A19907	Synthetic nucleotide s	0.00e+00
14	504	43.9	6889	25	I26928	Sequence 2 from patent	0.00e+00
15	499	43.5	2061	25	A20255	55kD receptor gene for	0.00e+00
16	473	41.2	483	25	A29099	Synthetic DNA for TNF-	0.00e+00
17	468	40.8	600	25	A20257	Synthetic nucleotide s	0.00e+00
18	467	40.7	510	25	A21525	oligonucleotide probe.	0.00e+00
19	464	40.5	600	25	I43808	Sequence 47 from paten	0.00e+00
20	375	32.7	504	25	A20713	Synthetic nucleotide s	0.00e+00
21	375	32.7	504	25	I43813	Sequence 56 from paten	0.00e+00
22	373	32.5	501	25	I43786	Sequence 1 from patent	0.00e+00
23	366	31.9	500	25	A20254	Synthetic nucleotide 5	0.00e+00
24	364	31.7	372	25	I43787	Sequence 3 from patent	0.00e+00
25	364	31.7	372	25	A20253	Synthetic nucleotide 5	0.00e+00
26	345	30.1	474	25	A20259	Synthetic nucleotide s	4.80e-289
27	345	30.1	474	25	I43809	Sequence 49 from paten	4.80e-289
28	316	27.6	66495	27	HUMGHCSA	Human growth hormone (	2.26e-261
29	307	26.8	581	15	FCU72344	Felis catus tumour nec	8.40e-253
30	301	26.2	2004	15	SSU19994	Sus scrofa p55 TNF rec	4.30e-247
31	289	25.2	1826	25	I02855	Sequence 1 from Patent	1.09e-235
32	288	25.1	1964	27	HSGROW2	Human germ line gene f	9.72e-235
33	288	25.1	1964	27	HUMGH	Human growth hormone (	9.72e-235
34	288	25.1	2771	25	I41411	Sequence 5 from patent	9.72e-235
35	287	25.0	2657	27	HUMGHN	Human growth hormone g	8.66e-234
36	287	25.0	4283	25	I63120	Sequence 3 from patent	8.66e-234
37	263	22.9	2130	14	RATTNFR	Rat tumor necrosis fac	4.84e-211
38	262	22.8	621	27	HSGONA	Human messenger RNA fo	4.28e-210
39	255	22.2	477	25	A20263	Synthetic nucleotide s	1.77e-203
40	255	22.2	477	25	I43811	Sequence 53 from paten	1.77e-203
41	252	22.0	1956	14	MUSTNFR2	Murine tumor necrosis	1.21e-200
42	252	22.0	2048	14	MUSMTNFR1	Mouse tumor necrosis f	1.21e-200
43	252	22.0	2063	14	MMP55R	Murine mRNA for p55 tu	1.21e-200
44	252	22.0	2154	14	MUSTNFX	Mus musculus Tumor Nec	1.21e-200
45	252	22.0	2179	14	MMTNFRE5	Mouse mRNA for 55-kDa	1.21e-200

ALIGNMENTS

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RESULT    1
LOCUS       A29103       1331 bp    DNA             PAT       03-JUL-1995

DEFINITION  H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29103
NID         g1247517
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1331)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 53 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1. .1331
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      298 a    407 c    343 g    283 t
ORIGIN

  Query Match           44.1%;  Score 506;  DB 25;  Length 1331;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db     333 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 392
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Qy     344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db     393 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 452
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Qy     404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db     453 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 512
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Qy     464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523
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Db    513 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 572
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Db    573 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 632
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    633 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 692
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    693 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 752
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    753 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 812
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    813 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCCTGGT 862
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874
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RESULT 2
LOCUS A29098 1368 bp DNA PAT 03-JUL-1995

DEFINITION Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION A29098
NID g1248892
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1368)
AUTHORS Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL Patent: EP 0393438-A 48 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

FEATURES Location/Qualifiers
source 1. .1368
/organism="unidentified"
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source 1. .1368
/organism="artificial sequence"
/db_xref="taxon:29278"

BASE COUNT 293 a 424 c 375 g 276 t
ORIGIN

Query Match 44.1%; Score 506; DB 25; Length 1368;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCCTGGT 650
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874
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RESULT 3
LOCUS HUMTNFRP 2050 bp mRNA PRI 11-OCT-1991

DEFINITION Human tumor necrosis factor receptor(TNF) mRNA, complete cds.
ACCESSION M60275 M37764
NID g339759
KEYWORDS TNF receptor; transmembrane receptor; tumor necrosis factor receptor.
SOURCE Human placenta, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2050)
AUTHORS Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.
TITLE Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
MEDLINE 91017509
COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-AUG-1990.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/tissue_type="placenta"
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/gene="TNF receptor"
CDS 155. .1516
/codon_start=1
/product="TNF receptor"
/db_xref="PID:g339760"
/translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
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gene 155. .274
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mat_peptide 275. .1513
/product="TNF receptor"

BASE COUNT 429 a 611 c 566 g 444 t
ORIGIN

Query Match 44.1%; Score 506; DB 27; Length 2050;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCCTGGT 804
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    4
LOCUS       A21522       2062 bp    RNA             PAT       26-JUL-1994

DEFINITION  TNF alpha gene.
ACCESSION   A21522
NID         g579599
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   .
  JOURNAL   Patent: GB 2246569-A 1 05-FEB-1992;
FEATURES             Location/Qualifiers
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                     /gene="TNF alpha gene"
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                     /db_xref="PID:g579600"
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
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                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
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BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

  Query Match           44.1%;  Score 506;  DB 25;  Length 2062;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCCTGGT 804
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    5
LOCUS       I43805       2062 bp    DNA             PAT       10-JUL-1997

DEFINITION  Sequence 24 from patent US 5633145.
ACCESSION   I43805
NID         g2468903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE     TNF.alpha. receptor-derived binding protein
  JOURNAL   Patent: US 5633145-A 24 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .2062
                     /organism="unknown"
BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

  Query Match           44.1%;  Score 506;  DB 25;  Length 2062;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT 804
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874
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RESULT    6
LOCUS       HUMTNFR      2087 bp    mRNA            PRI       10-NOV-1993

DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61, 361-370 (1990)
  MEDLINE   90235285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
FEATURES             Location/Qualifiers
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     CDS             182. .1549
                     /note="tumor necrosis factor receptor"
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                     /db_xref="PID:g339745"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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                     SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
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                     PSLLR"
BASE COUNT      433 a    624 c    581 g    449 t
ORIGIN
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  Query Match           44.1%;  Score 506;  DB 27;  Length 2087;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;
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Db    302 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 361
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    362 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 421
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    422 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 481
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    482 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 541
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    542 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 601
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    602 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 661
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    662 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 721
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    722 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 781
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    782 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT 831
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874
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RESULT    7
LOCUS       HUMTNFRB     2111 bp    mRNA            PRI       14-NOV-1990

DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID         g339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cell line HL60, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
  TITLE     Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
  JOURNAL   Cell 61, 351-359 (1990)
  MEDLINE   90235284
FEATURES             Location/Qualifiers
     source          1. .2111
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                     /cell_line="HL60"
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                     /product="tumor necrosis factor receptor"
     CDS             187. .1554
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                     /note="55 kDa"
                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /db_xref="PID:g339754"
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                     SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
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  Query Match           44.1%;  Score 506;  DB 27;  Length 2111;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 546
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    547 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 606
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
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Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 726
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    727 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 786
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    787 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT 836
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    8
LOCUS       A26412       2111 bp    DNA             PAT       26-APR-1995

DEFINITION  cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
            patent EP0417563.
ACCESSION   A26412
NID         g904968
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 24 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .2111
                     /organism="Artificial sequences"
     CDS             187. .1554
                     /note="pid:e161624"
                     /codon_start=1
                     /product="55 kD TNF-BP"
                     /db_xref="PID:g904969"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
                     PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           44.1%;  Score 506;  DB 25;  Length 2111;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 546
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    547 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 606
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
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Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 726
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    727 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 786
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    787 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT 836
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    9
LOCUS       HUMTNFRC     2112 bp    mRNA            PRI       30-SEP-1991

DEFINITION  Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
            cds.
ACCESSION   M63121 M75861
NID         g339755
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2112)
  AUTHORS   Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
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            Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C. and
            Adolf,G.R.
  TITLE     Molecular cloning and expression of human and rat tumor necrosis
            factor receptor chain (p60) and its soluble derivative, tumor
            necrosis factor-binding protein
  JOURNAL   DNA Cell Biol. 9, 705-715 (1990)
  MEDLINE   91090841
FEATURES             Location/Qualifiers
     source          1. .2112
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                     /db_xref="taxon:9606"
     sig_peptide     207. .293
                     /gene="TNF receptor"
     CDS             207. .1574
                     /gene="TNF receptor"
                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /db_xref="PID:g339756"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
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     gene            207. .1574
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     mat_peptide     294. .1571
                     /gene="TNF receptor"
                     /product="tumor necrosis factor receptor"
BASE COUNT      435 a    632 c    589 g    456 t
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  Query Match           44.1%;  Score 506;  DB 27;  Length 2112;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    327 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 386
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    387 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 446
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    447 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 506
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    507 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 566
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    567 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 626
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    627 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 686
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Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    687 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 746
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    747 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 806
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    807 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT 856
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT   10
LOCUS       HSTNFR1A     2161 bp    RNA             PRI       18-JAN-1993

DEFINITION  H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION   X55313
NID         g37223
KEYWORDS    TNF-R gene; tumor necrosis factor receptor 1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2161)
  AUTHORS   Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
            Aderka,D., Holtmann,H. and Wallach,D.
  TITLE     Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
            for the type I TNF-R, cloned using amino acid sequence data of its
            soluble form, encodes both the cell surface and a soluble form of
            the receptor
  JOURNAL   EMBO J. 9 (10), 3269-3278 (1990)
  MEDLINE   91006021
FEATURES             Location/Qualifiers
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                     /product="tumor necrosis factor receptor type 1"
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                     /db_xref="SWISS-PROT:P19438"
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BASE COUNT      459 a    642 c    604 g    456 t
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  Query Match           44.1%;  Score 506;  DB 27;  Length 2161;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
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Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCCTGGT 905
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT   13
LOCUS       A19907       2176 bp    DNA             PAT       04-OCT-1994

DEFINITION  Synthetic nucleotide sequence Type I TNF receptor gene.
ACCESSION   A19907
NID         g641222
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2176)
  AUTHORS   Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
            Aderka,D.
  TITLE     Expression of the recombinant tumor necrosis factor binding protein
            I (TBP-I)
  JOURNAL   Patent: EP 0433900-A 28 26-JUN-1991;
            YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED
FEATURES             Location/Qualifiers
     source          1. .2176
                     /organism="Artificial sequences"
BASE COUNT      474 a    642 c    604 g    456 t
ORIGIN

  Query Match           44.1%;  Score 506;  DB 25;  Length 2176;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

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Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCCTGGT 905
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT   14
LOCUS       I26928       6889 bp    DNA             PAT       01-OCT-1996

DEFINITION  Sequence 2 from patent US 5561053.
ACCESSION   I26928
NID         g1606798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6889)
  AUTHORS   Crowley,C.W.
  TITLE     Method for selecting high-expressing host cells
  JOURNAL   Patent: US 5561053-A 2 01-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .6889
                     /organism="unknown"
BASE COUNT     1729 a   1826 c   1681 g   1653 t
ORIGIN

  Query Match           43.9%;  Score 504;  DB 25;  Length 6889;
  Best Local Similarity  99.0%;  Pred. No. 0.00e+00;
  Matches   509;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
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Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
          |||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db   2145 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 2204
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823
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Db   2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 857


RESULT   15
LOCUS       A20255       2061 bp    DNA             PAT       20-SEP-1995

DEFINITION  55kD receptor gene for human TNF-alpha.
ACCESSION   A20255
NID         g1247401
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2061)
  AUTHORS   .
  TITLE     MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL   Patent: WO 9207076-A 23 30-APR-1992;
FEATURES             Location/Qualifiers
     source          1. .2061
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      429 a    616 c    573 g    443 t
ORIGIN

  Query Match           43.5%;  Score 499;  DB 25;  Length 2061;
  Best Local Similarity  97.9%;  Pred. No. 0.00e+00;
  Matches   520;  Conservative    0;  Mismatches   9;  Indels   2;  Gaps   2;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCAC-TCTCCTGCCAGGAG 633
          |||||||||||||||||| |||||||||||||||||||||||||| ||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    634 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 693
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    694 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 753
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    754 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT 803
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


Search completed: Wed May  6 14:00:37 1998
Job time : 1184 secs.
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MPSRCH (TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:19:06 1998; MasPar time 149.10 Seconds
887.730 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-5
Description: (1-1147) from US08804166.seq
Perfect Score: 1147
N.A. Sequence: 1 TCGAGATGGCTACAGGTAAG.....AATCTTAAGGATCCCTCGAG 1147
Comp: AGCTCTACCGATGTCCATTC.....TTAGAATTCCTAGGGAGCTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.143; Variance 4.888; scale 1.870

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	506	44.1	1334	1	Q06282	Plasmid Tumour Necros	0.00e+00
2	506	44.1	1368	8	Q49932	Lambda-derived TNF-R	0.00e+00
3	506	44.1	2062	3	Q20973	TNF-alpha binding pro	0.00e+00
4	506	44.1	2062	4	Q24440	Encodes TNF-alpha 55k	0.00e+00
5	506	44.1	2088	2	Q10883	30kD TNF inhibitor pr	0.00e+00
6	506	44.1	2111	2	Q10955	Encodes human 55kD TN	0.00e+00
7	506	44.1	2175	15	Q90513	p55 TNF-R gene.	0.00e+00
8	504	43.9	2141	1	Q06285	Human Tumour Necrosis	0.00e+00
9	504	43.9	2176	2	Q12215	Type I TNF receptor.	0.00e+00
10	504	43.9	6889	18	T15931	DHFR/intron (WTrasSD)	0.00e+00
11	502	43.8	2170	9	Q50870	p55 Tumour necrosis f	0.00e+00
12	468	40.8	608	4	Q24441	Encodes truncated TNF	0.00e+00
13	375	32.7	504	4	Q24445	Encodes truncated TNF	1.89e-267
14	345	30.1	474	4	Q24442	Encodes truncated TNF	1.16e-243
15	288	25.1	2771	31	T76770	Rat Fabpl gut-specifi	1.27e-198
16	287	25.0	2160	33	T62826	Human growth hormone	7.82e-198
17	280	24.4	336	6	Q41459	Human growth hormone	2.55e-192
18	264	23.0	707	17	T03236	Single chain gonadotr	9.85e-180
19	264	23.0	719	17	T03235	Single chain gonadotr	9.85e-180
20	264	23.0	728	17	T03224	Single chain gonadotr	9.85e-180
21	264	23.0	743	17	T03219	Single chain gonadotr	9.85e-180
22	264	23.0	743	17	T03233	Single chain gonadotr	9.85e-180
23	264	23.0	743	17	T03231	Single chain gonadotr	9.85e-180
24	264	23.0	744	17	T03221	Single chain gonadotr	9.85e-180
25	264	23.0	752	17	T03227	Single chain gonadotr	9.85e-180
26	264	23.0	752	17	T03229	Single chain gonadotr	9.85e-180
27	264	23.0	836	17	T03212	Single chain gonadotr	9.85e-180
28	262	22.8	592	2	Q10075	Engineered human alph	3.67e-178
29	262	22.8	592	24	T41695	Dimeric glycoprotein	3.67e-178
30	256	22.3	312	17	T03237	Gonadotropin alpha su	1.89e-173
31	256	22.3	836	17	T03243	Single chain gonadotr	1.89e-173
32	255	22.2	477	4	Q24444	Encodes truncated TNF	1.15e-172
33	255	22.2	2173	1	Q06284	Rat Tumour Necrosis F	1.15e-172
34	213	18.6	462	4	Q24443	Encodes truncated TNF	8.39e-140
35	194	16.9	2660	4	N30032	Sequence of gene for	5.08e-125
36	178	15.5	608	1	Q03846	Porcine alpha subunit	1.27e-112
37	166	14.5	716	2	Q10059	Ovine FSH alpha subun	2.31e-103
38	164	14.3	731	1	Q03843	Bovine alpha subunit	8.03e-102
39	150	13.1	480	1	Q03849	Equine alpha subunit	4.52e-91
40	144	12.6	482	1	Q03820	Gene encoding equine	1.76e-86
41	130	11.3	1027	2	Q10878	Partial sequence of c	8.03e-76
42	101	8.8	345	11	Q65374	Fish gonadotropic hor	5.08e-54
43	99	8.6	340	2	N91174	Sequence encoding fis	1.55e-52
44	80	7.0	360	11	Q65373	Fish gonadotropic hor	1.40e-38
45	79	6.9	267	3	N50521	Sequence encoding sal	7.41e-38

ALIGNMENTS

RESULT 1
ID Q06282 standard; DNA; 1334 BP.
AC Q06282;
DT 29-JAN-1991 (first entry)
DE Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW pTNF-BP15; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 213..1325
FT /*tag= a
FT /product=TNF-BP
PN EP-393438-A.
PD 24-OCT-1990.
PF 06-APR-1990; 106624.
PR 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
PA (BOEH) BOEHRINGER INGELHEIMINT.
PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR WPI; 90-321987/43.
DR P-PSDB; R07449.
PT DNA encoding TNF binding protein and TNF- receptor - used in
PT tumour treatment and to understand mechanismsm to TNF action
PS Disclosure; Fig 1(1-3); 51pp; German.
CC pTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC from induced TNF-induced fibrosarcoma cells. A TNF-BP had been
CC isolated from the urine of patients with uraemia and probes/primers
CC were constructed from the determined amino acid sequence.
CC To produce a vector expressing a soluble form of TNF-binding
CC protein, this plasmid was cut with XmmI, amplified by PCR and the
CC amplified DNA cut with BamHI and EcoRI.
CC The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC (BRL) cut with the same enzymes to recover pTNF-BP. This was cut
CC with BamHI and EcoRI, and the recovered fragment inserted into
CC pAD-CMV1 (Q06283) to give the required plasmid pADTNF-BP.
CC See also Q06282-Q06285.
SQ Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T;

Query Match 44.1%; Score 506; DB 1; Length 1334;

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  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 392
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
          |||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    753 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 812
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    813 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 862
          ||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    2
ID    Q49932 standard; cDNA to mRNA; 1368 BP.
AC    Q49932;
DT    29-APR-1994  (first entry)
DE    Lambda-derived TNF-R cDNA.
KW    Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW    IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW    rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW    pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW    graft verses host disease; sepsis; inflammation; allergy;
KW    autoimmune dysfunction; ss.
OS    Homo sapiens.
OS    Lambda-gt10-7-ctnfbp.
FH    Key             Location/Qualifiers
FT    CDS             1..1366
FT    /*tag=  a
FT    /product= hTNF-R
FT    sig_peptide     1..120
FT    /*tag=  b
FT    mat_peptide     121..1363
FT    /*tag=  c
PN    WO9319777-A.
PD    14-OCT-1993.
PF    26-MAR-1993; U02938.
PR    30-MAR-1992; US-860710.
PA    (IMMV ) IMMUNEX CORP.
PI    Smith CA;
DR    WPI; 93-336592/42.
DR    P-PSDB; R42059.
PT    New fusion protein tumour necrosis factor and human interleukin-1
PT    receptor - useful in therapy, diagnosis and assays of e.g.
PT    rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS    Disclosure; Page 57-59; 85pp; English.

CC    The sequences given in Q49931-32 encode human tumour necrosis factor
CC    receptor (TNF-R) and the sequences in Q49933-34 encode human
CC    interleukin-1 receptor (IL-1R).  These sequences were used in the
CC    production of a fusion protein which conformed to one of the
CC    formulae:
CC    TNF-R-linker-TNF-R-linker-IL-1R
CC    IL-1R-linker-TNF-R-linker-TNF-R or
CC    TNF-R-linker-TNF-R
CC    The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC    Ser, Thr and Ala.  These linkers separate the individual moeities
CC    by such a distance that each component of the fusion protien is
CC    capable of folding into the secondary or tertiary structure required
CC    for its biological activity.  These fusion proteins may be used in
CC    therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC    particularly in conditions in which both TNF and IL-1 play a causitive
CC    role.  They may be used to treat cachexia, rheumatoid arthritis,
CC    diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC    cerebral malaria, allograft and xenograft rejection in graft verses
CC    host disease, sepsis, septic shock, inflammation, allergies and
CC    autoimmune dysfunctions.
SQ    Sequence   1368 BP;    292 A;    424 C;    376 G;    276 T;

  Query Match           44.1%;  Score 506;  DB 8;  Length 1368;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    121 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 180
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
          |||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    481 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 540
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    541 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 600
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    601 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 650
          ||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    3
ID    Q20973 standard; DNA; 2062 BP.
AC    Q20973;
DT    11-MAY-1992  (first entry)
DE    TNF-alpha binding protein gene.
KW    Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
KW    extracellular domain.
OS    Homo sapiens.
FH    Key             Location/Qualifiers
FT    CDS             155..1522
```

```
FT   /*tag= a
FT   sig_peptide     155..274
FT   /*tag= b
FT   mat_peptide     275..1522
FT   /*tag= c
FT   misc_feature    473..532
FT   /*tag= d
FT   /note= "homologous to probe Q20974"
FT   misc_feature    242..751
FT   /*tag= e
FT   /note= "encodes the extracellular domain of human
FT   TNF alpha receptor"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding tumour necrosis factor alpha
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence   2062 BP;    429 A;    616 C;    573 G;    444 T;

  Query Match           44.1%;  Score 506;  DB 3;  Length 2062;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          |||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 754
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    755 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 804
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874
```

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RESULT    4
ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-NOV-1992  (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             156..1517
FT   /*tag= a
FT   /product= human TNF-alpha
FT   mat_peptide     1265..1267
FT   /*tag= b
FT   /note= "3"
FT   mat_peptide     1265..1267
FT   /*tag= c
FT   /codon= seq:"TGG", aa:Thr
FT   mat_peptide     1258..1260
FT   /*tag= d
FT   /codon= Seq"AAG", aa:Leu
FT   mat_peptide     1433..1435
FT   /*tag= e
FT   /codon= Seq:"GAC", aa:Asn
FT   sig_peptide     156..274
FT   /*tag= f
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24000
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Claim 4; Fig 1; 43pp; English.
CC   This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC   library in gt10 was screened with probe Q29236. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in prTNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain. PCR with primers Q29237,8 generated a 300bp
CC   restriction fragment which was cloned into prTNFR, giving pTNFRecd.
CC   DNA sequencing confirmed this contained the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   2062 BP;    429 A;    618 C;    572 G;    443 T;

  Query Match           44.1%;  Score 506;  DB 4;  Length 2062;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523
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Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    695 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 754
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    755 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 804
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    5
ID   Q10883 standard; cDNA; 2088 BP.
AC   Q10883;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
KW   Tumour necrosis factor; inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             171..1536
FT   /*tag=  a
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   P-PSDB; R10986.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also Q10878, Q10884 and Q10907.
SQ   Sequence   2088 BP;    439 A;    626 C;    578 G;    445 T;

  Query Match           44.1%;  Score 506;  DB 2;  Length 2088;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    289 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    349 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    409 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    469 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    529 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    589 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 648
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Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    649 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 708
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    709 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 768
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    769 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 818
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    6
ID   Q10955 standard; cDNA; 2111 BP.
AC   Q10955;
DT   24-MAY-1991  (first entry)
DE   Encodes human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   sig_peptide     187..273
FT   /*tag=  a
FT   mat_peptide     274..1551
FT   /*tag=  b
FT   /product= 55kD TNF-BP
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   P-PSDB; R11082.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 4; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   2111 BP;    445 A;    628 C;    588 G;    450 T;

  Query Match           44.1%;  Score 506;  DB 2;  Length 2111;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    307 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403
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Db    367 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 426
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    427 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    487 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    547 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    607 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 666
          |||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    667 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 726
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Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    727 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 786
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Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    787 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 836
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Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874
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RESULT    7
ID   Q90513 standard; DNA; 2175 BP.
AC   Q90513;
DT   19-JAN-1996  (first entry)
DE   p55 TNF-R gene.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT   /*tag= a
FT   /product= p55 TNF-R
FT   misc_signal     2143..2149
FT   /*tag= b
FT   /note= "possible poly-A signal"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
DR   WPI; 95-194342/26.
DR   P-PSDB; R75084.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment.  The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type.  The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain.  This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain.  The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11.  This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.  The
CC   mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3.  These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence   2175 BP;    474 A;    642 C;    603 G;    456 T;
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  Query Match           44.1%;  Score 506;  DB 15;  Length 2175;
  Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
  Matches   521;  Conservative    0;  Mismatches   9;  Indels   1;  Gaps   1;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
          |||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 855
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    856 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 905
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874
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RESULT    8
ID   Q06285 standard; DNA; 2141 BP.
AC   Q06285;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   lambdaTNF-R2; raTNF-R8; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             213..1577
FT   /*tag= a
FT   /label=huTNF-R
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
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DR   WPI; 90-321987/43.
DR   P-PSDB; R07451.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).
CC   See also Q06282-Q06285.
SQ   Sequence   2141 BP;    455 A;    633 C;    593 G;    460 T;

  Query Match           43.9%;  Score 504;  DB 1;  Length 2141;
  Best Local Similarity  97.9%;  Pred. No. 0.00e+00;
  Matches   520;  Conservative    0;  Mismatches  10;  Indels   1;  Gaps   1;

Db    333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
          |||||||||||||||||| |||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    753 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattcag 812
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    813 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 862
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT    9
ID   Q12215 standard; DNA; 2176 BP.
AC   Q12215;
DT   12-SEP-1991  (first entry)
DE   Type I TNF receptor.
KW   Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   terminator      244..246
FT   /*tag=  a
FT   /note= "in-frame termination codon"
FT   CDS             256..1620
FT   /*tag=  a
FT   /product= type I TNF receptor
FT   sig_peptide     256..318
FT   /*tag=  b
FT   mat_peptide     319..1620
FT   /*tag=  c
FT   misc_RNA        319..864
FT   /*tag=  d
FT   /label= soluble_domain
FT   /note= "may be 2 codons shorter or a few codons
FT   longer"
FT   misc_feature    376..414
FT   /*tag=  e
FT   /note= "TBP-I derived sequence"
FT   misc_feature    583..627
FT   /*tag=  f
FT   /note= "TBP-I derived sequence"
FT   misc_feature    850..858
FT   /*tag=  g
FT   /note= "TBP-I derived sequence"
FT   misc_RNA        889..957
FT   /*tag=  h
FT   /label= transmembrane_domain
FT   repeat_unit     385..504
FT   /*tag=  i
FT   /number= 1
FT   repeat_unit     505..633
FT   /*tag=  j
FT   /number= 2
FT   repeat_unit     634..756
FT   /*tag=  k
FT   /number= 3
FT   repeat_unit     757..858
FT   /*tag=  l
FT   /number= 4
FT   polyA_signal    2145..2150
FT   /*tag=  m
PN   EP-433900-A.
PD   26-JUN-1991.
PF   13-DEC-1990; 124133.
PR   13-DEC-1989; IL-092697.
PR   12-JUL-1990; IL-095064.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI   Aderka D;
DR   WPI; 91-186774/26.
DR   P-PSDB; R12550.
PT   Recombinant tumour necrosis factor binding protein I - prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PT   acid encoding human type T TNF receptor or soluble domain
PS   Disclosure; Fig 1(D); 30pp; English.
CC   The Tumour Necrosis Factor Binding Protein I is the soluble form of
CC   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA.  The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also Q12212-15.
SQ   Sequence   2176 BP;    475 A;    644 C;    602 G;    455 T;

  Query Match           43.9%;  Score 504;  DB 2;  Length 2176;
  Best Local Similarity  97.9%;  Pred. No. 0.00e+00;
  Matches   520;  Conservative    0;  Mismatches  10;  Indels   1;  Gaps   1;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgcagtacc 435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 855
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    856 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 905
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT   10
ID   T15931 standard; DNA; 6889 BP.
AC   T15931;
DT   20-JUN-1996  (first entry)
DE   DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.
KW   Recombinant host cell; dihydrofolate reductase; selectable marker;
KW   DHFR; ras splice donor; dicistronic vector; gene expression;
KW   immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
OS   Synthetic.
PN   WO9604391-A1.
PD   15-FEB-1996.
PF   28-JUL-1995; U09576.
PR   05-AUG-1994; US-286740.
PA   (GETH ) GENENTECH INC.
PI   Crowley CW;
DR   WPI; 96-129407/13.
PT   Improved process for the selection of recombinant host cells
PT   expressing high level of a desired product - uses eukaryotic host
PT   cells contg. a DNA construct comprising a selectable gene
PS   Example 2; Page 36-42; 137pp; English.
CC   A dicistronic vector (T15930) comprises a regulatory region
CC   derived from the cytomegalovirus immediate-early gene, a
CC   selectable dihydrofolate reductase gene positioned within an
CC   intron having a 5' wild-type ras splice donor site, a downstream
CC   sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
CC   tumour necrosis factor, and a poly-A sequence.  Transfection of CHO
CC   DHFR- cells and subsequent methotrexate amplification and growth of
CC   the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC   ug/ml (15-fold higher compared to conventional vector amplified
CC   pools).
SQ   Sequence   6889 BP;    1729 A;    1826 C;    1681 G;    1653 T;

  Query Match           43.9%;  Score 504;  DB 18;  Length 6889;
  Best Local Similarity  99.0%;  Pred. No. 0.00e+00;
  Matches   509;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db   1725 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 1784
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db   1785 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 1844
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db   1845 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 1904
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db   1905 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 1964
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   1965 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 2024
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db   2025 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 2084
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db   2085 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 2144
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db   2145 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 2204
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db   2205 aatgttaagggcactgaggactcaggcaccacag 2238
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 857


RESULT   11
ID   Q50870 standard; DNA; 2170 BP.
AC   Q50870;
DT   13-MAY-1994  (first entry)
DE   p55 Tumour necrosis factor receptor coding sequence.
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT   /*tag= a
FT   /product= p55 Tumour necrosis factor receptor.
PN   EP-568925-A.
PD   10-NOV-1993.
PF   29-APR-1993; 106981.
PR   03-MAY-1992; IL-101769.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Brakebusch C,  Wallach D;
DR   WPI; 93-353057/45.
DR   P-PSDB; R42197.
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
PS   Claim 2; Figure 1; 17pp; English.
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor.  This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock.  They can also
CC   be used to treat overdoses of exogenous TNF.
SQ   Sequence   2170 BP;    474 A;    657 C;    584 G;    455 T;

  Query Match           43.8%;  Score 502;  DB 9;  Length 2170;
  Best Local Similarity  97.7%;  Pred. No. 0.00e+00;
  Matches   519;  Conservative    0;  Mismatches  11;  Indels   1;  Gaps   1;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523
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Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgcgaccgtgcacctctcctgccaggag 735
          |||||||||||||||||| |||||||||||||| |||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    796 tcctgtagtaactgtaagaaaagcctgcagtgcacgaagttgtgcctaccccagattgag 855
          |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db    856 aatgttaagggcactgaggactcaggcaccacagt-gctgttgcccctggt 905
          |||||||||||||||||||||||||||||||||  | || |||||| |||
Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCCAGGT 874


RESULT   12
ID   Q24441 standard; DNA; 608 BP.
AC   Q24441;
DT   05-NOV-1992  (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (197 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24080.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
CC   derivative, as present in pTNFRecd. This was produced as described in
CC   Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC   the cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   608 BP;    148 A;    159 C;    165 G;    136 T;

  Query Match           40.8%;  Score 468;  DB 4;  Length 608;
  Best Local Similarity  98.8%;  Pred. No. 0.00e+00;
  Matches   474;  Conservative    0;  Mismatches   6;  Indels   0;  Gaps   0;

Db    129 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    189 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 248
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463

Db    249 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    309 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    369 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    429 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 488
          |||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    489 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 548
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763

Db    549 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagatttag 608
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823


RESULT   13
ID   Q24445 standard; DNA; 504 BP.
AC   Q24445;
DT   05-NOV-1992  (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (165 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24084.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 11; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
CC   derivative, as present in pdeltaIV. This construct was generated by
CC   cloning of the BglII/HindIII digested product of a PCR using
CC   primers 5A and 4D into BglII/HindIII 5'-deltaCla. This introduced
CC   a termination codon after amino acid 167, to yield pdeltaIV.
CC   This derivative lacks the membrane proximal 4th subdomain, yet
CC   retains the ability to bind TNF-alpha with high affinity
CC   (10power8 - 10power9 Mpower-1) The deriv. can be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis. The deriv. is given at 10-100ug/dose.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   504 BP;    122 A;    137 C;    138 G;    107 T;

  Query Match           32.7%;  Score 375;  DB 4;  Length 504;
  Best Local Similarity  99.0%;  Pred. No. 1.89e-267;
  Matches   379;  Conservative    0;  Mismatches   4;  Indels   0;  Gaps   0;

Db    121 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGAC 463
```

```
Db    241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db    301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
          |||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Qy    644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAG 703

Db    481 aaacagaacaccgtgtgcacctg 503
          ||||||||||||| ||||||||
Qy    704 AAACAGAACACCGTCTGCACCTG 726
```

RESULT 14
ID Q24442 standard; DNA; 474 BP.
AC Q24442;
DT 05-NOV-1992 (first entry)
DE Encodes truncated TNF-alpha 55kD receptor (155 amino acids).
KW tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningitis; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
PN WO9207076-A.
PD 30-APR-1992.
PF 18-OCT-1991; G01826.
PR 18-OCT-1990; GB-022648.
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR WPI; 92-167156/20.
DR P-PSDB; R24081.
PT New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
PS Example; Fig 8; 43pp; English.
CC This sequence encodes the designed TNF-alpha 55kD receptor
CC derivative, as present in pdeltaI. This construct was generated by
CC joining PCR fragments by means of overlaps introduced into the
CC primers used for PCR. Gel purified products of PCR's using
CC 5'Cla, IA, IB, and 5D primers were mixed and subjected to further
CC amplification using 5'Cla and 5D as primers. The resulting fragment
CC was digested with ClaI and BglII and cloned into ClaI/BglII
CC digested pTNFRecd, to yield pdeltaI, containing the sequence given.
CC This derivative could be used to regulate TNF-alpha mediated responses
CC by binding and sequestering human TNF-alpha e.g. in the treatment of
CC pulmonary diseases, septic shock, HIV infection, malaria, viral
CC meningitis, graft versus host disease and autoimmune diseases, esp.
CC rheumatoid arthritis.
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ Sequence 474 BP; 110 A; 126 C; 132 G; 106 T;

Query Match 30.1%; Score 345; DB 4; Length 474;
Best Local Similarity 98.3%; Pred. No. 1.16e-243;
Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Db    118 agagagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctcagc 177
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    467 AGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGC 526

Db    178 tgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggaccgg 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    527 TGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGG 586

Db    238 gacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctttttc 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    587 GACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTC 646

Db    298 cagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggagaaa 357
          |||||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||
Qy    647 CAGTGCTTCAATTGCACCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGTCAGGAGAAA 706

Db    358 cagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtctcc 417
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    707 CAGAACACCGTCTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCC 766

Db    418 tgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagatttag 474
          |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Qy    767 TGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823
```

RESULT 15
ID T76770 standard; cDNA; 2771 BP.
AC T76770;
DT 15-SEP-1997 (first entry)
DE Rat Fabpl gut-specific promoter and human growth hormone exon 1.
KW Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
KW GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase;
KW alpha 1,2 FT; alpha 1,3/4 FT; tissue-specific promoter;
KW rat liver fatty acid binding protein; transgene; transgenic mouse;
KW animal model; intestinal adhesion; Helicobacter pylori infection;
KW stomach; small intestine; gut; epithelial cell; surface receptor;
KW carbohydrate antigen; gastritis; peptic ulcer; neoplasia;
KW gastric adenocarcinoma; Lewis antigen; fucosylation; ds.
OS Chimeric - Homo sapiens.
OS Chimeric - Rattus sp.
FH Key Location/Qualifiers
FT promoter 1..617
FT /*tag= a
FT /note= "Corresponds to nucleotides -596 to +21 of
FT the rat liver fatty acid binding protein
FT gene"
FT exon 620..2771
FT /*tag= b
FT /number= 1
FT /note= "Corresponds to nucleotides +3 to +2150 of
FT the human growth hormone (hGH) gene; it is
FT desirable for cDNA coding for a human
FT fucosyltransferase to be inserted into
FT exon 1 of the hGH gene"
PN US5625124-A.
PD 29-APR-1997.
PF 11-JUL-1994; 273411.
PR 11-JUL-1994; US-273411.
PA (UNIW) UNIV WASHINGTON.
PI Falk P, Gordon JI;
DR WPI; 97-258275/23.
PT Animal model for Helicobacter pylori infection - comprising
PT transgenic mouse expressing human enzyme promoting intestinal
PT adhesion
PS Example 2; Columns 25-28; 24pp; English.
CC A claimed transgenic mouse expresses, in its intestinal epithelial
CC cells, the enzyme human GDP-L-fucose:beta-D-galactoside 2-alpha-L-
CC fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose:
CC beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also
CC called alpha 1,3/4 FT). The enzyme is expressed under the
CC control of a gut epithelial cell-specific promoter and Helicobacter
CC pylori adheres to the transgenic cells. The transgenic mouse and
CC intestinal epithelial cells from it are useful as models for screening
CC compounds for the ability to inhibit adhesion of H. pylori to gut
CC epithelial cells. The first 617 nucleotides of the present chimeric
CC sequence encode the promoter from rat liver fatty acid binding protein
CC (Fabpl) which can direct foreign gene expression to the pit cell
CC lineage of the mouse gastric epithelium, to proliferating and non-
CC proliferating cells in intestinal crypts, as well as to the four
CC principal differentiated cell lineages along the crypt-to-villus axis
CC of the small intestine. The remainder of the chimeric sequence
CC corresponds to exon 1 of the human growth hormone (hGH) gene, into
CC which a sequence coding for a human fucosyltransferase (hFT) can be

```
CC   inserted. No hGH will be produced because the initiator Met codon
CC   and the first translation stop codon will be from the hFT sequence
CC   and there is no ribosome re-entry sequence. The hGH exon 1 ensures
CC   efficient splicing of the transgene primary transcript, improves
CC   stability of the cytoplasmic hFT mRNA and allows transgene
CC   expression to be monitored by in situ hybridisation using a
CC   digoxigenin-labelled hGH oligonucleotide.
SQ   Sequence   2771 BP;    666 A;    718 C;    704 G;    683 T;

  Query Match           25.1%;  Score 288;  DB 31;  Length 2771;
  Best Local Similarity  95.6%;  Pred. No. 1.27e-198;
  Matches   323;  Conservative    0;  Mismatches  11;  Indels   4;  Gaps   3;

Db    680 atggctacaggtaagcgcccctaaaatccctttgggcacaatgtgtcctgaggggagagg 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db    740 cagcgacctgtagatgggacgggggcactaaccctcaggtttggggcttctgaatg--ag 797
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||  ||
Qy     66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTTTGAATGTGAG 125

Db    798 tatcgccatgtaagcccagtatg-gcc-aatctcagaaagctcctggtccctggagggat 855
          ||| ||||||||||||||||||  ||| ||||||||||||||||||||||||||||||||
Qy    126 TATGGCCATGTAAGCCCAGTATTTGCCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 185

Db    856 ggagagagaaaaacaaacagctcctggagcagggagagtgctggcctcttgctctccggc 915
          |||||||||||||||||||||||||||||||| | | ||||||||||||||| ||||
Qy    186 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGACACTCCTGGCCTCTTGCTCTGCGGC 245

Db    916 tccctctgttgccctctggtttctccccaggctcccggacgtccctgctcctggcttttg 975
          ||| | ||||||||| ||||||||||||| ||||||||||||||||||||||||||||||
Qy    246 TCCGTGTGTTGCCCTGTGGTTTCTCCCCACGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 305

Db    976 gcctgctctgcctgccctggcttcaagagggcagtgcc 1013
          |||||||||||||||||||||||||||||||||||||
Qy    306 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343


Search completed: Wed May  6 14:21:41 1998
Job time : 155 secs.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:00:59 1998; MasPar time 1055.78 Seconds
1320.756 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-5
Description: (1-1147) from US08804166.seq
Perfect Score: 1147
N.A. Sequence: 1 TCGAGATGGCTACAGGTAAG.....AATCTTAAGGATCCCTCGAG 1147
Comp: AGCTCTACCGATGTCCATTC.....TTAGAATTCCTAGGGAGCTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est8 8:em_gss 9:em_est13
Database: genbank-est
10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13
25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.165; Variance 1.901; scale 5.873

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	262	22.8	373	23	HUM505B08B	Human placenta cDNA 5'	0.00e+00
2	262	22.8	379	23	C18240	Human placenta cDNA 5'	0.00e+00
3	262	22.8	392	11	R76249	yi72b05.r1 Homo sapien	0.00e+00
4	261	22.8	423	12	H00861	yj31h01.r1 Homo sapien	0.00e+00
5	262	22.8	464	23	C17209	Human placenta cDNA 5'	0.00e+00
6	262	22.8	467	11	R71429	yi51d03.r1 Homo sapien	0.00e+00
7	260	22.7	433	11	R23843	yh48c04.r1 Homo sapien	0.00e+00
8	260	22.7	452	12	H00781	yj30d01.r1 Homo sapien	0.00e+00
9	258	22.5	478	23	C17142	Human placenta cDNA 5'	0.00e+00
10	255	22.2	330	23	C18403	Human placenta cDNA 5'	0.00e+00
11	254	22.1	458	11	R77385	yi75d11.r1 Homo sapien	0.00e+00
12	250	21.8	482	12	H03289	yj44h10.r1 Homo sapien	0.00e+00
13	249	21.7	336	23	HUM530G10B	Human placenta cDNA 5'	0.00e+00
c 14	238	20.7	519	31	AA779136	zj46h11.s1 Soares feta	0.00e+00
15	236	20.6	423	23	C17966	Human placenta cDNA 5'	0.00e+00
16	232	20.2	519	23	C18044	Human placenta cDNA 5'	0.00e+00
17	230	20.1	386	17	W86567	zh63h08.r1 Soares feta	0.00e+00
18	231	20.1	403	11	R65664	yi16a09.r1 Homo sapien	0.00e+00
19	231	20.1	471	12	H47149	yp73d07.r1 Homo sapien	0.00e+00
20	229	20.0	430	12	H00795	yj30f02.r1 Homo sapien	0.00e+00
21	228	19.9	439	12	H01069	yj26c09.r1 Homo sapien	0.00e+00
22	223	19.4	513	23	AA441787	zw62b09.s1 Soares tota	0.00e+00
23	221	19.3	336	11	R79875	yi85a07.r1 Homo sapien	0.00e+00
24	221	19.3	468	11	R23095	yh31g05.r1 Homo sapien	0.00e+00
25	220	19.2	365	23	HUM505C02B	Human placenta cDNA 5'	0.00e+00
26	220	19.2	526	16	H94810	yu21c05.r1 Soares feta	0.00e+00
c 27	219	19.1	527	31	AA777267	zi96b03.s1 Soares feta	0.00e+00
28	218	19.0	294	10	T48916	yb07c06.r1 Homo sapien	0.00e+00
29	218	19.0	360	14	HSC32B021	H. sapiens partial cDN	0.00e+00
30	217	18.9	429	13	H77743	yu23f09.r1 Homo sapien	0.00e+00
31	216	18.8	348	11	R33236	yh84d10.r1 Homo sapien	0.00e+00
c 32	216	18.8	478	31	AA778170	zf45c10.s1 Soares feta	0.00e+00
33	212	18.5	420	10	T49525	ya76f03.r1 Homo sapien	0.00e+00
34	207	18.0	291	23	HUM511F08B	Human placenta cDNA 5'	0.00e+00
c 35	207	18.0	465	29	AA704477	zj19d06.s1 Soares feta	0.00e+00
36	205	17.9	365	11	R23453	yh39b02.r1 Homo sapien	0.00e+00
37	205	17.9	393	11	R33285	yh81d04.r1 Homo sapien	0.00e+00
38	205	17.9	438	14	N57230	yw65f07.r1 Homo sapien	0.00e+00
39	204	17.8	261	23	HUM525D05B	Human placenta cDNA 5'	0.00e+00
40	201	17.5	465	14	W01919	za35c04.r1 Soares feta	0.00e+00
c 41	198	17.3	450	12	H04324	yj20g12.s1 Homo sapien	0.00e+00
c 42	198	17.3	450	29	AA677403	zj62g07.s1 Soares feta	0.00e+00
43	198	17.3	479	11	R68866	yi37d02.r1 Homo sapien	0.00e+00
44	197	17.2	347	11	R34458	yh85b04.r1 Homo sapien	0.00e+00
45	193	16.8	344	11	R27121	yh52h07.r1 Homo sapien	0.00e+00

ALIGNMENTS

RESULT 1
LOCUS HUM505B08B 373 bp mRNA EST 21-MAY-1996

DEFINITION Human placenta cDNA 5'-end GEN-505B08.
ACCESSION D58574
NID g968208
KEYWORDS EST; EST(expressed sequence tag); Human placenta; similar to known(May 29,1995).
SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human placenta polyA+ mRNA (#6518).
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 373)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
TITLE Unpublished(004)
JOURNAL Unpublished (1995)
REFERENCE 2 (bases 1 to 373)
AUTHORS Fujiwara,T.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035)
COMMENT Submitted (30-May-1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888

```
          Fax  : 0886-37-1035.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Clontech human placenta polyA+ mRNA (#6518)"
BASE COUNT       94 a     88 c     84 g    107 t
ORIGIN

  Query Match           22.8%;  Score 262;  DB 23;  Length 373;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   262;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      47 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db     107 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     167 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     227 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db     287 TTGTTATTATCACAAATCTTAA 308
           |||||||||||||||||||||
Qy    1114 TTGTTATTATCACAAATCTTAA 1135


RESULT    2
LOCUS       C18240        379 bp    mRNA            EST       09-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-559D08.
ACCESSION   C18240
NID         g1579842
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:559D08.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 379)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
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                     /clone="559D08"
                     /tissue_type="placenta"
BASE COUNT       94 a     95 c     85 g    104 t      1 others
ORIGIN

  Query Match           22.8%;  Score 262;  DB 23;  Length 379;
  Best Local Similarity  99.6%;  Pred. No. 0.00e+00;
  Matches   261;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      67 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db     127 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTARGGTCCAAGAAGAC 186
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     187 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     247 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db     307 TTGTTATTATCACAAATCTTAA 328
           |||||||||||||||||||||
Qy    1114 TTGTTATTATCACAAATCTTAA 1135


RESULT    3
LOCUS       R76249        392 bp    mRNA            EST       06-JUN-1995

DEFINITION  yi72b05.r1 Homo sapiens cDNA clone 144753 3' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R76249
NID         g850931
KEYWORDS    EST.
SOURCE      human clone=144753 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=Promega -21m13 Rsite1=Not I Rsite2=Eco RI Female
            placenta obtained at birth (full term). 1st strand cDNA was primed
            with a Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 328
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .392
                     /organism="Homo sapiens"
                     /clone="144753"
BASE COUNT      100 a     90 c     89 g    112 t      1 others
ORIGIN

  Query Match           22.8%;  Score 262;  DB 11;  Length 392;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
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  Matches   262;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      35 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 94
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db      95 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     155 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 214
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     215 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 274
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db     275 TTGTTATTATCACAAATCTTAA 296
           |||||||||||||||||||||
Qy    1114 TTGTTATTATCACAAATCTTAA 1135


RESULT    4
LOCUS       H00861        423 bp    mRNA            EST       19-JUN-1995

DEFINITION  yj31h01.r1 Homo sapiens cDNA clone 150385 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00861
NID         g863794
KEYWORDS    EST.
SOURCE      human clone=150385 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 344
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .423
                      /organism="Homo sapiens"
                      /clone="150385"
BASE COUNT      109 a     95 c     95 g    119 t      5 others
ORIGIN

  Query Match           22.8%;  Score 261;  DB 12;  Length 423;
  Best Local Similarity  99.6%;  Pred. No. 0.00e+00;
  Matches   261;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      18 TTGCCCAGAATGCACGCTACAGGANAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 77
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db      78 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     138 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     198 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db     258 TTGTTATTATCACAAATCTTAA 279
           |||||||||||||||||||||
Qy    1114 TTGTTATTATCACAAATCTTAA 1135


RESULT    5
LOCUS       C17209        464 bp    mRNA            EST       04-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-541F08.
ACCESSION   C17209
NID         g1571916
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:541F08.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 464)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES              Location/Qualifiers
     source           1. .464
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="541F08"
                      /tissue_type="placenta"
BASE COUNT      114 a    117 c     95 g    138 t
ORIGIN

  Query Match           22.8%;  Score 262;  DB 23;  Length 464;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   262;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      39 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 98
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db      99 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     159 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 218
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db    219 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 278
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db    279 TTGTTATTATCACAAATCTTAA 300
          ||||||||||||||||||||||
Qy   1114 TTGTTATTATCACAAATCTTAA 1135


RESULT    6
LOCUS       R71429        467 bp    mRNA            EST       01-JUN-1995

DEFINITION  yi51d03.r1 Homo sapiens cDNA clone 142757 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R71429
NID         g844946
KEYWORDS    EST.
SOURCE      human clone=142757 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 386
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .467
                     /organism="Homo sapiens"
                     /clone="142757"
BASE COUNT      113 a    114 c     98 g    139 t      3 others
ORIGIN

  Query Match           22.8%;  Score 262;  DB 11;  Length 467;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   262;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     50 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db    110 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db    170 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db    230 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db    290 TTGTTATTATCACAAATCTTAA 311
          ||||||||||||||||||||||
Qy   1114 TTGTTATTATCACAAATCTTAA 1135


RESULT    7
LOCUS       R23843        433 bp    mRNA            EST       20-APR-1995

DEFINITION  yh48c04.r1 Homo sapiens cDNA clone 132966 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R23843
NID         g778731
KEYWORDS    EST.
SOURCE      human clone=132966 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 334
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Homo sapiens"
                     /clone="132966"
BASE COUNT      111 a    104 c     90 g    127 t      1 others
ORIGIN

  Query Match           22.7%;  Score 260;  DB 11;  Length 433;
  Best Local Similarity 98.9%;  Pred. No. 0.00e+00;
  Matches   263;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db      2 CAGGATTGCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAA 61
          |||| |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    870 CAGGTTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAA 929

Db     62 TACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    930 TACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 989
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Db    122 AGACGATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCAT 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    990 AGACGATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCAT 1049

Db    182 ATAACAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCA 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1050 ATAACAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCA 1109

Db    242 GTACTTGTTATTATCACAAATCTTAA 267
          |||||||||||||||||||||||||
Qy   1110 GTACTTGTTATTATCACAAATCTTAA 1135


RESULT    8
LOCUS       H00781        452 bp    mRNA            EST       19-JUN-1995

DEFINITION  yj30d01.r1 Homo sapiens cDNA clone 150241 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00781
NID         g863714
KEYWORDS    EST.
SOURCE      human clone=150241 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 322
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .452
                      /organism="Homo sapiens"
                      /clone="150241"
BASE COUNT      107 a    104 c    103 g    133 t      5 others
ORIGIN

  Query Match           22.7%;  Score 260;  DB 12;  Length 452;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   260;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     44 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db    104 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db    164 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db    224 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db    284 TTGTTATTATCACAAATCTT 303
          ||||||||||||||||||||
Qy   1114 TTGTTATTATCACAAATCTT 1133


RESULT    9
LOCUS       C17142        478 bp    mRNA            EST       04-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-539G04.
ACCESSION   C17142
NID         g1571849
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:539G04.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 478)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES              Location/Qualifiers
     source           1. .478
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="539G04"
                      /tissue_type="placenta"
BASE COUNT      125 a    113 c     96 g    144 t
ORIGIN

  Query Match           22.5%;  Score 258;  DB 23;  Length 478;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   258;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 CCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    878 CCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAG 937

Db     61 TGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    938 TGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATG 997

Db    121 TTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    998 TTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGG 1057

Db    181 GTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1058 GTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGT 1117

Db    241 TATTATCACAAATCTTAA 258
          ||||||||||||||||||
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Qy   1118 TATTATCACAAATCTTAA 1135


RESULT   10
LOCUS       C18403        330 bp    mRNA            EST       09-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-561H02.
ACCESSION   C18403
NID         g1580005
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:561H02.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 330)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="561H02"
                     /tissue_type="placenta"
BASE COUNT       82 a     87 c     73 g     88 t
ORIGIN

  Query Match           22.2%;  Score 255;  DB 23;  Length 330;
  Best Local Similarity  99.6%;  Pred. No. 0.00e+00;
  Matches   261;  Conservative    0;  Mismatches   0;  Indels   1;  Gaps   1;

Db      67 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db     127 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     187 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     247 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGA-CCACACGGCGTGCCACTGCAGTAC 305
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db     306 TTGTTATTATCACAAATCTTAA 327
           |||||||||||||||||||||
Qy    1114 TTGTTATTATCACAAATCTTAA 1135


RESULT   11
LOCUS       R77385        458 bp    mRNA            EST       06-JUN-1995

DEFINITION  yi75d11.r1 Homo sapiens cDNA clone 145077 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R77385
NID         g852017
KEYWORDS    EST.
SOURCE      human clone=145077 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 458)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 393
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .458
                     /organism="Homo sapiens"
                     /clone="145077"
BASE COUNT      119 a    109 c     97 g    133 t
ORIGIN

  Query Match           22.1%;  Score 254;  DB 11;  Length 458;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   254;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      16 AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAGTGCA 75
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     882 AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACTTCAGTGCA 941

Db      76 TGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATGTTGG 135
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     942 TGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATGTTGG 1001

Db     136 TCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCA 195
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1002 TCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCA 1061

Db     196 CAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTTATT 255
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1062 CAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTTATT 1121

Db     256 ATCACAAATCTTAA 269
           ||||||||||||||
Qy    1122 ATCACAAATCTTAA 1135


RESULT   12
LOCUS       H03289        482 bp    mRNA            EST       20-JUN-1995

DEFINITION  yj44h10.r1 Homo sapiens cDNA clone 151651 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H03289
NID         g866222
KEYWORDS    EST.
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SOURCE      human clone=151651 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.  .
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 482)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 301
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .482
                      /organism="Homo sapiens"
                      /clone="151651"
BASE COUNT      111 a    106 c    118 g    142 t      5 others
ORIGIN

  Query Match           21.8%;  Score 250;  DB 12;  Length 482;
  Best Local Similarity  99.2%;  Pred. No. 0.00e+00;
  Matches   262;  Conservative    0;  Mismatches   0;  Indels   2;  Gaps   2;

Db      51 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db     111 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     171 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     231 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGGAGAACCACACGGGCGTGCCACTGCAGT 290
           |||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGG-AGAACCACACGG-CGTGCCACTGCAGT 1111

Db     291 ACTTGTTATTATCACAAATCTTAA 314
           |||||||||||||||||||||||||
Qy    1112 ACTTGTTATTATCACAAATCTTAA 1135


RESULT   13
LOCUS       HUM530G10B     336 bp    mRNA            EST       13-DEC-1995

DEFINITION  Human placenta cDNA 5'-end GEN-530G10.
ACCESSION   D79076
NID         g1180949
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone_lib:human placenta
            polyA+.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
  TITLE     Large-scale sequencing project at Otsuka GEN Research Institute
  JOURNAL   Unpublished (1995)
REFERENCE   2  (bases 1 to 336)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan
COMMENT     Submitted (7-Nov-1995) to DDBJ by:
            Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical CO.,Ltd
            463-10 Kagasuno Kawauchi-cho
            Tokushima, Tokushima
            771-01
            Japan
            Phone:0886-65-2888
            Fax  :0886-37-1035.
FEATURES              Location/Qualifiers
     source           1. .336
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="human placenta polyA+"
                      /tissue_type="placenta"
BASE COUNT       76 a     89 c     78 g     93 t
ORIGIN

  Query Match           21.7%;  Score 249;  DB 23;  Length 336;
  Best Local Similarity  98.8%;  Pred. No. 0.00e+00;
  Matches   252;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db      47 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db     107 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     167 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     227 CAGGGTCACAGTAATGGGGGGTTTCATAGTGGGGACCCACACGGCGTGCCACTGCAGTAC 286
           |||||||||||||||||||||||||| ||||| || ||||||||||||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db     287 TTGTTATTATCACAA 301
           |||||||||||||||
Qy    1114 TTGTTATTATCACAA 1128


RESULT   14
LOCUS       AA779136       519 bp    mRNA            EST       05-FEB-1998

DEFINITION  zj46h11.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA
            clone 453381 3' similar to gb:V00518 GLYCOPROTEIN HORMONES ALPHA
            CHAIN PRECURSOR (HUMAN);.
ACCESSION   AA779136
NID         g2838467
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KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 519)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 316.
FEATURES             Location/Qualifiers
     source          1. .519
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                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.  1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
                     /db_xref="GDB:1389737"
                     /db_xref="taxon:9606"
                     /clone="453381"
                     /clone_lib="Soares fetal liver spleen 1NFLS S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
BASE COUNT      156 a     98 c    127 g    138 t
ORIGIN

  Query Match          20.7%;  Score 238;  DB 31;  Length 519;
  Best Local Similarity  96.6%;  Pred. No. 0.00e+00;
  Matches   257;  Conservative    0;  Mismatches   7;  Indels   2;  Gaps   2;

Db     253 TTAAGATTTGTGATAATAACAAGTACTGCAGTGGCACGCCGTGTGGTTCTCCACTTTGAA 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1135 TTAAGATTTGTGATAATAACAAGTACTGCAGTGGCACGCCGTGTGGTTCTCCACTTTGAA 1076

Db     313 ACCCCCCATTACTGTGACCCTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1075 ACCCCCCATTACTGTGACCCTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 1016

Db     373 GACGTTCTTTTGGACCAACATCGTCTTCTTGGACCTTAGTGGAGTGGGATATGCTCTAGA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1015 GACGTTCTTTTGGACCAACATCGTCTTCTTGGACCTTAGTGGAGTGGGATATGCTCTAGA 956

Db     433 GAAGCAGCAGCCCATGCACTGAAGTAGTGGGGCACCGGGCTCGTAGAAGAATGGGGTTTC 492
           |||||||||||||||||||||||| |||||||| |||| | |||||||||||| ||||
Cp     955 GAAGCAGCAGCCCATGCACTGAAGTATTGGGGCACCCGGCTGGGAGAAGAATGGGTTTTC 896

Db     493 CTG-AGCGTG-ATTCTGGGGAATCTG 516
           ||| |||||| |||||||| || |||
Cp     895 CTGTAGCGTGCATTCTGGGCAACCTG 870

RESULT  15

LOCUS       C17966        423 bp    mRNA            EST       09-SEP-1996

DEFINITION  Human placenta cDNA 5'-end GEN-555E01.
ACCESSION   C17966
NID         g1579568
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:555E01.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 423)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1. .423
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="555E01"
                     /tissue_type="placenta"
BASE COUNT      113 a    117 c     90 g    103 t
ORIGIN

  Query Match          20.6%;  Score 236;  DB 23;  Length 423;
  Best Local Similarity  98.0%;  Pred. No. 0.00e+00;
  Matches   251;  Conservative    0;  Mismatches   3;  Indels   2;  Gaps   2;

Db     169 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     874 TTGCCCAGAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT 933

Db     229 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     934 TCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Db     289 GATGTTGGTCCAAAAGACCGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 348
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Qy     994 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 1053

Db     349 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGA-CCACACGGCGTGCCACTGCAGTAC 407
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Qy    1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTAC 1113

Db     408 TTTTTTTTTATCACAA 423
           || || || |||||||
Qy    1114 TTGTTATT-ATCACAA 1128


Search completed: Wed May  6 14:18:45 1998
Job time : 1066 secs.
```

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:01:34 1998; MasPar time 9.14 Seconds
466.133 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6
Description: (1-285) from US08804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 31.870; Variance 121.907; scale 0.261

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	2183	100.0	285	26	W33359	TBP(20-190)/hCG-alpha	2.81e-227
2	1667	76.4	256	26	W33357	TBP(20-161)/hCG-alpha	1.50e-169
3	1505	68.9	336	26	W33360	TBP(20-190)/hCG-beta	1.76e-151
4	1306	59.8	371	2	R07449	Tumour Necrosis Facto	2.45e-129
5	1305	59.8	451	13	R70107	TNF-R-GBP 130 fusion	3.16e-129
6	1306	59.8	455	4	R24000	TNF-alpha 55kD recept	2.45e-129
7	1306	59.8	455	14	R75084	p55 TNF-R.	2.45e-129
8	1306	59.8	455	4	R20787	TNF-alpha binding pro	2.45e-129
9	1306	59.8	455	8	R42059	Lambda derived TNF-R.	2.45e-129
10	1306	59.8	455	2	R10986	30kD TNF inhibitor pr	2.45e-129
11	1306	59.8	455	2	R11082	Human 55kD TNF-bindin	2.45e-129
12	1305	59.8	900	13	R70103	TNF-R-GBP 130 fusion	3.16e-129
13	1303	59.7	309	13	R70108	TNF-R-GBPH fusion pro	5.28e-129
14	1303	59.7	455	2	R07451	Human Tumour Necrosis	5.28e-129
15	1303	59.7	547	13	R70104	TNF-R-GBPH fusion pro	5.28e-129
16	1303	59.7	1604	13	R70105	TNF-R-EBA 175 fusion	5.28e-129
17	1301	59.6	1245	13	R70106	TNF-R-Pl. vivax Duffy	8.81e-129
18	1297	59.4	433	8	R51032	Mutant p55 tumour nec	2.45e-128
19	1297	59.4	443	8	R51033	Mutant p55 tumour nec	2.45e-128
20	1297	59.4	455	8	R42197	p55 Tumour necrosis f	2.45e-128
21	1297	59.4	455	8	R51034	Mutant p55 tumour nec	2.45e-128
22	1292	59.2	455	3	R12550	Type I TNF receptor.	8.80e-128
23	1289	59.0	307	26	W33358	TBP(20-161)/hCG-beta	1.90e-127
24	1247	57.1	161	5	R27496	Native 30 kD TNF inhi	8.73e-123
25	1247	57.1	884	13	R70109	TNF-R-GBP 130 fusion	8.73e-123
26	1236	56.6	199	4	R24080	Truncated TNF-alpha 5	1.45e-121
27	994	45.5	168	4	R24084	Truncated TNF-alpha 5	8.84e-95
28	912	41.8	158	4	R24081	Truncated TNF-alpha 5	9.63e-86
29	907	41.5	461	2	R07450	Rat Tumour Necrosis F	3.42e-85
30	715	32.8	234	15	R86254	Single chain gonadotr	3.80e-64
31	705	32.3	234	15	R86266	Partially deglycosyla	4.68e-63
32	705	32.3	234	15	R86276	Single chain gonadotr	4.68e-63
33	699	32.0	234	15	R86248	Single chain gonadotr	2.11e-62
34	697	31.9	234	15	R86249	Single chain gonadotr	3.49e-62
35	696	31.9	234	15	R86253	Single chain gonadotr	4.48e-62
36	694	31.8	226	15	R86255	Single chain gonadotr	7.40e-62
37	693	31.7	222	15	R86256	Single chain gonadotr	9.51e-62
38	693	31.7	222	15	R86268	Partially deglycosyla	9.51e-62
39	689	31.6	234	15	R86270	Single chain gonadotr	2.60e-61
40	689	31.6	234	15	R86260	Partially deglycosyla	2.60e-61
41	689	31.6	237	15	R86252	Single chain gonadotr	2.60e-61
42	687	31.5	229	15	R86250	Single chain gonadotr	4.29e-61
43	687	31.5	234	15	R86271	Single chain gonadotr	4.29e-61
44	687	31.5	234	15	R86261	Partially deglycosyla	4.29e-61
45	686	31.4	234	15	R86275	Single chain gonadotr	5.51e-61

ALIGNMENTS

RESULT 1
ID W33359 standard; Protein; 285 AA.
AC W33359;
DT 19-MAR-1998 (first entry)
DE TBP(20-190)/hCG-alpha fusion protein.
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW alpha subunit; hCG-alpha.
OS Homo sapiens.
PN WO9730161-A1.
PD 21-AUG-1997.
PF 20-FEB-1997; U02315.
PR 20-FEB-1996; US-011936.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PI Campbell RK, Chappel SC, Jameson BA;
DR WPI; 97-425036/39.
DR N-PSDB; T94021.
PT Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation
PS Example; Pages 37-38; 60pp; English.
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein hormone capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC (hCG-alpha) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed.
SQ Sequence 285 AA;

Query Match 100.0%; Score 2183; DB 26; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.81e-227;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db     121 nlfqcfnctlclngtvhlscqekqntvctchagfflrenecvscsnckkslectklslpq 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     121 NLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ 180

Db     181 ienvkgtedsgttagaapgcpectlqenpffsqpgapilqcmgccfsrayptplrskktm 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     181 IENVKGTEDSGTTAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTM 240

Db     241 lvqknvtsestccvaksynrvtvmggfkvenhtachcstcyyhks 285
           |||||||||||||||||||||||||||||||||||||||||||||
Qy     241 LVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    2
ID   W33357 standard; Protein; 256 AA.
AC   W33357;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94007.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 32-33; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   256 AA;

  Query Match           76.4%;  Score 1667;  DB 26;  Length 256;
  Best Local Similarity  89.1%;  Pred. No. 1.50e-169;
  Matches   254;  Conservative    2;  Mismatches   0;  Indels  29;  Gaps   1;

Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvsc---------------- 164
          ||||||||:|||||||||||||||||||||||||||||||||
Qy    121 NLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ 180

Db    165 ----------agaapgcpectlqenpffsqpgapilqcmgccfsrayptplrskktm 211
                     ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 IENVKGTEDSGTTAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTM 240

Db    212 lvqknvtsestccvaksynrvtvmggfkvenhtgchcstcyyhks 256
          |||||||||||||||||||||||||||||||:||||||||||
Qy    241 LVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    3
ID   W33360 standard; Protein; 336 AA.
AC   W33360;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94022.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 39-40; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   336 AA;

  Query Match           68.9%;  Score 1505;  DB 26;  Length 336;
  Best Local Similarity  98.0%;  Pred. No. 1.76e-151;
  Matches   196;  Conservative    2;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db    121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscsnckkslectklclpq 180
          ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    121 NLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ 180

Db    181 ienvkgtedsgttagagprc 200
          ||||||||||||||||:| |
Qy    181 IENVKGTEDSGTTAGAAPGC 200


RESULT    4
ID   R07449 standard; protein; 371 AA.
AC   R07449;
DT   29-JAN-1991  (first entry)
DE   Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06282.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
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PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of
CC   e.g. COS7 cells.  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   371 AA;

  Query Match           59.8%;  Score 1306;  DB 2;  Length 371;
  Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           |||||||||||||||||||||||||||||| ||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    5
ID   R70107 standard; Protein; 451 AA.
AC   R70107;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 53-54; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence   451 AA;

  Query Match           59.8%;  Score 1305;  DB 13;  Length 451;
  Best Local Similarity  98.3%;  Pred. No. 3.16e-129;
  Matches   169;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtna 191
           |||||||||||||||||||||||||||||| |||||||||||||| |
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTTA 194


RESULT    6
ID   R24000 standard; Protein; 455 AA.
AC   R24000;
DT   05-NOV-1992  (first entry)
DE   TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /label= signal peptide
FT   modified_site   54..56
FT                   /label= N linked glycosylation site
FT                   /note= "potential"
FT   modified_site   145..147
FT                   /label= N linked glycosylation site
FT                   /note= "potential "
FT   modified_site   151..153
FT                   /label= N linked glycosylation site
FT                   /note= "potential"
FT   domain          212..234
FT                   /label= transmembrane domain
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   N-PSDB; Q24440.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 1; 43pp; English.
CC   This sequence was deduced from human TNF-alpha cDNA isolated as in
CC   Q24440. The first 35 amino acids are generally quite hydrophobic
CC   and probably represent a signal sequence. Residues 35-40  are highly
CC   charged (DREKR) and this is not normally found in secretory
CC   signal sequences. It is possible the receptor is processed by
CC   proteolysis after residue 40 which contains a dibasic cleavage site
CC   (KR). Hydropathy analysis of this sequence predicts a single
CC   transmembrane domain of 23 amino acids, dividing the sequence into
CC   an extracellular domain of 171 residues and a cytoplasmic domain of
CC   221 residues. The sequence contains a large number of cysteine
CC   residues, the arrangement of which is similar to that of other cell
CC   surface proteins, suggesting the TNF-alpha receptor is structurally
CC   related to a family of receptors.
CC   NOTE:- Residues 371,2 given in the sequence as T,L, are encoded by
CC   TGG (W) and AAG (K).
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   455 AA;

  Query Match           59.8%;  Score 1306;  DB 4;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;
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Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
          ||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    7
ID    R75084 standard; Protein; 455 AA.
AC    R75084;
DT    19-JAN-1996  (first entry)
DE    p55 TNF-R.
KW    p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW    epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW    phorbol myristate acetate; PMA.
OS    Homo sapiens.
FH    Key             Location/Qualifiers
FT    peptide         41..53
FT                    /note= "N terminus of soluble p55 TNF-R"
FT    modified_site   54..56
FT                    /note= "glycosylation site"
FT    modified_site   145..147
FT                    /note= "glycosylation site"
FT    modified_site   161..163
FT                    /note= "glycosylation site"
FT    peptide         193..210
FT                    /note= "peptide used in creation of chimeras"
FT    region          198..210
FT                    /note= "spacer region"
FT    misc_difference 201
FT                    /note= "major C terminus for soluble p55 TNF-R"
FT    misc_difference 202
FT                    /note= "essential for shedding reaction"
FT    misc_difference 203
FT                    /note= "minor C terminus for soluble p55 TNF-R"
FT    region          212..234
FT                    /note= "transmembrane region"
PN    AU9475742-A.
PD    04-MAY-1995.
PF    11-OCT-1994; 075742.
PR    12-OCT-1993; IL-107268.
PA    (YEDA ) YEDA RES & DEV CO LTD.
PI    Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
DR    WPI; 95-194342/26.
DR    N-PSDB; Q90513.
PT    New protease capable of cleaving soluble tumour necrosis factor
PT    (TNF) receptor  - from cell-bound TNF- receptor, useful for
PT    antagonising deleterious effects of TNF.
PS    Disclosure; Fig 1; 40pp; English.
CC    This sequence represents human p55 tumour necrosis factor (TNF-R).
CC    Expression of this receptor is regulated by shedding of the extracellular
CC    receptor fragment.  The p55 TNF-R can be shed in response to different
CC    inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC    type.  The only region of the receptor whose structure affects the
CC    shedding response is the spacer region (see R75012) in the extracellular
CC    domain.  This region is located close to a site of cleavage of the
CC    molecule, and links the Cys rich module to the transmembrane domain.  The
CC    spacer region of the encoded protein was used to create the chimeras
CC    between human p55 TNF-R and murine epidermal growth factor receptor
CC    (EGF-R) that are represented by R75007-11.  This spacer region was
CC    subjected to deletion mutations (R75013-25) and substitutions
CC    (R75026-47).  Of the spacer region, the most important residues are
CC    Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC    important of these.  The shedding of the receptor is independent of the
CC    side chain identity of these residues, with the exception of a limited
CC    dependence on the identity of Val 173.  Mutations which alter the
CC    conformation of the protein adversely effect the shedding process.
CC    The mutations shown in R75013-47 were introduced in order to create an
CC    inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC    from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC    R75017-9, R75025, R75033-5 and R75042-3.  These protease inhibitors can
CC    be used for enhancing TNF function.
SQ    Sequence   455 AA;

  Query Match           59.8%;  Score 1306;  DB 14;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
          ||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    8
ID    R20787 standard; Protein; 455 AA.
AC    R20787;
DT    11-MAY-1992  (first entry)
DE    TNF-alpha binding protein.
KW    Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW    extracellular domain.
OS    Homo sapiens.
FH    Key             Location/Qualifiers
FT    peptide         1..40
FT                    /note= "signal peptide"
FT    peptide         41..455
FT                    /note= "mature peptide"
FT    domain          30..199
FT                    /note= "extracellular domain"
FT    domain          212..234
FT                    /note= "transmembrane domain"
FT    modified_site   145..147
FT                    /note= "potential N-glycosylation site"
FT    modified_site   151..153
FT                    /note= "potential N-glycosylation site"
PN    GB2246569-A.
PD    05-FEB-1992.
PF    15-JUN-1990; 013410.
PR    15-JUN-1990; GB-013410.
PA    (CHAR-) CHARING CROSS SUNLE.
PI    Feldman M, Gray P, Turner M, Brennan F;
DR    WPI; 92-043613/06.
DR    N-PSDB; Q20973.
PT    New tumour necrosis factor alpha binding protein and polypeptide
PT    - useful in treating cachexia, sepsis and auto immune diseases
PT    e.g. rheumatoid arthritis
PS    Disclosure; Fig 1; 25pp; English.
CC    The amino acid sequence is that of tumour necrosis factor alpha
CC    binding protein which contains the extracellular domain of human TNF
CC    alpha receptor. It is soluble and can be used in the regulation of
CC    TNF-mediated responses by binding and sequestering the cytokine. It
CC    can therefore be used therapeutically to treat disorders such as
CC    cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC    arthritis.
SQ    Sequence   455 AA;

  Query Match           59.8%;  Score 1306;  DB 4;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           |||||||||||||||||||||||||||||||| ||||||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    9
ID   R42059 standard; Protein; 455 AA.
AC   R42059;
DT   29-APR-1994  (first entry)
DE   Lambda derived TNF-R.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction.
OS   Homo sapiens.
OS   Lambda-gt10-7ctnfbp.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "Signal peptide"
FT   protein         41..455
FT                   /note= "Mature hTNF-R"
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   N-PSDB; Q49932.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.
CC   The sequences given in R42058-59 repressent human tumour necrosis
CC   factor receptor (TNF-R) and the sequences in R42060-61 represent
CC   human interleukin-1 receptor (IL-1R).  These sequences were used in
CC   the production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence   455 AA;

  Query Match           59.8%;  Score 1306;  DB 8;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           |||||||||||||||||||||||||||||||| ||||||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT   10
ID   R10986 standard; Protein; 455 AA.
AC   R10986;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor.
KW   Tumour necrosis factor; inhibitor.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cleavage_site   40..41
FT                   note=" cleavage gives active protein "
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   N-PSDB; Q10883.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC   from which the sequence was deduced was isolated from a cDNA
CC   library prepd. from RNA form U937 cells treated with PMA/PHA.
CC   The whole gene can be inserted into expression vectors for prepn.
CC   of TNF inhibitor for use in the treatment of inflammatory and
CC   degenerative diseases.  The active protein is claimed (Claim 8).
CC   See also R10984 and R11001.
SQ   Sequence   455 AA;

  Query Match           59.8%;  Score 1306;  DB 2;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           |||||||||||||||||||||||||||||||| ||||||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT   11
ID   R11082 standard; Protein; 455 AA.
AC   R11082;
DT   24-MAY-1991  (first entry)
DE   Human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   modified_site   54
FT                   /label= putative N-glycosylation site
FT   modified_site   145
FT                   /label= putative N-glycosylation site
FT   modified_site   151
FT                   /label= putative N-glycosylation site
FT   modified_site   270
FT                   /label= putative N-glycosylation site
FT   region          212..230
FT                   /label= transmembrane region
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FT   peptide          1..28
FT                    /label= signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   455 AA;

  Query Match           59.8%;  Score 1306;  DB 2;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           ||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT   12
ID   R70103 standard; Protein; 900 AA.
AC   R70103;
DT   02-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 46-47; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70103 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence   900 AA;

  Query Match           59.8%;  Score 1305;  DB 13;  Length 900;
  Best Local Similarity  98.3%;  Pred. No. 3.16e-129;
  Matches   169;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtna 191
           ||||||||||||||||||||||||||||||| |||||||||||||||| |
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTTA 194


RESULT   13
ID   R70108 standard; Protein; 309 AA.
AC   R70108;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
FH   Key              Location/Qualifiers
FT   misc_difference  230..269
FT                    /label= repeat_region
FT                    /note= "can be repeated n times, where n is a real
FT                    number"
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 54-55; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The
CC   use of cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
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CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   309 AA;

  Query Match           59.7%;  Score 1303;  DB 13;  Length 309;
  Best Local Similarity  98.2%;  Pred. No. 5.28e-129;
  Matches   168;  Conservative    2;  Mismatches   1;  Indels   0;  Gaps   0;

Db      20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db      80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts 190
           ||||||||||||||||||||||||||||||||| ||||||||||||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT   14
ID   R07451 standard; protein; 455 AA.
AC   R07451;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06285.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282). The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha). They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   455 AA;

  Query Match           59.7%;  Score 1303;  DB 2;  Length 455;
  Best Local Similarity  98.2%;  Pred. No. 5.28e-129;
  Matches   168;  Conservative    2;  Mismatches   1;  Indels   0;  Gaps   0;

Db      41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 kqntvctchagfflrenecvscsnckkslectklclpqiqnvkgtedsgtt 211
           ||||||||||||||||||||||||||||||| ||||:||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT   15
ID   R70104 standard; Protein; 547 AA.
AC   R70104;
DT   02-NOV-1995  (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 47-48; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70104 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The use of
CC   cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   547 AA;

  Query Match           59.7%;  Score 1303;  DB 13;  Length 547;
  Best Local Similarity  98.2%;  Pred. No. 5.28e-129;
  Matches   168;  Conservative    2;  Mismatches   1;  Indels   0;  Gaps   0;

Db      20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db      80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts 190
           ||||||||||||||||||||||||||||||||| ||||||||||||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


Search completed: Wed May  6 09:03:11 1998
Job time : 97 secs.
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****

MPSRCH (TM)

****

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:00:43 1998; MasPar time 12.89 Seconds
807.727 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6
Description: (1-285) from US08804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 40.957; Variance 71.278; scale 0.575

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1306	59.8	455	1	GQHUT1	tumor necrosis factor	1.60e-278
2	1241	56.8	160	5	1EXTA	tumor necrosis factor	8.41e-263
3	1222	56.0	158	5	1EXTB	tumor necrosis factor	3.27e-258
4	1119	51.3	142	5	1NCFB	tumor necrosis factor	2.28e-233
5	1103	50.5	139	5	1TNRR	tumor necrosis factor	1.62e-229
6	1096	50.2	140	5	1NCFA	tumor necrosis factor	7.85e-228
7	1012	46.4	461	2	JC4302	tumor necrosis factor	1.20e-207
8	944	43.2	454	2	I57826	tumor necrosis factor	2.33e-191
9	944	43.2	454	1	GQMST1	tumor necrosis factor	2.33e-191
10	928	42.5	461	1	GQRTT1	tumor necrosis factor	1.56e-187
11	672	30.8	116	1	TTHUAP	glycoprotein hormones	8.42e-127
12	650	29.8	86	5	1HRPA	chorionic gonadotropi	1.23e-121
13	648	29.7	85	5	1XULA	chorionic gonadotropi	3.63e-121
14	648	29.7	85	5	1HCNA	Human chorionic gonad	3.63e-121
15	552	25.3	120	2	A39555	glycoprotein hormones	8.95e-99
16	547	25.1	96	2	A05096	glycoprotein hormones	1.29e-97
17	549	25.1	120	1	TTBOA	glycoprotein hormones	4.44e-98
18	549	25.1	120	1	UTSHA	glycoprotein hormones	4.44e-98
19	544	24.9	120	1	TTRTA	glycoprotein hormones	6.39e-97
20	542	24.8	96	2	PN0138	glycoprotein hormones	1.86e-96
21	542	24.8	120	1	UTPGA	glycoprotein hormones	1.86e-96
22	542	24.8	120	1	TTMSA	glycoprotein hormones	1.86e-96
23	540	24.7	120	2	G00021	chorionic gonadotropi	5.39e-96
24	537	24.6	120	2	A45585	glycoprotein hormones	2.67e-95
25	537	24.6	120	2	I51241	pituitary glycoprotei	2.67e-95
26	507	23.2	118	2	A40554	glycoprotein hormones	2.25e-88
27	505	23.1	120	2	S53062	glycoprotein hormones	6.50e-88
28	503	23.0	96	1	TTHOA	glycoprotein hormones	1.88e-87
29	500	22.9	118	2	S16762	gonadotropin alpha ch	9.19e-87
30	500	22.9	118	1	UTCAA	glycoprotein hormones	9.19e-87
31	500	22.9	118	2	A60626	glycoprotein hormones	9.19e-87
32	478	21.9	93	2	S07091	glycoprotein hormones	1.03e-81
33	479	21.9	97	2	S20287	lutropin alpha chain	6.10e-82
34	474	21.7	117	2	A37198	glycoprotein hormones	8.53e-81
35	452	20.7	119	2	I51229	gonadotropin alpha 1	9.07e-76
36	450	20.6	114	2	B60627	glycoprotein hormones	2.59e-75
37	448	20.5	108	2	A60627	glycoprotein hormones	7.40e-75
38	448	20.5	114	2	I51230	gonadotropin alpha 2	7.40e-75
39	434	19.9	117	2	I50992	gonadotropin alpha-su	1.13e-71
40	245	11.2	435	2	I54182	tumor necrosis factor	4.53e-30
41	228	10.4	38	2	A60583	glycoprotein hormones	1.59e-26
42	225	10.3	325	2	B43692	T2 protein - rabbit f	6.62e-26
43	221	10.1	326	1	GQVZML	T2 protein - myxoma v	4.42e-25
44	214	9.8	349	2	D36858	gene G4R protein - va	1.20e-23
45	212	9.7	427	1	GQHUN	nerve growth factor r	3.08e-23

ALIGNMENTS

RESULT 1
ENTRY GQHUT1 #type complete

TITLE tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAM
CONTAINS tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-Oct-1997
ACCESSIONS A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE A38208
#authors Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
#journal Genomics (1992) 13:219-224
#title Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to chromosome 12p13.
#accession A38208
##molecule_type DNA
##residues 1-455 ##label FUC
##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748; PID:g339750
REFERENCE A34899
#authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.
#journal Cell (1990) 61:351-359
#title Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.
#cross-references MUID:90235284
#accession A34899
##molecule_type mRNA
##residues 1-455 ##label LOE
##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
##experimental_source placenta
##note part of this sequence, including the amino end of the mature protein, confirmed by protein sequencing
REFERENCE A34900
#authors Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab, H.; Kohr, W.J.; Goeddel, D.V.
#journal Cell (1990) 61:361-370
#title Molecular cloning and expression of a receptor for human tumor necrosis factor.
#cross-references MUID:90235285
#accession A34900
##molecule_type mRNA
##residues 1-455 ##label SCH
##cross-references GB:M33294; NID:g339744; PID:g339745

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REFERENCE       A36555
  #authors      Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                  Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                  Stratowa, C.; Adolf, G.R.
  #journal      DNA Cell Biol. (1990) 9:705-715
  #title        Molecular cloning and expression of human and rat tumor
                  necrosis factor receptor chain (p60) and its soluble
                  derivative, tumor necrosis factor-binding protein.
  #cross-references MUID:91090841
  #accession    A36555
    ##molecule_type mRNA
    ##residues      1-455 ##label HIM
    ##cross-references GB:M63121; NID:g339755; PID:g339756
  #accession    C36555
    ##molecule_type protein
    ##residues      30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
                     107-128;162-167,'X',169-201 ##label HI2
    ##note          the purified protein, called tumor necrosis factor
                     binding protein, is a soluble derivative of the
                     receptor
REFERENCE       A38281
  #authors      Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
                  M.
  #journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
  #title        Cloning of human tumor necrosis factor (TNF) receptor cDNA
                  and expression of recombinant soluble TNF-binding protein.
  #cross-references MUID:91017509
  #accession    A38281
    ##molecule_type mRNA
    ##residues      1-455 ##label GRA
    ##cross-references GB:M37764
    ##note          the authors translated the codon TGG for residue 371 as
                     Thr, AAG for residue 372 as Leu, and GAC for residue
                     427 as Asn
REFERENCE       S12057
  #authors      Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
                  R.; Aderka, D.; Holtmann, H.; Wallach, D.
  #journal      EMBO J. (1990) 9:3269-3278
  #title        Soluble forms of tumor necrosis factor receptors (TNF-Rs).
                  The cDNA for the type I TNF-R, cloned using amino acid
                  sequence data of its soluble form, encodes both the cell
                  surface and a soluble form of the receptor.
  #cross-references MUID:91006021
  #accession    S12057
    ##molecule_type mRNA
    ##residues      1-455 ##label NOP
    ##cross-references EMBL:X55313; NID:g37223; PID:g37224
    ##note          parts of soluble TNF binding protein 1, including its
                     amino and carboxyl ends, were confirmed by protein
                     sequencing
REFERENCE       JT0758
  #authors      Kemper, O.; Wallach, D.
  #journal      Gene (1993) 134:209-216
  #title        Cloning and partial characterization of the promoter for the
                  human p55 tumor necrosis factor (TNF) receptor.
  #accession    JT0758
    ##molecule_type DNA
    ##residues      1-13 ##label KEM
REFERENCE       A60231
  #authors      Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
                  J.M.
  #journal      Eur. J. Immunol. (1990) 20:1167-1174
  #title        Tumor necrosis factor inhibitor: purification, NH-2-terminal
                  amino acid sequence and evidence for anti-inflammatory and
                  immunomodulatory activities.
  #cross-references MUID:90292116
  #accession    A60231
    ##molecule_type protein
    ##residues      41-43,'X',45-53,'X',55-57 ##label SEC
REFERENCE       A38258
  #authors      Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
                  J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
                  R.S.; Granger, G.A.
  #journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
  #title        Purification and characterization of an inhibitor (soluble
                  tumor necrosis factor receptor) for tumor necrosis factor
                  and lymphotoxin obtained from the serum ultrafiltrates of
                  human cancer patients.
  #cross-references MUID:91062364
  #accession    A38258
    ##molecule_type protein
    ##residues      41-60 ##label GAT
    ##experimental_source cancer patient serum
REFERENCE       A60594
  #authors      Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
                  Grubb, A.; Adolf, G.
  #journal      Eur. J. Haematol. (1989) 42:270-275
  #title        Isolation and characterization of a tumor necrosis factor
                  binding protein from urine.
  #accession    A60594
    ##molecule_type protein
    ##residues      41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
    ##experimental_source renal failure patient urine
REFERENCE       A35010
  #authors      Engelmann, H.; Novick, D.; Wallach, D.
  #journal      J. Biol. Chem. (1990) 265:1531-1536
  #title        Two tumor necrosis factor-binding proteins purified from
                  human urine. Evidence for immunological cross-reactivity
                  with cell surface tumor necrosis factor receptors.
  #cross-references MUID:90110215
  #accession    A35010
    ##molecule_type protein
    ##residues      41-45 ##label ENG
    ##experimental_source normal urine
REFERENCE       JC2404
  #authors      Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
  #journal      Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
  #title        Amino acid sequence of natural tumor necrosis factor alpha
                  inhibitor purified from human urine.
  #accession    JC2404
    ##molecule_type protein
    ##residues      41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
                     ##label KAJ
    ##experimental_source urine
COMMENT     This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
GENETICS
  #gene         GDB:TNFR1
    ##cross-references GDB:125913; OMIM:191190
  #map_position 12p13.2-12p13.2
  #introns      13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                  receptor repeat homology
KEYWORDS        duplication; glycoprotein; receptor; transmembrane protein
FEATURE
  1-21              #domain signal sequence #status predicted #label SIG\
  22-455            #product tumor necrosis factor receptor type 1 #status
                      predicted #label MAT\
  30-211            #domain extracellular #status predicted #label EXT\
  41-201            #product TNF binding protein 1 (tumor necrosis factor
                      alpha inhibitor) #status experimental #label TBP1\
  44-82             #domain NGF receptor repeat homology #label NG1\
  84-126            #domain NGF receptor repeat homology #label NG2\
  127-167           #domain NGF receptor repeat homology #label NG3\
  168-196           #domain NGF receptor repeat homology #label NG4\
  212-234           #domain transmembrane #status predicted #label MEM\
  235-455           #domain intracellular #status predicted #label INT\
  54,145,151        #binding_site carbohydrate (Asn) (covalent) #status
                      predicted
SUMMARY         #length 455  #molecular-weight 50494  #checksum 153

  Query Match            59.8%;  Score 1306;  DB 1;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 1.60e-278;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
          |||||||||||||||||||||||||||||| ||||||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    2
ENTRY             1EXTA      #type complete

TITLE             tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE         extracellular domain of the 55kda tumor necrosis factor
                    receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, the construct contains
                    residues 12 to 172 of the mature sequence of the entire
                    receptor. residue 11 is mutated to met as a result of the
                    expression system
REFERENCE         A65560
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, July 1996
   #cross-references PDB:1EXT
REFERENCE         TN026248
   #authors       Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
   #journal       J. Biol. Chem. (1995) 270:13303
   #title         Crystallographic evidence for dimerization of unliganded
                    tumor necrosis factor receptor.
REFERENCE         TN026249
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 1.85 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   66-68               #region helix (right hand 3-10)\
   141-143             #region helix (right hand 3-10)\
   151-154             #region helix (right hand alpha)\
   7-9,17-19           #region beta sheet\
   131-134,137-140     #region beta sheet\
   25-29,39-42         #region beta sheet\
   71-74,83-85         #region beta sheet\
   90-96,99-104        #region beta sheet\
   111-115,124-127     #region beta sheet\
   3-17                #disulfide_bonds\
   18-31               #disulfide_bonds\
   21-40               #disulfide_bonds\
   43-58               #disulfide_bonds\
   61-76               #disulfide_bonds\
   64-84               #disulfide_bonds\
   86-102              #disulfide_bonds\
   105-117             #disulfide_bonds\
   108-125             #disulfide_bonds\
   127-138             #disulfide_bonds\
   141-154             #disulfide_bonds\
   144-150             #disulfide_bonds
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  Best Local Similarity  98.8%;  Pred. No. 8.41e-263;
  Matches   158;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      24 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 83

Db      61 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 120
          ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Qy      84 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEK 143

Db     121 QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN 160
          |||||||||||||||||||||||||||||| ||||||
Qy     144 QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIEN 183


RESULT    3
ENTRY             1EXTB      #type complete

TITLE             tumor necrosis factor receptor extracellular domain, chain B
PDB_TITLE         extracellular domain of the 55kda tumor necrosis factor
                    receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, the construct contains
                    residues 12 to 172 of the mature sequence of the entire
                    receptor. residue 11 is mutated to met as a result of the
                    expression system
REFERENCE         A65560
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, July 1996
   #cross-references PDB:1EXT
REFERENCE         TN026251
   #authors       Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
   #journal       J. Biol. Chem. (1995) 270:13303
   #title         Crystallographic evidence for dimerization of unliganded
                    tumor necrosis factor receptor.
REFERENCE         TN026252
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 1.85 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   68-70               #region helix (right hand 3-10)\
   143-145             #region helix (right hand 3-10)\
   9-11,19-21          #region beta sheet\
   133-136,139-142     #region beta sheet\
   27-31,41-44         #region beta sheet\
   73-76,85-87         #region beta sheet\
   92-98,101-106       #region beta sheet\
   113-117,126-129     #region beta sheet\
   5-19                #disulfide_bonds\
   20-33               #disulfide_bonds\
   23-42               #disulfide_bonds\
   45-60               #disulfide_bonds\
   63-78               #disulfide_bonds\
   66-86               #disulfide_bonds\
   88-104              #disulfide_bonds\
   107-119             #disulfide_bonds\
   110-127             #disulfide_bonds\
   129-140             #disulfide_bonds\
```

```
   143-156            #disulfide_bonds\
   146-152            #disulfide_bonds
SUMMARY           #length 158  #molecular-weight 17827  #checksum 5022

  Query Match           56.0%;  Score 1222;  DB 5;  Length 158;
  Best Local Similarity  98.7%;  Pred. No. 3.27e-258;
  Matches   155;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 158
          |||||||||||||||||||||||||||||| ||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLP 179


RESULT    4
ENTRY             1NCFB      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain B - hu
ALTERNATE_NAMES   stnfr1; type i receptor
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029041
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   2-16                #disulfide_bonds\
   17-30               #disulfide_bonds\
   20-39               #disulfide_bonds\
   42-57               #disulfide_bonds\
   60-75               #disulfide_bonds\
   63-83               #disulfide_bonds\
   85-101              #disulfide_bonds\
   104-116             #disulfide_bonds\
   107-124             #disulfide_bonds\
   126-137             #disulfide_bonds
SUMMARY           #length 142  #molecular-weight 16046  #checksum 1225

  Query Match           51.3%;  Score 1119;  DB 5;  Length 142;
  Best Local Similarity  99.3%;  Pred. No. 2.28e-233;
  Matches   141;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db     61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQ 144

Db    121 NTVCTCHAGFFLRENECVSCSN 142
          ||||||||||||||||||||||
Qy    145 NTVCTCHAGFFLRENECVSCSN 166


RESULT    5
ENTRY             1TNRR      #type complete

TITLE             tumor necrosis factor receptor type 1 (P55 extracellular
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          recombinant form expressed in Baculovirus SF9
REFERENCE         A52442
   #authors       Banner, D.W.
   #submission    submitted to the Brookhaven Protein Data Bank, May 1994
   #cross-references PDB:1TNR
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
REFERENCE         TN034093
   #authors       D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
                    Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
                    Lesslauer, W.
   #journal       J. Mol. Biol. (1993) 229:555
   #title         Crystallization and preliminary analysis of tnf-beta and a
                    tnf-beta-55 kd tnf receptor complex.
COMMENT     Resolution: 2.85 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS          Complex(lymphokineRECEPTOR)
FEATURE
   1-15                #disulfide_bonds\
   16-29               #disulfide_bonds\
   19-38               #disulfide_bonds\
   41-56               #disulfide_bonds\
   59-74               #disulfide_bonds\
   62-82               #disulfide_bonds\
   84-100              #disulfide_bonds\
   103-115             #disulfide_bonds\
   106-123             #disulfide_bonds\
   125-136             #disulfide_bonds
SUMMARY           #length 139  #molecular-weight 15746  #checksum 5235

  Query Match           50.5%;  Score 1103;  DB 5;  Length 139;
  Best Local Similarity  99.3%;  Pred. No. 1.62e-229;
  Matches   138;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db     61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 120
          ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Qy     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQN 145

Db    121 TVCTCHAGFFLRENECVSC 139
          |||||||||||||||||||
Qy    146 TVCTCHAGFFLRENECVSC 164


RESULT    6
ENTRY             1NCFA      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain A - hu
ALTERNATE_NAMES   stnfr1; type i receptor
```

```
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029039
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   5-19                #disulfide_bonds\
   20-33               #disulfide_bonds\
   23-42               #disulfide_bonds\
   45-60               #disulfide_bonds\
   63-78               #disulfide_bonds\
   66-86               #disulfide_bonds\
   88-104              #disulfide_bonds\
   107-119             #disulfide_bonds\
   110-127             #disulfide_bonds\
   129-140             #disulfide_bonds
SUMMARY           #length 140  #molecular-weight 15889  #checksum 6622

  Query Match           50.2%;  Score 1096;  DB 5;  Length 140;
  Best Local Similarity  99.3%;  Pred. No. 7.85e-228;
  Matches   138;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
          ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENEC 140
          |||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENEC 161


RESULT    7
ENTRY             JC4302     #type complete

TITLE             tumor necrosis factor receptor p55 - pigORGANISM         #formal_name S
DATE              29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                    12-Dec-1997
ACCESSIONS        JC4302; PC4093
REFERENCE         JC4302
   #authors       Suter, B.; Pauli, U.
   #journal       Gene (1995) 163:263-266
   #title         Cloning of the cDNA encoding the porcine p55 tumor necrosis
                    factor receptor.
   #accession     JC4302
      ##molecule_type mRNA
      ##residues       1-461 ##label SUT
      ##cross-references GB:U19994; NID:g1141752; PID:g1141753
   #accession     PC4093
      ##molecule_type protein
      ##residues       1-7 ##label SU2
      ##experimental_source kidney cell line 15
GENETICS
   #gene          tnfr
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
   1-29               #domain signal sequence #status predicted #label SIG\
   30-461             #product tumor necrosis factor receptor p55 #status
                        predicted #label MAT\
   44-194             #domain extracellular cysteine rich #status predicted
                        #label EXT\
   44-82              #domain NGF receptor repeat homology #label NG1\
   211-231            #domain transmembrane #status predicted #label TMM\
   361-447            #domain signal transduction #status predicted #label
                        SIT\
   54,145,151         #binding_site carbohydrate (Asn) (covalent) #status
                        predicted
SUMMARY           #length 461  #molecular-weight 50696  #checksum 8079

  Query Match           46.4%;  Score 1012;  DB 2;  Length 461;
  Best Local Similarity  71.9%;  Pred. No. 1.20e-207;
  Matches   123;  Conservative   25;  Mismatches  22;  Indels   1;  Gaps   1;

Db     41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|:|||||| |||| |||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |||||| ||:|||||:|||||||||||||||| |||| ||||:||:|| ||||:|:| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPATSETRNDFQDTGTT 210
          ||:|:| ||:|||||::||||| |||:: :| :|  :  |  :  :|:|||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    8
ENTRY             I57826     #type complete

TITLE             tumor necrosis factor receptor - mouseORGANISM         #formal_name
DATE              02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                    23-May-1997
ACCESSIONS        I57826
REFERENCE         I57826
   #authors       Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
                    Steinmetz, M.
   #journal       Mol. Immunol. (1993) 30:165-176
   #title         Genomic organization and promoter function of the murine
                    tumor necrosis factor receptor beta gene.
   #cross-references MUID:93156721
   #accession     I57826
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-454 ##label RES
      ##cross-references GB:M76656; NID:g202100; PID:g202102
GENETICS
   #gene          TNFR-2
   #introns       13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          cytokine receptor
SUMMARY           #length 454  #molecular-weight 50030  #checksum 4267

  Query Match           43.2%;  Score 944;  DB 2;  Length 454;
  Best Local Similarity  67.4%;  Pred. No. 2.33e-191;
  Matches   116;  Conservative   28;  Mismatches  27;  Indels   1;  Gaps   1;

Db     41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
```

```
          ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|: |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
          ||||| |||||||||:|||:||:|||: || || ||  : ||   :||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ-IENVKGTEDSGTT 193


RESULT    9
ENTRY             GQMST1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    05-Sep-1997
ACCESSIONS        A38634; B40254; S16677; S19021; I54532
REFERENCE         A38634
   #authors       Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
                    G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
   #title         Cloning and expression of cDNAs for two distinct murine tumor
                    necrosis factor receptors demonstrate one receptor is
                    species specific.
   #cross-references MUID:91187885
   #accession     A38634
      ##molecule_type mRNA
      ##residues       1-454 ##label LEW
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         A40254
   #authors       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
                    C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
   #journal       Mol. Cell. Biol. (1991) 11:3020-3026
   #title         Molecular cloning and expression of the type 1 and type 2
                    murine receptors for tumor necrosis factor.
   #cross-references MUID:91246168
   #accession     B40254
      ##molecule_type mRNA
      ##residues       1-454 ##label GO2
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         S16677
   #authors       Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis,
                    A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
   #journal       Eur. J. Immunol. (1991) 21:1649-1656
   #title         Cloning, expression and cross-linking analysis of the murine
                    p55 tumor necrosis factor receptor.
   #cross-references MUID:91285014
   #accession     S16677
      ##molecule_type mRNA
      ##residues       1-454 ##label BAR
      ##cross-references EMBL:X59238; NID:g53578; PID:g53579
REFERENCE         S19021
   #authors       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
   #journal       Immunogenetics (1991) 34:338-340
   #title         Molecular cloning and expression of the mouse Tnf receptor
                    type b.
   #cross-references MUID:92039815
   #accession     S19021
      ##molecule_type mRNA
      ##residues       1-454 ##label ROT
      ##cross-references EMBL:X57796; NID:g54848; PID:g54849
REFERENCE         I54532
   #authors       Bebo, B.F.
   #journal       Immunogenetics (1994) 39:450-451
   #title         Nucleotide sequence of the TNF type I receptor from a mouse
                    endothelioma cell line.
   #cross-references MUID:94245292
   #accession     I54532
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-454 ##label RES
      ##cross-references GB:L26349; NID:g430732; PID:g430733
COMMENT     This protein is one of two distantly related receptors for both
              TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                 #domain signal sequence #status predicted #label SIG\
   30-454               #product tumor necrosis factor receptor type 1 #status
                          predicted #label MAT\
   30-212               #domain extracellular #status predicted #label EXT\
   44-82                #domain NGF receptor repeat homology #label NG1\
   84-126               #domain NGF receptor repeat homology #label NG2\
   127-167              #domain NGF receptor repeat homology #label NG3\
   168-204              #domain NGF receptor repeat homology #label NG4\
   213-235              #domain transmembrane #status predicted #label MEM\
   236-454              #domain intracellular #status predicted #label INT\
   54,151,202           #binding_site carbohydrate (Asn) (covalent) #status
                          predicted
SUMMARY           #length 454  #molecular-weight 50129  #checksum 4839

  Query Match           43.2%;  Score 944;  DB 1;  Length 454;
  Best Local Similarity  67.4%;  Pred. No. 2.33e-191;
  Matches   116;  Conservative   28;  Mismatches  27;  Indels   1;  Gaps   1;

Db     41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:|||:| ||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  |||||:|||||:|  |:|||||: ||:::| ||  ||| :|: |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
          ||||| |||||||||:|||:||:|||: || || ||  : ||   :||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ-IENVKGTEDSGTT 193


RESULT   10
ENTRY             GQRTT1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
                    05-Sep-1997
ACCESSIONS        B36555
REFERENCE         A36555
   #authors       Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                    Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                    Stratowa, C.; Adolf, G.R.
   #journal       DNA Cell Biol. (1990) 9:705-715
   #title         Molecular cloning and expression of human and rat tumor
                    necrosis factor receptor chain (p60) and its soluble
                    derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
   #accession     B36555
      ##molecule_type mRNA
      ##residues       1-461 ##label HIM
      ##cross-references GB:M63122; NID:g207361; PID:g207362
COMMENT     This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                 #domain signal sequence #status predicted #label SIG\
   30-461               #product tumor necrosis factor receptor type 1 #status
                          predicted #label MAT\
   30-211               #domain extracellular #status predicted #label EXT\
   30-201               #product tumor necrosis factor binding protein #status
                          predicted #label TBP\
   44-82                #domain NGF receptor repeat homology #label NG1\
   84-126               #domain NGF receptor repeat homology #label NG2\
   127-167              #domain NGF receptor repeat homology #label NG3\
   168-204              #domain NGF receptor repeat homology #label NG4\
   212-234              #domain transmembrane #status predicted #label MEM\
```

```
   235-461          #domain intracellular #status predicted #label INT\
   54,151,201       #binding_site carbohydrate (Asn) (covalent) #status
                      predicted
SUMMARY          #length 461  #molecular-weight 50969  #checksum 1617

  Query Match           42.5%;  Score 928;  DB 1;  Length 461;
  Best Local Similarity  66.1%;  Pred. No. 1.56e-187;
  Matches   113;  Conservative   26;  Mismatches  32;  Indels   0;  Gaps   0;

Db      41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
           |::|||||| || ||||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  ||||| |||||:|  | ||||||:|||:::| ||  ||| :|: |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTA 211
           |||||| ||||||| ||| :||:|||: || || || : ||   :||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT   11
ENTRY            TTHUAP     #type complete

TITLE            glycoprotein hormones alpha chain precursor - humanALTERNATE_NAMES  cho
                   alpha chain; follitropin alpha chain; interstitial
                   cell-stimulating hormone alpha chain; luteinizing hormone
                   alpha chain; lutropin alpha chain; thyroid-stimulating
                   hormone alpha chain; thyrotropin alpha chain
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             13-Jul-1981 #sequence_revision 23-Oct-1981 #text_change
                   05-Sep-1997
ACCESSIONS       A93213; A92832; B92303; A90751; A90179; A91461; A92184;
                   A94552; B92181; A92141; I58200; A01481
REFERENCE        A93213
   #authors      Fiddes, J.C.; Goodman, H.M.
   #journal      Nature (1979) 281:351-356
   #title        Isolation, cloning and sequence analysis of the cDNA for the
                   alpha-subunit of human chorionic gonadotropin.
   #cross-references MUID:80011660
   #accession    A93213
      ##molecule_type mRNA
      ##residues      1-116 ##label FID
      ##cross-references GB:V00518; NID:g31868; PID:g31869
REFERENCE        A92832
   #authors      Fiddes, J.C.; Goodman, H.M.
   #journal      J. Mol. Appl. Genet. (1981) 1:3-18
   #title        The gene encoding the common alpha subunit of the four human
                   glycoprotein hormones.
   #cross-references MUID:82267643
   #accession    A92832
      ##molecule_type DNA
      ##residues      1-98 ##label FI2
      ##cross-references GB:V00484
REFERENCE        A92303
   #authors      Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
   #journal      J. Biol. Chem. (1981) 256:1816-1823
   #title        The amino acid sequences of the prepeptides contained in the
                   alpha and beta subunits of human choriogonadotropin.
   #cross-references MUID:81117268
   #accession    B92303
      ##molecule_type protein
      ##residues      1-24 ##label BIR
      ##note          restriction endonuclease evidence indicates that a
                       single gene codes for the alpha chain common to the
                       four dimeric hormones: thyrotropin, lutropin,
                       follitropin, and choriogonadotropin
      ##note          previously the mature alpha chain (residues 25-116) was
                       isolated from each of the hormones and its sequence
                       was determined, as documented below
REFERENCE        A90751
   #authors      Sairam, M.R.; Li, C.H.
   #journal      Can. J. Biochem. (1977) 55:755-760
   #title        Human pituitary thyrotropin. The primary structure of the
                   alpha and beta subunits.
   #cross-references MUID:77243687
   #accession    A90751
      ##molecule_type protein
      ##residues      28-107,'SC',110-116 ##label SAI
REFERENCE        A90179
   #authors      Sairam, M.R.; Papkoff, H.; Li, C.H.
   #journal      Biochem. Biophys. Res. Commun. (1972) 48:530-537
   #title        Human pituitary interstitial cell stimulating hormone:
                   primary structure of the alpha subunit.
   #cross-references MUID:72242988
   #accession    A90179
      ##molecule_type protein
      ##residues      28-107,'SC',110-116 ##label SA2
REFERENCE        A91461
   #authors      Keutmann, H.T.; Williams, R.M.; Bishop, W.H.; Ryan, R.J.
   #journal      Fed. Proc. (1978) 37:1828
   #title        Structure of human luteninizing hormone.
   #accession    A91461
      ##molecule_type protein
      ##residues      28-116 ##label KEU
REFERENCE        A92184
   #authors      Rathnam, P.; Saxena, B.B.
   #journal      J. Biol. Chem. (1975) 250:6735-6746
   #title        Primary amino acid sequence of follicle-stimulating hormone
                   from human pituitary glands.
   #cross-references MUID:76005558
   #accession    A92184
      ##molecule_type protein
      ##residues      25-28,'E',30-116 ##label RAT
REFERENCE        A94552
   #authors      Shome, B.; Parlow, A.F.
   #submission   submitted to the Atlas, April 1975
   #accession    A94552
      ##molecule_type protein
      ##residues      28-116 ##label SHO
REFERENCE        A92181
   #authors      Morgan, F.J.; Birken, S.; Canfield, R.E.
   #journal      J. Biol. Chem. (1975) 250:5247-5258
   #title        The amino acid sequence of human chorionic gonadotropin. The
                   alpha subunit and beta subunit.
   #cross-references MUID:75211304
   #accession    B92181
      ##molecule_type protein
      ##residues      25-116 ##label MOR
      ##note          heterogeneity is found at the amino end. Approximately
                       10 and 30% of the chains lack residues 1-2 and 1-3,
                       respectively
REFERENCE        A92141
   #authors      Bellisario, R.; Carlsen, R.B.; Bahl, O.P.
   #journal      J. Biol. Chem. (1973) 248:6796-6809
   #title        Human chorionic gonadotropin. Linear amino acid sequence of
                   the alpha subunit.
   #cross-references MUID:74011266
   #accession    A92141
      ##molecule_type protein
      ##residues      25-116 ##label BEL
REFERENCE        A92760
   #authors      Shome, B.; Parlow, A.F.
   #journal      J. Clin. Endocrinol. Metab. (1974) 39:199-202
   #title        Human follicle stimulating hormone (hFSH): first proposal for
                   the amino acid sequence of the alpha-subunit (hFSHalpha)
                   and first demonstration of its identity with the
                   alpha-subunit of human luteinizing hormone (hLHalpha).
   #cross-references MUID:74262937
   #contents     annotation
REFERENCE        A90632
   #authors      Fujiki, Y.; Rathnam, P.; Saxena, B.B.
   #journal      Biochim. Biophys. Acta (1980) 624:428-435
   #title        Studies on the disulfide bonds in human pituitary
                   follicle-stimulating hormone.
```

```
   #cross-references MUID:81021713
   #contents      annotation; preliminary disulfide bonds
REFERENCE         A44674
   #authors       Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                    J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                    N.W.
   #journal       Nature (1994) 369:455-461
   #title         Crystal structure of human chorionic gonadotropin.
   #contents      annotation; X-ray crystallography, 3.0 angstroms; correction
                    of disulfide bonds
REFERENCE         I58200
   #authors       Miyoshi, I.; Kasai, N.; Hayashizaki, Y.
   #journal       Nippon Rinsho (1994) 52:940-947
   #title         [Structure and regulation of human thyroid-stimulating
                    hormone (TSH) gene].
   #cross-references MUID:94254248
   #accession     I58200
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-116 ##label RES
      ##cross-references GB:S70585; NID:g546844; PID:g546845
GENETICS
   #gene          GDB:CGA
      ##cross-references GDB:119774; OMIM:118850
   #map_position 6q14-6q21
   #introns       30/1; 91/3
CLASSIFICATION    #superfamily glycoprotein hormones alpha chain
KEYWORDS          glycoprotein; heterodimer; hormone; pituitary
FEATURE
   1-24                #domain signal sequence #status experimental #label SIG\
   25-116              #product glycoprotein hormones alpha chain #status
                         experimental #label MAT\
   31-55,34-84,52-106,
   56-108,83-111       #disulfide_bonds #status experimental\
   76,102              #binding_site carbohydrate (Asn) (covalent) #status
                         experimental
SUMMARY           #length 116  #molecular-weight 13075  #checksum 1664

  Query Match           30.8%;  Score 672;  DB 1;  Length 116;
  Best Local Similarity  93.5%;  Pred. No. 8.42e-127;
  Matches    87;  Conservative    1;  Mismatches   5;  Indels   0;  Gaps   0;

Db      24 SAPDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC 83
           :|    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     193 TAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC 252

Db      84 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 116
           ||||||||||||||||||||||||||||||||
Qy     253 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT   12
ENTRY             1HRPA      #type complete

TITLE             chorionic gonadotropin, chain A - humanORGANISM         #formal_name Ho
   #note          placental origin, urinary extracted
REFERENCE         A52806
   #authors       Lapthorn, A.J.; Harris, D.C.; Isaacs, N.W.
   #submission    submitted to the Brookhaven Protein Data Bank, August 1994
   #cross-references PDB:1HRP
REFERENCE         TN022062
   #authors       Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                    J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                    N.W.
   #journal       Nature (1994) 369:455
   #title         Crystal structure of human chorionic gonadotropin.
REFERENCE         TN022063
   #authors       Harris, D.C.; Machin, K.J.; Evin, G.M.; Morgan, F.J.; Isaacs,
                    N.W.
   #journal       J. Biol. Chem. (1989) 264:6705
   #title         Preliminary x-ray diffraction analysis of human chorionic
                    gonadotropin.
COMMENT     Resolution: 3.0 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS          hormone
FEATURE
   4-28                #disulfide_bonds\
   7-57                #disulfide_bonds\
   25-79               #disulfide_bonds\
   29-81               #disulfide_bonds\
   56-84               #disulfide_bonds
SUMMARY           #length 86  #molecular-weight 9572  #checksum 1371

  Query Match           29.8%;  Score 650;  DB 5;  Length 86;
  Best Local Similarity  96.5%;  Pred. No. 1.23e-121;
  Matches    83;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 TQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 60
           : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     197 APGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 256

Db      61 SYNRVTVMGGFKVENHTACHCSTCYY 86
           ||||||||||||||||||||||||||
Qy     257 SYNRVTVMGGFKVENHTACHCSTCYY 282


RESULT   13
ENTRY             1XULA      #type complete

TITLE             chorionic gonadotropin, chain A - humanPDB_TITLE        theoretical
                    receptor complexed with human chorionic gonadotropin
ORGANISM          #formal_name Homo sapiens #common_name man
REFERENCE         A66957
   #authors       Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                    Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #submission    submitted to the Brookhaven Protein Data Bank, December 1996
   #cross-references PDB:1XUL
REFERENCE         TN032623
   #authors       Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                    Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #journal       Structure (London) (1996) 3:1341
   #title         Structural predictions for the ligand-binding region of
                    glycoprotein hormone receptors and the nature of
                    hormone-receptor interactions structure.
REFERENCE         TN032624
   #authors       Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                    Hendrickson, W.A.
   #journal       Structure (London) (1994) 2:545
   #title         Structure of human chorionic gonadotropin at 2.6 a resolution
                    from mad analysis of the selenomethionyl protein.
COMMENT     Resolution: not applicable
COMMENT     Determination: theoretical model
KEYWORDS          complex; glycoprotein hormone receptor glycoprotein; hormone;
                    phosphorylation; receptor
FEATURE
   37-41               #region helix (right hand alpha)\
   7-10,22-25          #region beta sheet\
   49-53,26-34         #region beta sheet\
   61-65,71-75         #region beta sheet\
   55-60,77-81         #region beta sheet\
   3-27                #disulfide_bonds\
   6-56                #disulfide_bonds\
   24-78               #disulfide_bonds\
   28-80               #disulfide_bonds\
   55-83               #disulfide_bonds
SUMMARY           #length 85  #molecular-weight 9471  #checksum 9656

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  Best Local Similarity 100.0%;  Pred. No. 3.63e-121;
  Matches    83;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       3 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     200 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db      63 RVTVMGGFKVENHTACHCSTCYY 85
```

```
          ||||||||||||||||||||||
Qy    260 RVTVMGGFKVENHTACHCSTCYY 282


RESULT   14
ENTRY            1HCNA      #type complete

TITLE            Human chorionic gonadotropin, chain A - humanORGANISM        #formal_n
REFERENCE        A52587
   #authors      Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                   Hendrickson, W.A.
   #submission   submitted to the Brookhaven Protein Data Bank, July 1994
   #cross-references PDB:1HCN
REFERENCE        TN020262
   #authors      Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                   Hendrickson, W.A.
   #journal      Structure (1994) 2:545
   #title        Structure of human chorionic gonadotropin at 2.6 angstroms
                   resolution from mad analysis of the selenomethionyl
                   protein.
COMMENT     Resolution: 2.6 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS         Hormone
FEATURE
   36-43              #region helix (right hand alpha)\
   4-11,21-28         #region beta sheet\
   29-35,48-54        #region beta sheet\
   3-27               #disulfide_bonds\
   6-56               #disulfide_bonds\
   24-78              #disulfide_bonds\
   28-80              #disulfide_bonds\
   55-83              #disulfide_bonds
SUMMARY          #length 85  #molecular-weight 9471  #checksum 9656

  Query Match           29.7%;  Score 648;  DB 5;  Length 85;
  Best Local Similarity 100.0%;  Pred. No. 3.63e-121;
  Matches    83;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      3 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    200 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db     63 RVTVMGGFKVENHTACHCSTCYY 85
          |||||||||||||||||||||||
Qy    260 RVTVMGGFKVENHTACHCSTCYY 282


RESULT   15
ENTRY            A39555     #type complete

TITLE            glycoprotein hormones alpha chain precursor - rhesus macaqueORGANISM
DATE             08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change
                   13-Jan-1995
ACCESSIONS       A39555
REFERENCE        A39555
   #authors      Golos, T.G.; Durning, M.; Fisher, J.M.
   #journal      DNA Cell Biol. (1991) 10:367-380
   #title        Molecular cloning of the rhesus glycoprotein hormone
                   alpha-subunit gene.
   #cross-references MUID:91321740
   #accession    A39555
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type DNA
      ##residues      1-120 ##label GOL
CLASSIFICATION   #superfamily glycoprotein hormones alpha chain
KEYWORDS         glycoprotein
SUMMARY          #length 120  #molecular-weight 13785  #checksum 5074

  Query Match           25.3%;  Score 552;  DB 2;  Length 120;
  Best Local Similarity 83.5%;  Pred. No. 8.95e-99;
  Matches    71;  Conservative    4;  Mismatches  10;  Indels   0;  Gaps   0;

Db     35 CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94
          ||||  :|| ||| ||||| ||||||||||||:||||||||||||||||||||||
Qy    200 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db     95 RVMVMGSVRVENHTECHCSTCYYHK 119
          || |||: :||||| ||||||||||
Qy    260 RVTVMGGFKVENHTACHCSTCYYHK 284


Search completed: Wed May  6 09:01:17 1998
Job time : 34 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:58:14 1998; MasPar time 8.40 Seconds
851.426 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6
Description: (1-285) from US08804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 42.622; Variance 62.749; scale 0.679

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1306	59.8	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	0.00e+00
2	1012	46.4	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	1.63e-244
3	944	43.2	454	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	2.69e-225
4	928	42.5	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	8.75e-221
5	672	30.8	116	1	GLHA_HUMAN	GLYCOPROTEIN HORMONES	3.55e-149
6	552	25.3	120	1	GLHA_MACMU	GLYCOPROTEIN HORMONES	3.70e-116
7	547	25.1	96	1	GLHA_RABIT	GLYCOPROTEIN HORMONES	8.57e-115
8	549	25.1	120	1	GLHA_BOVIN	GLYCOPROTEIN HORMONES	2.44e-115
9	549	25.1	120	1	GLHA_SHEEP	GLYCOPROTEIN HORMONES	2.44e-115
10	544	24.9	120	1	GLH1_RAT	GLYCOPROTEIN HORMONES	5.64e-114
11	542	24.8	96	1	GLHA_BALAC	GLYCOPROTEIN HORMONES	1.98e-113
12	542	24.8	120	1	GLH2_RAT	GLYCOPROTEIN HORMONES	1.98e-113
13	542	24.8	120	1	GLHA_MOUSE	GLYCOPROTEIN HORMONES	1.98e-113
14	542	24.8	120	1	GLHA_PIG	GLYCOPROTEIN HORMONES	1.98e-113
15	539	24.7	96	1	GLHA_STRCA	GLYCOPROTEIN HORMONES	1.30e-112
16	540	24.7	120	1	GLHA_CALJA	GLYCOPROTEIN HORMONES	6.95e-113
17	536	24.6	96	1	GLHA_PHYCA	GLYCOPROTEIN HORMONES	8.55e-112
18	537	24.6	120	1	GLHA_MELGA	GLYCOPROTEIN HORMONES	4.57e-112
19	507	23.2	118	1	GLH2_CYPCA	GLYCOPROTEIN HORMONES	6.51e-104
20	505	23.1	120	1	GLHA_EQUAS	GLYCOPROTEIN HORMONES	2.27e-103
21	503	23.0	96	1	GLHA_HORSE	GLYCOPROTEIN HORMONES	7.90e-103
22	499	22.9	116	1	GLHA_CLAGA	GLYCOPROTEIN HORMONES	9.58e-102
23	500	22.9	118	1	GLHA_HYPMO	GLYCOPROTEIN HORMONES	5.13e-102
24	500	22.9	118	1	GLH1_CYPCA	GLYCOPROTEIN HORMONES	5.13e-102
25	500	22.9	118	1	GLHA_CTEID	GLYCOPROTEIN HORMONES	5.13e-102
26	478	21.9	93	1	GLHA_MURCI	GLYCOPROTEIN HORMONES	4.53e-96
27	479	21.9	97	1	GLHA_RANCA	GLYCOPROTEIN HORMONES	2.43e-96
28	474	21.7	117	1	GLHA_ANGAN	GLYCOPROTEIN HORMONES	5.42e-95
29	450	20.6	114	1	GLH2_ONCKE	GLYCOPROTEIN HORMONES	1.53e-88
30	448	20.5	108	1	GLH1_ONCKE	GLYCOPROTEIN HORMONES	5.27e-88
31	427	19.6	94	1	GLHA_THUOB	GLYCOPROTEIN HORMONES	2.17e-82
32	424	19.4	117	1	GLHA_ACALA	GLYCOPROTEIN HORMONES	1.37e-81
33	376	17.2	125	1	GLHA_FUNHE	GLYCOPROTEIN HORMONES	6.97e-69
34	247	11.3	417	1	WSL1_HUMAN	WSL-1 PROTEIN PRECURSO	6.68e-36
35	245	11.2	435	1	TNRC_HUMAN	LYMPHOTOXIN-BETA RECEP	2.07e-35
36	225	10.3	325	1	VT2_SFVKA	TUMOR NECROSIS FACTOR	1.55e-30
37	221	10.1	326	1	VT2_MYXVL	TUMOR NECROSIS FACTOR	1.43e-29
38	216	9.9	415	1	TNRC_MOUSE	LYMPHOTOXIN-BETA RECEP	2.26e-28
39	214	9.8	349	1	VC22_VARV	PROTEIN C22/B28 HOMOLO	6.80e-28
40	211	9.7	425	1	NGFR_RAT	LOW-AFFINITY NERVE GRO	3.53e-27
41	212	9.7	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GRO	2.04e-27
42	212	9.7	474	1	TNR2_MOUSE	TUMOR NECROSIS FACTOR	2.04e-27
43	204	9.3	260	1	CD27_HUMAN	CD27L RECEPTOR PRECURS	1.61e-25
44	191	8.7	323	1	FASA_BOVIN	FASL RECEPTOR PRECURSO	1.77e-22
45	183	8.4	595	1	CD30_HUMAN	CD30L RECEPTOR PRECURS	1.24e-20

ALIGNMENTS

RESULT 1
ID TNR1_HUMAN STANDARD; PRT; 455 AA.
AC P19438;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
GN TNFR1 OR TNFAR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 90235285.
RA SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL CELL 61:361-370(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90235284.
RA LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA TABUCHI H., LESSLAUER W.;
RL CELL 61:351-359(1990).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE; 91006021.
RA NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA ADERKA D., HOLTMANN H., WALLACH D.;
RL EMBO J. 9:3269-3278(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91090841.
RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL DNA CELL BIOL. 9:705-715(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 91017509.
RA GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92250049.
RA FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;

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RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RL   CELL 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KHONO H., SPRANG S.R.;
RL   STRUCTURE 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; X55313; G37224; -.
DR   EMBL; M33294; G339745; -.
DR   EMBL; M58286; G339754; -.
DR   EMBL; M63121; G339756; -.
DR   EMBL; M75866; G339750; -.
DR   EMBL; M75864; G339750; JOINED.
DR   EMBL; M75865; G339750; JOINED.
DR   EMBL; M60275; G339760; -.
DR   EMBL; A21522; G579600; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL       1    21
FT   CHAIN       22   455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN       41   291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN      22   211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212   234       POTENTIAL.
FT   DOMAIN     235   455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43   196       4 X TNFR-CYS.
FT   REPEAT      43    82       TNFR-CYS 1.
FT   REPEAT      83   125       TNFR-CYS 2.
FT   REPEAT     126   166       TNFR-CYS 3.
FT   REPEAT     167   196       TNFR-CYS 4.
FT   DOMAIN     356   441       DEATH DOMAIN.
FT   DISULFID    44    58
FT   DISULFID    59    72
FT   DISULFID    62    81
FT   DISULFID    84    99
FT   DISULFID   102   117
FT   DISULFID   105   125
FT   DISULFID   127   143
FT   DISULFID   146   158
FT   DISULFID   149   166
FT   DISULFID   168   179
FT   DISULFID   182   191
FT   DISULFID   185   195
FT   CARBOHYD    54    54       POTENTIAL.
FT   CARBOHYD   145   145       POTENTIAL.
FT   CARBOHYD   151   151       POTENTIAL.
FT   CONFLICT   412   412       MISSING (IN REF. 4).
FT   CONFLICT   443   446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  CE0EA06F CRC32;

  Query Match           59.8%;  Score 1306;  DB 1;  Length 455;
  Best Local Similarity  98.8%;  Pred. No. 0.00e+00;
  Matches   169;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
           ||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    2
ID   TNR1_PIG       STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUTER B., PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; U19994; G1141753; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL       1    21       POTENTIAL.
FT   CHAIN       22   461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN      22   210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   211   233       POTENTIAL.
FT   DOMAIN     234   461       CYTOPLASMIC (POTENTIAL).
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FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      362    447       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD     86     86       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
SQ   SEQUENCE   461 AA;  50696 MW;  8E2C350A CRC32;

  Query Match           46.4%;  Score 1012;  DB 1;  Length 461;
  Best Local Similarity  71.9%;  Pred. No. 1.63e-244;
  Matches   123;  Conservative   25;  Mismatches  22;  Indels   1;  Gaps   1;

Db      41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
           :|:|||||| |||| ||||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
           |||||| ||:|||||:|||||||||||||||||| |||| ||||:||:|| ||||:|:| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPATSETRNDFQDTGTT 210
           ||:|:| ||:||||||::||||| |||:: :| :|  :  |  :  :|:|||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    3
ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL   MOL. CELL. BIOL. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL   EUR. J. IMMUNOL. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL   IMMUNOGENETICS 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RL   IMMUNOGENETICS 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL   MOL. IMMUNOL. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M60468; G199826; -.
DR   EMBL; M59377; G202097; -.
DR   EMBL; X59238; G53579; -.
DR   EMBL; X57796; G54849; -.
DR   EMBL; L26349; G430733; -.
DR   EMBL; M76656; G202102; -.
DR   EMBL; M88067; G202102; JOINED.
DR   EMBL; M76655; G202102; JOINED.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1TNR.
DR   MGD; MGI:98781; TNFR1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235       POTENTIAL.
FT   DOMAIN      236    454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      356    441       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    202    202       POTENTIAL.
FT   CONFLICT    394    394       R -> G (IN REF. 6).
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SQ   SEQUENCE   454 AA;  50129 MW;  4B6EEC09 CRC32;

  Query Match           43.2%;  Score 944;  DB 1;  Length 454;
  Best Local Similarity  67.4%;  Pred. No. 2.69e-225;
  Matches   116;  Conservative   28;  Mismatches  27;  Indels   1;  Gaps   1;

Db      41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
           ||:|||||:|: ||||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  |||||:|||||:|  |:||||||: ||:::| ||  ||| :|: |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
           ||||| |||||||||:|||:||:|||: || || ||  : ||   :||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ-IENVKGTEDSGTT 193


RESULT    4
ID   TNR1_RAT       STANDARD;      PRT;   461 AA.
AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M63122; G207362; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      363    448       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    201    201       POTENTIAL.
SQ   SEQUENCE   461 AA;  50969 MW;  82F68B08 CRC32;

  Query Match           42.5%;  Score 928;  DB 1;  Length 461;
  Best Local Similarity  66.1%;  Pred. No. 8.75e-221;
  Matches   113;  Conservative   26;  Mismatches  32;  Indels   0;  Gaps   0;

Db      41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
           |::|||||| || |||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  ||||| ||||:|  | ||||||:|||:::| ||  ||| :|: |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTA 211
           |||||| |||||||  ||| :||:|||: || || || : ||   :||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193


RESULT    5
ID   GLHA_HUMAN     STANDARD;      PRT;   116 AA.
AC   P01215;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 80011660.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 281:351-356(1979).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94254248.
RA   MIYOSHI I., KASAI N., HAYASHIZAKI Y.;
RL   NIPPON RINSHO 52:940-947(1994).
RN   [3]
RP   SEQUENCE OF 1-98 FROM N.A.
RX   MEDLINE; 82267643.
RA   FIDDES J.C., GOODMAN H.M.;
RL   J. MOL. APPL. GENET. 1:3-18(1981).
RN   [4]
RP   SEQUENCE OF 1-24.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 77243687.
RA   SAIRAM M.R., LI C.H.;
RL   CAN. J. BIOCHEM. 55:755-760(1977).
RN   [6]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 72242988.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 48:530-537(1972).
RN   [7]
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RP   SEQUENCE, AND REVISIONS.
RA   KEUTMANN H.T., WILLIAMS R.M., BISHOP W.H., RYAN R.J.;
RL   FED. PROC. 37:1828-1828(1978).
RN   [8]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 76005558.
RA   RATHNAM P., SAXENA B.B.;
RL   J. BIOL. CHEM. 250:6735-6746(1975).
RN   [9]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 74262937.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 39:199-202(1974).
RN   [10]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 75211304.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [11]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 74011266.
RA   BELLISARIO R., CARLSEN R.B., BAHL O.P.;
RL   J. BIOL. CHEM. 248:6796-6809(1973).
RN   [12]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81021713.
RA   FUJIKI Y., RATHNAM P., SAXENA B.B.;
RL   BIOCHIM. BIOPHYS. ACTA 624:428-435(1980).
RN   [13]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81006887.
RA   MISE T., BAHL O.P.;
RL   J. BIOL. CHEM. 255:8516-8522(1980).
RN   [14]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 91122088.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
RN   [16]
RP   STRUCTURE BY NMR.
RX   MEDLINE; 97054614.
RA   DE BEER T., VAN ZUYLEN C.W.E.M., LEEFLANG B.R., HARD K., BOELENS R.,
RA   KAPTEIN R., KAMERLING J.P., VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 241:229-242(1996).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; J00152; G183319; -.
DR   EMBL; J00150; G183319; JOINED.
DR   EMBL; J00151; G183319; JOINED.
DR   EMBL; S70585; G546845; -.
DR   EMBL; S70583; G546845; JOINED.
DR   EMBL; S70584; G546845; JOINED.
DR   EMBL; V00518; G31869; -.
DR   EMBL; V00485; G669156; -.
DR   EMBL; V00486; G669156; JOINED.
DR   EMBL; V00487; G669156; JOINED.
DR   PIR; A01481; TTHUAP.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   MIM; 118850; -.
DR   MIM; 188530; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT   SIGNAL        1     24
FT   CHAIN        25    116       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     31     55
FT   DISULFID     34     84
FT   DISULFID     52    106
FT   DISULFID     56    108
FT   DISULFID     83    111
FT   CARBOHYD     63     63
FT   CARBOHYD     76     76
FT   CARBOHYD    102    102
FT   CONFLICT     29     29       Q -> E (IN REF. 8).
FT   CONFLICT    108    109       CS -> SC (IN REF. 5 AND 6).
SQ   SEQUENCE   116 AA;  13075 MW;  3BA19E2F CRC32;

  Query Match           30.8%;  Score 672;  DB 1;  Length 116;
  Best Local Similarity  93.5%;  Pred. No. 3.55e-149;
  Matches    87;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Db      24 SAPDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC 83
           :|     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     193 TAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC 252

Db      84 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 116
           ||||||||||||||||||||||||||||||||
Qy     253 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    6
ID   GLHA_MACMU     STANDARD;      PRT;   120 AA.
AC   P22762;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   MACACA MULATTA (RHESUS MACAQUE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91321740.
RA   GOLOS T.G., DURNING M., FISHER J.M.;
RL   DNA CELL BIOL. 10:367-380(1991).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; A39555; A39555.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     67     67       BY SIMILARITY.
FT   CARBOHYD     80     80       BY SIMILARITY.
FT   CARBOHYD    106    106       BY SIMILARITY.
SQ   SEQUENCE   120 AA;  13785 MW;  85E1F9F4 CRC32;

  Query Match           25.3%;  Score 552;  DB 1;  Length 120;
  Best Local Similarity  83.5%;  Pred. No. 3.70e-116;
  Matches    71;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Db      35 CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94
           ||||  :|| ||| ||||| |||||||||||||:|||||||||||||||||||||||
Qy     200 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db      95 RVMVMGSVRVENHTECHCSTCYYHK 119
           || |||: :||||| ||||||||||
Qy     260 RVTVMGGFKVENHTACHCSTCYYHK 284
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RESULT    7
ID   GLHA_RABIT     STANDARD;      PRT;    96 AA.
AC   P07474;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN   CGA.
OS   ORYCTOLAGUS CUNICULUS (RABBIT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; LAGOMORPHA.
RN   [1]
RP   SEQUENCE.
RA   GLENN S.D., NAHM H.S., WARD D.N.;
RL   J. PROTEIN CHEM. 3:143-156(1984).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; A05096; A05096.
DR   HSSP; P01233; 1HRP.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID     11     35       BY SIMILARITY.
FT   DISULFID     14     64       BY SIMILARITY.
FT   DISULFID     32     86       BY SIMILARITY.
FT   DISULFID     36     88       BY SIMILARITY.
FT   DISULFID     63     91       BY SIMILARITY.
FT   CARBOHYD     56     56
FT   CARBOHYD     82     82
SQ   SEQUENCE   96 AA;  10663 MW;  CD56D255 CRC32;

  Query Match           25.1%;  Score 547;  DB 1;  Length 96;
  Best Local Similarity  76.7%;  Pred. No. 8.57e-115;
  Matches    69;  Conservative    6;  Mismatches  15;  Indels   0;  Gaps   0;

Db       7 AMQGCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVA 66
           |  ||||| | || :||  |||| ||||||||||||||| |||||||| ||:|||:|||||
Qy     196 AAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVA 255

Db      67 KAFTKATVMGNAKVENHTECHCSTCYYHKS 96
           |:: : ||||  |||||| ||||||||||
Qy     256 KSYNRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    8
ID   GLHA_BOVIN     STANDARD;      PRT;   120 AA.
AC   P01217;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84041490.
RA   GOODWIN R.G., MONCMAN C.L., ROTTMAN F.M., NILSON J.H.;
RL   NUCLEIC ACIDS RES. 11:6873-6882(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84024633.
RA   ERWIN C., CROYLE M.L., DONELSON J., MAURER R.;
RL   BIOCHEMISTRY 22:4856-4860(1983).
RN   [3]
RP   SEQUENCE OF 8-133 FROM N.A.
RX   MEDLINE; 83161058.
RA   NILSON J.H., THOMASON A.R., CSERBAK M.T., MONCMAN C.L., WOYCHIK R.P.;
RL   J. BIOL. CHEM. 258:4679-4682(1983).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 71111428.
RA   LIAO T.-H., PIERCE J.G.;
RL   J. BIOL. CHEM. 246:850-865(1971).
RN   [5]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 71111429.
RA   PIERCE J.G., LIAO T.-H., CARLSEN R.B., REIMO T.;
RL   J. BIOL. CHEM. 246:866-872(1971).
RN   [6]
RP   SEQUENCE OF 80-91 AND 100-120.
RX   MEDLINE; 72012932.
RA   MAGHUIN-ROGISTER G., HENNEN G.P.;
RL   EUR. J. BIOCHEM. 21:489-497(1971).
RN   [7]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 74307752.
RA   CORNELL J.S., PIERCE J.G.;
RL   J. BIOL. CHEM. 249:4166-4174(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X00003; E274391; -.
DR   EMBL; X00004; E274391; JOINED.
DR   EMBL; X00050; G607; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A05132; A05132.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80
FT   CARBOHYD    106    106
FT   CONFLICT     13     13       A -> T (IN REF. 2).
FT   CONFLICT     37     37       E -> Q (IN REF. 4).
FT   CONFLICT     52     52       P -> A (IN REF. 2).
FT   CONFLICT     84     87       EATC -> AZCT (IN REF. 6).
SQ   SEQUENCE   120 AA;  13616 MW;  99C153C5 CRC32;

  Query Match           25.1%;  Score 549;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 2.44e-115;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | || :|| | ||| |||||||||||||| |||||||| ||:|||:||||||::
Qy     199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db      94 TKATVMGNVRVENHTECHCSTCYYHKS 120
             : ||||  :|||||| ||||||||||
Qy     259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    9
ID   GLHA_SHEEP     STANDARD;      PRT;   120 AA.
AC   P01218;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   OVIS ARIES (SHEEP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90098887.
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RA   BELLO P.A., MOUNTFORD P.S., BRANDON M.R., ADAMS T.E.;
RL   NUCLEIC ACIDS RES. 17:10494-10494(1989).
RN   [2]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 72211144.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., LAMKIN W.M., BAKER H.N.,
RA   WARD D.N.;
RL   J. BIOL. CHEM. 247:4351-4364(1972).
RN   [3]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 73190034.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:554-571(1972).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 82113052.
RA   SAIRAM M.R.;
RL   BIOCHEM. J. 197:535-539(1981).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RA   CHUNG D., SAIRAM M.R., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973).
RN   [6]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 91006170.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X16977; G1366; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A01484; UTSHA.
DR   PIR; S06935; S06935.
DR   PIR; S13200; S13200.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80
FT   CARBOHYD    106    106
FT   CONFLICT     27     27       D -> N (IN REF. 2).
FT   CONFLICT     29     29       E -> Q (IN REF. 2).
FT   CONFLICT     37     37       E -> Q (IN REF. 2 TO 4).
FT   CONFLICT    112    113       CS -> SC (IN REF. 3).
SQ   SEQUENCE   120 AA;  13588 MW;  13BA4DE1 CRC32;

  Query Match           25.1%;  Score 549;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 2.44e-115;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | || :|| | ||| |||||||||||||| |||||||| ||:|||:|||||::
Qy     199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db      94 TKATVMGNVRVENHTECHCSTCYYHKS 120
             : ||||  :||||| ||||||||||
Qy     259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT   10
ID   GLH1_RAT       STANDARD;      PRT;   120 AA.
AC   P11962; P70516;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN 1 PRECURSOR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=PITUITARY;
RX   MEDLINE; 82214055.
RA   GODINE J.E., CHIN W.W., HABENER J.F.;
RL   J. BIOL. CHEM. 257:8368-8371(1982).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89196918.
RA   BURNSIDE J., BUCKLAND P.R., CHIN W.W.;
RL   GENE 70:67-74(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   ZOOL. SCI. 7:877-885(1990).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01252; G56580; -.
DR   EMBL; J00757; G206111; -.
DR   EMBL; M22829; -; NOT_ANNOTATED_CDS.
DR   EMBL; M25543; G204470; -.
DR   EMBL; M25544; G204471; -.
DR   EMBL; D00575; G220842; -.
DR   PIR; JT0408; TTRTA.
DR   PIR; S27385; S27385.
DR   HSSP; P01233; 1HRP.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN 1.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80       PROBABLE.
FT   CARBOHYD    106    106       PROBABLE.
FT   CONFLICT     84     84       E -> Q (IN G206111).
SQ   SEQUENCE   120 AA;  13453 MW;  5E507A0D CRC32;

  Query Match           24.9%;  Score 544;  DB 1;  Length 120;
  Best Local Similarity  78.2%;  Pred. No. 5.64e-114;
  Matches    68;  Conservative    6;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKSF 93
           ||||| | || :||  |||| |||||||||||||| |||||||| ||:|||:|||||||:
Qy     199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db      94 TKATVMGNARVENHTDCHCSTCYYHKS 120
             : ||||  :||||| ||||||||||
Qy     259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT   11
ID   GLHA_BALAC     STANDARD;      PRT;    96 AA.
AC   P37036;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN   CGA.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.
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RA   KARASEV V.S., PANKOV Y.A.;
RL   BIOKHIMIIA 50:1972-1986(1985).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; PN0138; PN0138.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID     11     35       BY SIMILARITY.
FT   DISULFID     14     64       BY SIMILARITY.
FT   DISULFID     32     86       BY SIMILARITY.
FT   DISULFID     36     88       BY SIMILARITY.
FT   DISULFID     63     91       BY SIMILARITY.
FT   CARBOHYD     56     56
FT   CARBOHYD     82     82
SQ   SEQUENCE   96 AA;  10720 MW;  E2CD30DF CRC32;

  Query Match           24.8%;  Score 542;  DB 1;  Length 96;
  Best Local Similarity  70.1%;  Pred. No. 1.98e-113;
  Matches    61;  Conservative   13;  Mismatches  13;  Indels   0;  Gaps   0;

Db      10 GCPZCKLKZBKYFSKLGAPIYZCMGCCFSRAYPTPARSKKTMLVPKNITSZATCCVAKAF 69
           |||:| | :: :|| ||||  ||||||||||||||| |||||||| ||:||::||||||::
Qy     199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db      70 TKATVMGBARVZNHTZCHCSTCYYHKS 96
             : ||||  :|:||| ||||||||||
Qy     259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT   12
ID   GLH2_RAT       STANDARD;      PRT;   120 AA.
AC   P11963;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN 2 PRECURSOR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 82214055.
RA   GODINE J.E., CHIN W.W., HABENER J.F.;
RL   J. BIOL. CHEM. 257:8368-8371(1982).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01253; G56583; -.
DR   PIR; S27386; S27386.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN 2.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80       PROBABLE.
FT   CARBOHYD    106    106       PROBABLE.
SQ   SEQUENCE   120 AA;  13565 MW;  4E4FAB2E CRC32;

  Query Match           24.8%;  Score 542;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 1.98e-113;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | || :||  |||| |||||||||||||| |||||||| ||:|||:||||||::
Qy     199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db      94 TKATVMGNARVENHTECHCSTCYYHKS 120
             : ||||  :||||| ||||||||||
Qy     259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT   13
ID   GLHA_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01216;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 82060239.
RA   CHIN W.W., KRONENBERG H.M., DEE P.C., MALOOF F., HABENER J.F.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:5329-5333(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89170115.
RA   GORDON D.F., WOOD W.M., RIDGWAY E.C.;
RL   DNA 7:679-690(1988).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; J00643; G202180; -.
DR   EMBL; V00852; G54799; -.
DR   EMBL; M22991; -; NOT_ANNOTATED_CDS.
DR   EMBL; M22992; G575520; -.
DR   PIR; A01482; TTMSA.
DR   PIR; A31598; A31598.
DR   HSSP; P01215; 1HCN.
DR   MGD; MGI:88390; CGA.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80       PROBABLE.
FT   CARBOHYD    106    106       PROBABLE.
SQ   SEQUENCE   120 AA;  13565 MW;  86F1F31A CRC32;

  Query Match           24.8%;  Score 542;  DB 1;  Length 120;
  Best Local Similarity  77.0%;  Pred. No. 1.98e-113;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db      34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | || :||  |||| |||||||||||||| |||||||| ||:|||:||||||::
Qy     199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db      94 TKATVMGNARVENHTECHCSTCYYHKS 120
             : ||||  :||||| ||||||||||
Qy     259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT   14
ID   GLHA_PIG       STANDARD;      PRT;   120 AA.
AC   P01219;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
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GN   CGA.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89325834.
RA   HIRAI T., TAKIKAWA H., KATO Y.;
RL   MOL. CELL. ENDOCRINOL. 63:209-217(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SEQUENCE OF 31-120.
RX   MEDLINE; 74075725.
RA   MAGHUIN-ROGISTER G., COMBARNOUS Y., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:255-263(1973).
RN   [4]
RP   PRELIMINARY SEQUENCE OF 25-120.
RA   CLOSSET J., MAGHUIN-ROGISTER G., HENNEN G.;
RL   ENDOCRINOL. EXP. 8:164(1974).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 75093922.
RA   COMBARNOUS Y., HENNEN G.;
RL   BIOCHEM. SOC. TRANS. 2:915-917(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; D00768; G217699; -.
DR   EMBL; D00767; G217699; JOINED.
DR   PIR; A01485; UTPGA.
DR   PIR; A30339; A30339.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     80     80
FT   CARBOHYD    106    106
SQ   SEQUENCE   120 AA;  13532 MW;  8749DBA5 CRC32;

  Query Match           24.8%;  Score 542;  DB 1;  Length 120;
  Best Local Similarity 77.0%;  Pred. No. 1.98e-113;
  Matches    67;  Conservative    7;  Mismatches  13;  Indels   0;  Gaps   0;

Db     34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
          ||||| | || :||  |||| ||||||||||||||| |||||||| ||:|||:||||||::
Qy    199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db     94 TKATVMGNARVENHTECHCSTCYYHKS 120
            : ||||  :||||| ||||||||||
Qy    259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT   15
ID   GLHA_STRCA     STANDARD;      PRT;    96 AA.
AC   P80665;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
OS   STRUTHIO CAMELUS (OSTRICH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES;
OC   PALAEOGNATHAE; STRUTHIONIFORMES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 97025333.
RA   KOIDE Y., PAPKOFF H., KAWAUCHI H.;
RL   EUR. J. BIOCHEM. 240:262-267(1996).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID     11     35       BY SIMILARITY.
FT   DISULFID     14     64       BY SIMILARITY.
FT   DISULFID     32     86       BY SIMILARITY.
FT   DISULFID     36     88       BY SIMILARITY.
FT   DISULFID     63     91       BY SIMILARITY.
FT   CARBOHYD     56     56       POTENTIAL.
FT   CARBOHYD     82     82       POTENTIAL.
SQ   SEQUENCE   96 AA;  10781 MW;  DDF7B4BB CRC32;

  Query Match           24.7%;  Score 539;  DB 1;  Length 96;
  Best Local Similarity 74.7%;  Pred. No. 1.30e-112;
  Matches    65;  Conservative   10;  Mismatches  12;  Indels   0;  Gaps   0;

Db     10 GCPECKLGENRFFSKPGAPVYQCTGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKAF 69
          ||||| | || ||| ||||: || ||||||||||||||||||| ||:|||:||||||::
Qy    199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db     70 TKITLKDNVKIENHTECHCSTCYYHKS 96
             ::|::   |:|||| ||||||||||
Qy    259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


Search completed: Wed May  6 08:58:56 1998
Job time : 42 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:59:13 1998; MasPar time 14.96 Seconds
802.180 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6
Description: (1-285) from US08804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 41.694; Variance 64.494; scale 0.646

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	959	43.9	471	4	O19131	TUMOR NECROSIS FACTOR-	7.07e-219
2	943	43.2	180	4	Q95185	TUMOUR NECROSIS FACTOR	1.42e-214
3	453	20.8	107	12	Q90286	GONADOTROPIN ALPHA SUB	3.04e-85
4	454	20.8	108	12	Q90287	GONADOTROPIN ALPHA SUB	1.68e-85
5	452	20.7	119	12	Q91370	GONADOTROPHIN ALPHA 1	5.48e-85
6	448	20.5	114	12	Q91371	GONADOTROPHIN ALPHA 2	5.78e-84
7	433	19.8	117	12	Q91119	GLYCOPROTEIN HORMONES	3.90e-80
8	334	15.3	55	10	Q62589	ALPHA SUBUNIT OF GLYCO	2.97e-55
9	249	11.4	277	2	O14866	SOLUBLE DEATH RECEPTOR	1.12e-34
10	249	11.4	426	2	O14865	DEATH RECEPTOR 3 BETA.	1.12e-34
11	247	11.3	253	2	O00276	LYMPHOCYTE ASSOCIATED	3.31e-34
12	247	11.3	380	2	O00280	LYMPHOCYTE ASSOCIATED	3.31e-34
13	247	11.3	418	2	O00275	LYMPHOCYTE ASSOCIATED	3.31e-34
14	214	9.8	348	11	Q85407	HOMOLOG OF VACCINIA VI	1.52e-26
15	214	9.8	349	11	Q89118	SOMALIA-1977 RIGHT NEA	1.52e-26
16	214	9.8	349	11	Q89098	GARCIA-1966 RIGHT NEAR	1.52e-26
17	210	9.6	355	11	Q85308	SECRETED RECEPTOR BIND	1.24e-25
18	206	9.4	459	10	Q62327	TUMOR NECROSIS FACTOR	1.00e-24
19	204	9.3	401	10	O08727	OSTEOPROTEGERIN.	2.84e-24
20	194	8.9	401	2	O00300	OSTEOPROTEGERIN.	5.02e-22
21	191	8.7	401	10	O08712	OSTEOPROTEGERIN.	2.34e-21
22	187	8.6	267	4	O02764	OX40 PRECURSOR (FRAGME	1.80e-20
23	181	8.3	324	10	Q63199	FAS ANTIGEN PRECURSOR.	3.77e-19
24	181	8.3	411	2	O15517	CYTOTOXIC TRAIL RECEPT	3.77e-19
25	181	8.3	411	2	O15508	P53-REGULATED DNA DAMA	3.77e-19
26	181	8.3	411	2	O14720	DEATH RECEPTOR 5.	3.77e-19
27	181	8.3	440	2	O15531	APOPTOSIS INDUCING PRO	3.77e-19
28	181	8.3	440	2	O14763	APOPTOSIS INDUCING REC	3.77e-19
29	180	8.2	259	2	O14755	TRAIL RECEPTOR 3.	6.24e-19
30	180	8.2	283	2	Q92956	HERPESVIRUS ENTRY MEDI	6.24e-19
31	178	8.2	299	2	O14798	CYTOTOXIC TRAIL RECEPT	1.71e-18
32	179	8.2	425	2	Q16042	TUMOR NECROSIS FACTOR	1.03e-18
33	173	7.9	625	10	O35305	RANK.	2.08e-17
34	167	7.7	202	2	Q14405	SOMATOTROPIN PRECURSOR	4.07e-16
35	167	7.7	217	2	Q16631	SOMATOTROPIN PRECURSOR	4.07e-16
36	160	7.3	202	2	O14643	PLACENTAL GROWTH HORMO	1.25e-14
37	160	7.3	245	2	O14644	PLACENTAL GROWTH HORMO	1.25e-14
38	159	7.3	468	2	O00220	CYTOTOXIC LIGAND TRAIL	2.04e-14
39	154	7.1	199	2	Q14406	CHORIONIC SOMATOMAMMOT	2.28e-13
40	155	7.1	217	2	Q14407	CHORIONIC SOMATOMAMMOT	1.41e-13
41	150	6.9	274	2	Q13663	CELL SURFACE ANTIGEN O	1.54e-12
42	147	6.7	217	4	Q07367	SOMATOTROPIN 1 PRECURS	6.39e-12
43	146	6.7	217	4	Q07369	SOMATOTROPIN 3 PRECURS	1.02e-11
44	143	6.6	212	4	Q07368	SOMATOTROPIN 2 PRECURS	4.19e-11
45	142	6.5	314	2	Q14293	FAS SOLUBLE PROTEIN.	6.68e-11

ALIGNMENTS

RESULT 1
ID O19131 PRELIMINARY; PRT; 471 AA.

AC O19131;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR-RECEPTOR I.
GN TNF-RI.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AORTA;
RA LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U90937; G2290398; -.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
SQ SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;

Query Match 43.9%; Score 959; DB 4; Length 471;
Best Local Similarity 66.7%; Pred. No. 7.07e-219;
Matches 114; Conservative 28; Mismatches 28; Indels 1; Gaps 1;

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Db     41 ESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCL 100
          :| |||||| ||||::||||||||||||||||||||:||||| | :|:::|| |||||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160
          |||:|| || |||||:| |||||||||||||| ||:|  |:|:||:|| ||||:::|||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161 RQDTICHCHMGFFLKGAKCISCHDCKNK-ECEKLCPTRPSTGKDSQDPGTT 210
          :|:|:| || ||||:   |:|| :||:  || ||   :    | ::|:|||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
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RESULT 2
ID Q95185 PRELIMINARY; PRT; 180 AA.

AC Q95185;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

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DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN   TNFR-1.
OS   FELIS SILVESTRIS CATUS (CAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CARNIVORA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   DUTHIE S., NASIR L., ECKERSALL P.D.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72344; G1613880; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
FT   NON_TER       1      1
FT   NON_TER     180    180
SQ   SEQUENCE   180 AA;  20399 MW;  5452A6B2 CRC32;

  Query Match           43.2%;  Score 943;  DB 4;  Length 180;
  Best Local Similarity  85.3%;  Pred. No. 1.42e-214;
  Matches   116;  Conservative   10;  Mismatches  10;  Indels   0;  Gaps   0;

Db     45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
          ||||||||||:|||||||||||||||||:||| ||||||||:|:|||||| ||:|||||
Qy     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db    105 KCRKEMYQVEISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQN 164
          |||||| |||||:||| |||||||||||| |||| |||:||:|||||||::|| | ||
Qy     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQN 145

Db    165 TVCTCHAGFFLRGNEC 180
          |||||||||||| |||
Qy    146 TVCTCHAGFFLRENEC 161


RESULT    3
ID   Q90286         PRELIMINARY;   PRT;   107 AA.

AC   Q90286;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
RL   SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D86551; G1469836; -.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11959 MW;  880C6840 CRC32;

  Query Match           20.8%;  Score 453;  DB 12;  Length 107;
  Best Local Similarity  72.0%;  Pred. No. 3.04e-85;
  Matches    59;  Conservative    7;  Mismatches  15;  Indels   1;  Gaps   1;

Db     27 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEV 86
          || || | || :|| |||| |||||||||||||||||||||| ||:|||:||||||
Qy    199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db     87 KRVLV-NDVRLVNHTDCHCSTC 107
          :|| |    :: ||| ||||||
Qy    259 NRVTVMGGFKVENHTACHCSTC 280


RESULT    4
ID   Q90287         PRELIMINARY;   PRT;   108 AA.

AC   Q90287;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
RL   SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D86552; G1469838; -.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  12129 MW;  B2B1A212 CRC32;

  Query Match           20.8%;  Score 454;  DB 12;  Length 108;
  Best Local Similarity  72.0%;  Pred. No. 1.68e-85;
  Matches    59;  Conservative    7;  Mismatches  15;  Indels   1;  Gaps   1;

Db     28 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKDITSEATCCVAKEV 87
          || || | || :|| |||| |||||||||||||||||||||| |::|||:||||||
Qy    199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db     88 KRVLV-DDVKLVNHTDCHCSTC 108
          :|| |    |: ||| ||||||
Qy    259 NRVTVMGGFKVENHTACHCSTC 280


RESULT    5
ID   Q91370         PRELIMINARY;   PRT;   119 AA.

AC   Q91370;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GONADOTROPHIN ALPHA 1 SUBUNIT.
OS   ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94197892.
RA   GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69273; G546258; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ   SEQUENCE   119 AA;  13131 MW;  2EEF28F4 CRC32;

  Query Match           20.7%;  Score 452;  DB 12;  Length 119;
  Best Local Similarity  67.8%;  Pred. No. 5.48e-85;
  Matches    59;  Conservative   11;  Mismatches  16;  Indels   1;  Gaps   1;

Db     34 GCEECKLKENKLFSNPGAPVYQCTGCCFSRAYPTPLQSKKAMLVPKNITSEATCCVAKEG 93
          || || | || :|| |||| || |||||||||||||:|||:||| ||:|||:||||||
Qy    199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258

Db     94 ERV-VVDNIKLTNHTECWCNTCYHHKS 119
          :|| |:  :|: ||| | |:||| |||
Qy    259 NRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    6
ID   Q91371         PRELIMINARY;   PRT;   114 AA.

AC   Q91371;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GONADOTROPHIN ALPHA 2 SUBUNIT.
OS   ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE; 94197892.
RA   GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69274; G546260; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ   SEQUENCE   114 AA;  12519 MW;  473D3C83 CRC32;

  Query Match           20.5%;  Score 448;  DB 12;  Length 114;
  Best Local Similarity  58.3%;  Pred. No. 5.78e-84;
  Matches    67;  Conservative   11;  Mismatches  33;  Indels   4;  Gaps   2;

Db       4 LKSTGLSLILSALLVIADSYPNSDKTNMGCEECTLKPNTIF--PN--IIQCTGCCFSRAY 59
           |  | |||     :  ::    :  :  || ||||  | :|  |   |:|| ||||||||
Qy     171 LECTKLSLPQIENVKGTEDSGTTAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAY 230

Db      60 PTPLRSKQTMLVPKNITSEATCCVAKEGERVTTKDGFPVTNHTECHCSTCYYHKS 114
           ||||||| |||| ||:|||:||||||  :||| : || | ||| ||||||||||
Qy     231 PTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    7
ID   Q91119         PRELIMINARY;   PRT;   117 AA.

AC   Q91119;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (GONADOTROPIN ALPHA
DE   CHAIN) (GTH-ALPHA).
OS   MORONE SAXATILIS (STRIPED BASS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   HASSIN S.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENSIS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
DR   EMBL; L35071; G2322657; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    117       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     34     57       BY SIMILARITY.
FT   DISULFID     37     86       BY SIMILARITY.
FT   DISULFID     54    107       BY SIMILARITY.
FT   DISULFID     58    109       BY SIMILARITY.
FT   DISULFID     85    112       BY SIMILARITY.
FT   CARBOHYD     78     78       POTENTIAL.
FT   CARBOHYD    103    103       POTENTIAL.
SQ   SEQUENCE   117 AA;  13066 MW;  CAFB9D0C CRC32;

  Query Match           19.8%;  Score 433;  DB 12;  Length 117;
  Best Local Similarity  65.5%;  Pred. No. 3.90e-80;
  Matches    57;  Conservative   14;  Mismatches  12;  Indels   4;  Gaps   4;

Db      33 GCEECTLRKNSVFSR-DRPVYQCMGCCFSRAYPTPLKAMKTMTIPKNITSEATCCVAKHS 91
           || ||||: |: ||:   |: |||||||||||||:::||| : ||:|||:|||||| |
Qy     199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK-S 257

Db      92 YE-TEV-AGIKVRNHTDCHCSTCYFHK 116
           |:   | :|:|| ||| |||||||:||
Qy     258 YNRVTVMGGFKVENHTACHCSTCYYHK 284


RESULT    8
ID   Q62589         PRELIMINARY;   PRT;    55 AA.

AC   Q62589;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   ALPHA SUBUNIT OF GLYCOPROTEIN HORMONES (FRAGMENT).
OS   PHODOPUS SUNGORUS (STRIPED HAIRY-FOOTED HAMSTER) (DJUNGARIAN HAMSTER).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 96198779.
RA   BOCKMANN J., BOCKERS T.M., VENNEMANN B., NIKLOWITZ P., MULLER J.,
RA   WITTKOWSKI W., SABEL B., KREUTZ M.R.;
RL   ENDOCRINOLOGY 137:1804-1813(1996).
DR   EMBL; X90776; E195654; -.
FT   NON_TER       1      1
SQ   SEQUENCE   55 AA;  6047 MW;  E5AAE0F8 CRC32;

  Query Match           15.3%;  Score 334;  DB 10;  Length 55;
  Best Local Similarity  76.4%;  Pred. No. 2.97e-55;
  Matches    42;  Conservative    6;  Mismatches   7;  Indels   0;  Gaps   0;

Db       1 PTPARSKKTMLVPKNITSEATCCVAKAFTKATVMGNARVENHTECHCSTCYYHKS 55
           ||| |||||||| ||:|||:|||||:: : ||||  :|||| ||||||||||
Qy     231 PTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285


RESULT    9
ID   O14866         PRELIMINARY;   PRT;   277 AA.

AC   O14866;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   SOLUBLE DEATH RECEPTOR 3 BETA.
GN   DR3.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026071; G2570833; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   277 AA;  29111 MW;  06E165C7 CRC32;

  Query Match           11.4%;  Score 249;  DB 2;  Length 277;
  Best Local Similarity  31.8%;  Pred. No. 1.12e-34;
  Matches    57;  Conservative   31;  Mismatches  76;  Indels  15;  Gaps  11;

Db      13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
           ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  |  ::
Qy       3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db      69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
             |  |   :| | |||     |  |  |  : :|| : :|:   || |||:   :     |
Qy      62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db     129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPPSL 186
           : :    | |  ||: |::|    | |  :::| | || :||: : : ||||:    ||
Qy     120 ENLFQC-FNCTLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSL 171


RESULT   10
ID   O14865         PRELIMINARY;   PRT;   426 AA.
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AC   O14865;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   DEATH RECEPTOR 3 BETA.
GN   DR3.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026070; G2570831; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   426 AA;  45950 MW;  87E00821 CRC32;

  Query Match           11.4%;  Score 249;  DB 2;  Length 426;
  Best Local Similarity  31.8%;  Pred. No. 1.12e-34;
  Matches    57;  Conservative   31;  Mismatches  76;  Indels  15;  Gaps  11;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  | ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
           |  |   :| | |||    |  |  |  : :|| : :|:   || |||:   :     |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPPSL 186
          : :    | |  ||: |::|    | |  :::| | || :||: : : ||||:    ||
Qy    120 ENLFQC-FNCTLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSL 171


RESULT   11
ID   O00276         PRELIMINARY;   PRT;   253 AA.

AC   O00276;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94503; G2071953; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   253 AA;  26934 MW;  A21C863E CRC32;

  Query Match           11.3%;  Score 247;  DB 2;  Length 253;
  Best Local Similarity  31.8%;  Pred. No. 3.31e-34;
  Matches    55;  Conservative   31;  Mismatches  72;  Indels  15;  Gaps  11;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  | ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
           |  |   :| | |||    |  |  |  : :|| : :|:   || |||:   :     |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
          : :    | |  ||: |::|    | |  :::| | || :||: : : ||||:
Qy    120 ENLFQC-FNCTLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCS 165


RESULT   12
ID   O00280         PRELIMINARY;   PRT;   380 AA.

AC   O00280;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94510; G2071967; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   380 AA;  41192 MW;  17C92A14 CRC32;

  Query Match           11.3%;  Score 247;  DB 2;  Length 380;
  Best Local Similarity  31.8%;  Pred. No. 3.31e-34;
  Matches    55;  Conservative   31;  Mismatches  72;  Indels  15;  Gaps  11;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
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Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
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Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
          : :    | |  ||: |::|    | |  :::| | || :||: : : ||||:
Qy    120 ENLFQC-FNCTLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCS 165


RESULT   13
ID   O00275         PRELIMINARY;   PRT;   418 AA.

AC   O00275;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94502; G2071951; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   418 AA;  45456 MW;  3D04954A CRC32;

  Query Match           11.3%;  Score 247;  DB 2;  Length 418;
  Best Local Similarity  31.8%;  Pred. No. 3.31e-34;
  Matches    55;  Conservative   31;  Mismatches  72;  Indels  15;  Gaps  11;

Db     13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
          ::|||   ||  :: | |:  : |   | : |     :||  |  | ||   |  | ::
Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
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Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
          : :    | |  ||: |::|    | |  :::| | || :||: : : ||||:
Qy    120 ENLFQC-FNCTLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCS 165
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RESULT   14
ID   Q85407         PRELIMINARY;   PRT;   348 AA.

AC   Q85407;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   HOMOLOG OF VACCINIA VIRUS CDS B28R.
GN   G2R.
OS   VARIOLA VIRUS.
OC   VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC   ORTHOPOXVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BANGLADESH-1975;
RX   MEDLINE; 94088747.
RA   MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
RA   KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
RL   NATURE 366:748-751(1993).
DR   EMBL; L22579; G439102; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   348 AA;  38075 MW;  2A911AF6 CRC32;

  Query Match            9.8%;  Score 214;  DB 11;  Length 348;
  Best Local Similarity  38.5%;  Pred. No. 1.52e-26;
  Matches    30;  Conservative   14;  Mismatches  32;  Indels   2;  Gaps   2;

Db     39 HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 96
          :::||  |  |||    | :   :|:|  | ||:||: :|||  ||||:  | :  |||
Qy     37 NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96

Db     97 RSCNTTHNRICECSPGYY 114
            ||   :: :| |    |
Qy     97 SSCTVDRDTVCGCRKNQY 114


RESULT   15
ID   Q89118         PRELIMINARY;   PRT;   349 AA.

AC   Q89118;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   SOMALIA-1977 RIGHT NEAR-TERMINAL REGION.
OS   VARIOLA VIRUS.
OC   VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC   ORTHOPOXVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SOMALIA-1977;
RA   MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,
RA   TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;
RL   SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U18341; G885855; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   349 AA;  38272 MW;  0FDCC784 CRC32;

  Query Match            9.8%;  Score 214;  DB 11;  Length 349;
  Best Local Similarity  38.5%;  Pred. No. 1.52e-26;
  Matches    30;  Conservative   14;  Mismatches  32;  Indels   2;  Gaps   2;

Db     40 HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 97
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Qy     37 NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96

Db     98 RSCNTTHNRICECSPGYY 115
            ||   :: :| |    |
Qy     97 SSCTVDRDTVCGCRKNQY 114


Search completed: Wed May  6 09:00:25 1998
Job time : 72 secs.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:22:01 1998; MasPar time 1326.51 Seconds
1499.916 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-7
Description: (1-1301) from US08804166.seq
Perfect Score: 1301
N.A. Sequence: 1 CTCGAGATGGCTACAGGTAA.....CACAATAAGGATCCCTCGAG 1301
Comp: GAGCTCTACCGATGTCCATT.....GTGTTATTCCTAGGGAGCTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl53
1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
13:em_pat
Database: genbank105
14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
26:gb_htg 27:gb_prl 28:gb_pr2

Statistics: Mean 11.236; Variance 5.267; scale 2.134

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	514	39.5	1331	25	A29103	H.sapiens mRNA for TNF	0.00e+00
2	514	39.5	1368	25	A29098	Synthetic DNA for TNF-	0.00e+00
3	514	39.5	2050	27	HUMTNFRP	Human tumor necrosis f	0.00e+00
4	514	39.5	2062	25	A21522	TNF alpha gene.	0.00e+00
5	514	39.5	2062	25	I43805	Sequence 24 from paten	0.00e+00
6	514	39.5	2087	27	HUMTNFR	Human tumor necrosis f	0.00e+00
7	514	39.5	2111	25	A26412	cDNA for (55kD TNF-BP)	0.00e+00
8	514	39.5	2111	27	HUMTNFRB	Homo sapiens tumor nec	0.00e+00
9	514	39.5	2112	27	HUMTNFRC	Human tumor necrosis f	0.00e+00
10	514	39.5	2161	27	HSTNFR1A	H.sapiens TNF-R mRNA f	0.00e+00
11	514	39.5	2175	25	A43873	Sequence 1 from Patent	0.00e+00
12	514	39.5	2175	25	I64751	Sequence 1 from patent	0.00e+00
13	514	39.5	2176	25	A19907	Synthetic nucleotide s	0.00e+00
14	514	39.5	6889	25	I26928	Sequence 2 from patent	0.00e+00
15	507	39.0	2061	25	A20255	55kD receptor gene for	0.00e+00
16	483	37.1	483	25	A29099	Synthetic DNA for TNF-	0.00e+00
17	477	36.7	510	25	A21525	oligonucleotide probe.	0.00e+00
18	478	36.7	600	25	A20257	Synthetic nucleotide s	0.00e+00
19	474	36.4	600	25	I43808	Sequence 47 from paten	0.00e+00
20	420	32.3	539	27	HUMCGB	Human chorionic gonado	0.00e+00
21	383	29.4	504	25	I43813	Sequence 56 from paten	0.00e+00
22	383	29.4	504	25	A20713	Synthetic nucleotide s	0.00e+00
23	381	29.3	501	25	I43786	Sequence 1 from patent	0.00e+00
24	374	28.7	500	25	A20254	Synthetic nucleotide 5	5.06e-297
25	372	28.6	372	25	A20253	Synthetic nucleotide 5	3.19e-295
26	372	28.6	372	25	I43787	Sequence 3 from patent	3.19e-295
27	354	27.2	474	25	A20259	Synthetic nucleotide s	4.88e-279
28	354	27.2	474	25	I43809	Sequence 49 from paten	4.88e-279
29	336	25.8	642	27	BABBCGA	Baboon beta-chorionic	7.02e-263
30	332	25.5	66495	27	HUMGHCSA	Human growth hormone (	2.71e-259
31	313	24.1	581	15	FCU72344	Felis catus tumour nec	2.83e-242
32	314	24.1	1665	27	HSGG02	Human chorionic gonado	3.60e-243
33	312	24.0	468	27	HUMCGBBA3	Human chorionic gonado	2.22e-241
34	312	24.0	475	27	HUMCGBEL03	Human chorionic gonado	2.22e-241
35	312	24.0	1665	27	HSCG01	Human chorionic gonado	2.22e-241
36	307	23.6	2004	15	SSU19994	Sus scrofa p55 TNF rec	6.58e-237
37	305	23.4	1826	25	I02855	Sequence 1 from Patent	4.04e-235
38	304	23.4	1964	27	HSGROW2	Human germ line gene f	3.16e-234
39	304	23.4	1964	27	HUMGH	Human growth hormone (	3.16e-234
40	304	23.4	2771	25	I41411	Sequence 5 from patent	3.16e-234
41	303	23.3	2657	27	HUMGHN	Human growth hormone g	2.48e-233
42	303	23.3	4283	25	I63120	Sequence 3 from patent	2.48e-233
43	285	21.9	426	25	I08477	Sequence 18 from Paten	2.90e-217
44	267	20.5	2130	14	RATTNFR	Rat tumor necrosis fac	3.10e-201
45	257	19.8	477	25	A20263	Synthetic nucleotide s	2.38e-192

ALIGNMENTS

```
RESULT    1
LOCUS       A29103       1331 bp    DNA             PAT       03-JUL-1995

DEFINITION  H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29103
NID         g1247517
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1331)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 53 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1. .1331
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      298 a    407 c    343 g    283 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 25;  Length 1331;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    333 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    393 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    453 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524
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Db    513 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 572
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    573 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    633 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    693 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    753 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 812
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    813 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 846
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    2
LOCUS       A29098       1368 bp    DNA             PAT       03-JUL-1995

DEFINITION  Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION   A29098
NID         g1248892
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1368)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 48 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1. .1368
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BASE COUNT      293 a    424 c    375 g    276 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 25;  Length 1368;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 634
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    3
LOCUS       HUMTNFRP     2050 bp    mRNA            PRI       11-OCT-1991

DEFINITION  Human tumor necrosis factor receptor(TNF) mRNA, complete cds.
ACCESSION   M60275 M37764
NID         g339759
KEYWORDS    TNF receptor; transmembrane receptor; tumor necrosis factor
            receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2050)
  AUTHORS   Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.
  TITLE     Cloning of human tumor necrosis factor (TNF) receptor cDNA and
            expression of recombinant soluble TNF-binding protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
  MEDLINE   91017509
COMMENT     Draft entry and computer-readable sequence for [Proc. Natl. Acad.
            Sci. U.S.A. (1990) In press] kindly submitted
            by P.W.Gray, 13-AUG-1990.
FEATURES             Location/Qualifiers
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                     /tissue_type="placenta"
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     CDS             155. .1516
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                     /db_xref="PID:g339760"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
                     PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
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                     GRCLREAQYSMLATWRRRTRREATLELLGRVLRDMDLLGCLEDIEEALCAPPLPPAPS
                     LLR"
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     mat_peptide     275. .1513
                     /product="TNF receptor"
BASE COUNT      429 a    611 c    566 g    444 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 27;  Length 2050;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 788
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    4
LOCUS       A21522       2062 bp    RNA             PAT       26-JUL-1994

DEFINITION  TNF alpha gene.
ACCESSION   A21522
NID         g579599
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   .
  JOURNAL   Patent: GB 2246569-A 1 05-FEB-1992;
FEATURES             Location/Qualifiers
     source          1. .2062
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                     /db_xref="taxon:9606"
     gene            155. .1522
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     CDS             155. .1522
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                     /codon_start=1
                     /db_xref="PID:g579600"
                     /db_xref="SWISS-PROT:P19438"
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                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
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BASE COUNT      429 a    617 c    573 g    443 t
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  Query Match           39.5%;  Score 514;  DB 25;  Length 2062;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
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Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 788
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    5
LOCUS       I43805       2062 bp    DNA             PAT       10-JUL-1997

DEFINITION  Sequence 24 from patent US 5633145.
ACCESSION   I43805
NID         g2468903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE     TNF.alpha. receptor-derived binding protein
  JOURNAL   Patent: US 5633145-A 24 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .2062
                     /organism="unknown"
BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 25;  Length 2062;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 634
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 788
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
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RESULT    6
LOCUS       HUMTNFR      2087 bp    mRNA            PRI       10-NOV-1993

DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61, 361-370 (1990)
  MEDLINE   90235285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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     CDS             182. .1549
                     /note="tumor necrosis factor receptor"
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                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
                     PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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                     PSLLR"
BASE COUNT      433 a    624 c    581 g    449 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 27;  Length 2087;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db    302 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 361
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    362 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 421
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    422 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 481
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    482 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 541
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    542 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 601
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    602 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 661
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    662 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 721
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    722 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 781
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    782 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 815
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
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RESULT    7
LOCUS       A26412       2111 bp    DNA             PAT       26-APR-1995

DEFINITION  cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
            patent EP0417563.
ACCESSION   A26412
NID         g904968
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 24 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
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                     /organism="Artificial sequences"
     CDS             187. .1554
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                     /db_xref="PID:g904969"
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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BASE COUNT      445 a    629 c    587 g    450 t
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  Query Match           39.5%;  Score 514;  DB 25;  Length 2111;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    547 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    727 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 786
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    787 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 820
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    8
LOCUS       HUMTNFRB     2111 bp    mRNA            PRI       14-NOV-1990

DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID         g339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cell line HL60, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
  TITLE     Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
  JOURNAL   Cell 61, 351-359 (1990)
  MEDLINE   90235284
FEATURES             Location/Qualifiers
     source          1. .2111
                     /organism="Homo sapiens"
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                     /cell_line="HL60"
     sig_peptide     187. .273
                     /gene="TNF receptor"
                     /product="tumor necrosis factor receptor"
     CDS             187. .1554
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                     /note="55 kDa"
                     /codon_start=1
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                     /db_xref="PID:g339754"
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
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BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 27;  Length 2111;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    307 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    367 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    427 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 546
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    547 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 606
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    727 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    787 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 820
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    9
LOCUS       HUMTNFRC     2112 bp    mRNA            PRI       30-SEP-1991

DEFINITION  Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
            cds.
ACCESSION   M63121 M75861
NID         g339755
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2112)
  AUTHORS   Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
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          Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C. and
          Adolf,G.R.
  TITLE   Molecular cloning and expression of human and rat tumor necrosis
          factor receptor chain (p60) and its soluble derivative, tumor
          necrosis factor-binding protein
  JOURNAL DNA Cell Biol. 9, 705-715 (1990)
  MEDLINE 91090841
FEATURES             Location/Qualifiers
     source          1. .2112
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     sig_peptide     207. .293
                     /gene="TNF receptor"
     CDS             207. .1574
                     /gene="TNF receptor"
                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /db_xref="PID:g339756"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
                     PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
                     SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
                     GRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
                     PSLLR"
     gene            207. .1574
                     /gene="TNF receptor"
     mat_peptide     294. .1571
                     /gene="TNF receptor"
                     /product="tumor necrosis factor receptor"
BASE COUNT      435 a    632 c    589 g    456 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 27;  Length 2112;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    327 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 386
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    387 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 446
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    447 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 506
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    507 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 566
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    567 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 626
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    627 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 686
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    687 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 746
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    747 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 806
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    807 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 840
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT   10
LOCUS       HSTNFR1A     2161 bp    RNA             PRI       18-JAN-1993

DEFINITION  H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION   X55313
NID         g37223
KEYWORDS    TNF-R gene; tumor necrosis factor receptor 1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2161)
  AUTHORS   Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
            Aderka,D., Holtmann,H. and Wallach,D.
  TITLE     Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
            for the type I TNF-R, cloned using amino acid sequence data of its
            soluble form, encodes both the cell surface and a soluble form of
            the receptor
  JOURNAL   EMBO J. 9 (10), 3269-3278 (1990)
  MEDLINE   91006021
FEATURES             Location/Qualifiers
     source          1. .2161
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /gene="TNF-R"
     CDS             256. .1623
                     /gene="TNF-R"
                     /codon_start=1
                     /product="tumor necrosis factor receptor type 1"
                     /db_xref="PID:g37224"
                     /db_xref="SWISS-PROT:P19438"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
                     PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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     repeat_region   505. .633
                     /gene="TNF-R"
     repeat_region   634. .756
                     /gene="TNF-R"
     repeat_region   757. .857
                     /gene="TNF-R"
     polyA_signal    2145. .2150
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                     /note="putative"
     polyA_site      2161
                     /gene="TNF-R"
BASE COUNT      459 a    642 c    604 g    456 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 27;  Length 2161;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 889
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
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RESULT   11
LOCUS       A43873       2175 bp    DNA             PAT       06-MAR-1997

DEFINITION  Sequence 1 from Patent EP0657536.
ACCESSION   A43873
NID         g2299022
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Proteases capable of shedding the soluble TNF-receptor and TNF-R
            derived peptides and antibodies against the proteases inhibiting
            the shedding
  JOURNAL   Patent: EP 0657536-A 1 14-JUN-1995;
            YEDA RES & DEV (IL)
COMMENT     Other publication ZA 9407962 951121
            Other publication JP 7194376 950801
            Other publication AU 7574294 950504
            Other publication CA 2133872 950413.
FEATURES             Location/Qualifiers
     source          1. .2175
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     CDS             256. .1623
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                     /db_xref="PID:g2299023"
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                     SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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                     PSLLR"
BASE COUNT      474 a    641 c    604 g    456 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 25;  Length 2175;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
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Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
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Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Db    796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 889
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
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RESULT   12
LOCUS       I64751       2175 bp    DNA             PAT       26-SEP-1997

DEFINITION  Sequence 1 from patent US 5665859.
ACCESSION   I64751
NID         g2481645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Molecules influencing the shedding of the TNF receptor, their
            preparation and their use
  JOURNAL   Patent: US 5665859-A 1 09-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .2175
                     /organism="unknown"
BASE COUNT      474 a    641 c    604 g    456 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 25;  Length 2175;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

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Db    796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 889
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT   13
LOCUS       A19907       2176 bp    DNA             PAT       04-OCT-1994

DEFINITION  Synthetic nucleotide sequence Type I TNF receptor gene.
ACCESSION   A19907
NID         g641222
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2176)
  AUTHORS   Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
            Aderka,D.
  TITLE     Expression of the recombinant tumor necrosis factor binding protein
            I (TBP-I)
  JOURNAL   Patent: EP 0433900-A 28 26-JUN-1991;
            YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED
FEATURES             Location/Qualifiers
     source          1. .2176
                     /organism="Artificial sequences"
BASE COUNT      474 a    642 c    604 g    456 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 25;  Length 2176;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
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Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 795
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 889
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT   14
LOCUS       I26928       6889 bp    DNA             PAT       01-OCT-1996

DEFINITION  Sequence 2 from patent US 5561053.
ACCESSION   I26928
NID         g1606798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6889)
  AUTHORS   Crowley,C.W.
  TITLE     Method for selecting high-expressing host cells
  JOURNAL   Patent: US 5561053-A 2 01-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .6889
                     /organism="unknown"
BASE COUNT     1729 a   1826 c   1681 g   1653 t
ORIGIN

  Query Match           39.5%;  Score 514;  DB 25;  Length 6889;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1725 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 1784
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1844
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   1845 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 2204
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Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824
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Db   2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT   15
LOCUS       A20255       2061 bp    DNA             PAT       20-SEP-1995

DEFINITION  55kD receptor gene for human TNF-alpha.
ACCESSION   A20255
NID         g1247401
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2061)
  AUTHORS   .
  TITLE     MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL   Patent: WO 9207076-A 23 30-APR-1992;
FEATURES             Location/Qualifiers
     source          1. .2061
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      429 a    616 c    573 g    443 t
ORIGIN

  Query Match           39.0%;  Score 507;  DB 25;  Length 2061;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   513;  Conservative    0;  Mismatches   0;  Indels   1;  Gaps   1;

Db    275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCAC-TCTCCTGCCAGGAG 633
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Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    634 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 693
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Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    694 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    754 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 787
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


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MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:           Wed May  6 15:05:10 1998;  MasPar time 167.20 Seconds
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Tabular output not generated.

Title:            >US-08-804-166-7
Description:      (1-1301) from US08804166.seq
Perfect Score:    1301
N.A. Sequence:         1 CTCGAGATGGCTACAGGTAA.........CACAATAAGGATCCCTCGAG 1301
     Comp:               GAGCTCTACCGATGTCCATT.........GTGTTATTCCTAGGGAGCTC

Scoring table:    TABLE default
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Nmatch   STD :    Dbase 0;  Query 0

Searched:         159651 seqs, 57698962 bases x 2

Post-processing:  Minimum Match 0%
                  Listing first 45 summaries

Database:         n-geneseq30
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                    8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                    14:part14 15:part15 16:part16 17:part17 18:part18
                    19:part19 20:part20 21:part21 22:part22 23:part23
                    24:part24 25:part25 26:part26 27:part27 28:part28
                    29:part29 30:part30 31:part31 32:part32 33:part33

Statistics:       Mean 9.269;  Variance 5.321;  scale 1.742

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

Result          %
   No.  Score  Query  Length DB  ID          Description            Pred. No.
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    1    514   39.5    1334  1  Q06282      Plasmid Tumour Necros  0.00e+00
    2    514   39.5    1368  8  Q49932      Lambda-derived TNF-R   0.00e+00
    3    514   39.5    2062  4  Q24440      Encodes TNF-alpha 55k  0.00e+00
    4    514   39.5    2062  3  Q20973      TNF-alpha binding pro  0.00e+00
    5    514   39.5    2088  2  Q10883      30kD TNF inhibitor pr  0.00e+00
    6    514   39.5    2111  2  Q10955      Encodes human 55kD TN  0.00e+00
    7    514   39.5    2175 15  Q90513      p55 TNF-R gene.        0.00e+00
    8    514   39.5    6889 18  T15931      DHFR/intron (WTrasSD)  0.00e+00
    9    512   39.4    2141  1  Q06285      Human Tumour Necrosis  0.00e+00
   10    512   39.4    2176  2  Q12215      Type I TNF receptor.   0.00e+00
   11    510   39.2    2170  9  Q50870      p55 Tumour necrosis f  0.00e+00
   12    478   36.7     608  4  Q24441      Encodes truncated TNF  0.00e+00
   13    416   32.0     579  3  Q14800      Human chorionic gonad  6.61e-279
   14    415   31.9     836 17  T03212      Single chain gonadotr  3.64e-278
   15    415   31.9     836 17  T03243      Single chain gonadotr  3.64e-278
   16    411   31.6     575 17  T03240      Human CG beta-subunit  3.34e-275
   17    383   29.4     504  4  Q24445      Encodes truncated TNF  1.75e-254
   18    354   27.2     474  4  Q24442      Encodes truncated TNF  4.64e-233
   19    321   24.7     743 17  T03219      Single chain gonadotr  9.76e-209
   20    304   23.4    2771 31  T76770      Rat Fabpl gut-specifi  3.12e-196
   21    303   23.3    2160 33  T62826      Human growth hormone   1.69e-195
   22    296   22.8     336  6  Q41459      Human growth hormone   2.35e-190
   23    285   21.9     426  2  N60524      Sequence encoding hum  2.78e-182
   24    282   21.7     743 17  T03231      Single chain gonadotr  4.41e-180
   25    282   21.7     743 17  T03233      Single chain gonadotr  4.41e-180
   26    282   21.7     752 17  T03229      Single chain gonadotr  4.41e-180
   27    276   21.2     744 17  T03221      Single chain gonadotr  1.10e-175
   28    267   20.5     752 17  T03227      Single chain gonadotr  4.31e-169
   29    259   19.9    2173  1  Q06284      Rat Tumour Necrosis F  3.07e-163
   30    257   19.8     477  4  Q24444      Encodes truncated TNF  8.89e-162
   31    221   17.0     462  4  Q24443      Encodes truncated TNF  1.56e-135
   32    215   16.5     525  1  Q03844      Bovine beta LH subuni  3.57e-131
   33    213   16.4     540  1  Q03851      Porcine beta LH subun  1.01e-129
   34    208   16.0    2660  4  N30032      Sequence of gene for   4.28e-126
   35    188   14.5     496  2  N60523      Sequence encoding dog  1.26e-111
   36    185   14.2     611  1  Q03848      Equine beta LH subuni  1.84e-109
   37    132   10.1    1027  2  Q10878      Partial sequence of c  1.41e-71
   38    101    7.8     114  2  N60522      Sequence encoding ami  7.09e-50
   39     99    7.6     138 13  Q80819      LH-beta -5 to 41 frag  1.71e-48
c  40     79    6.1    1047  2  Q10572      Human Natriuretic Pep  7.76e-35
   41     73    5.6    1047  2  Q10572      Human Natriuretic Pep  8.20e-31
   42     72    5.5     114  6  Q34669      DNA encoding hCG beta  3.81e-30
   43     71    5.5     651  2  N71239      Sequence encoding hum  1.76e-29
   44     71    5.5     700  2  N60678      Sequence encoding pre  1.76e-29
   45     71    5.5    3557  2  N60801      Human pro-growth horm  1.76e-29

                              ALIGNMENTS

RESULT    1
ID   Q06282 standard; DNA; 1334 BP.
AC   Q06282;
DT   29-JAN-1991  (first entry)
DE   Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             213..1325
FT   /*tag=  a
FT   /product=TNF-BP
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   P-PSDB; R07449.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   pTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC   from induced TNF-induced fibrosarcoma cells.  A TNF-BP had been
CC   isolated from the urine of patients with uraemia and probes/primers
CC   were constructed from the determined amino acid sequence.
CC   To produce a vector expressing a soluble form of TNF-binding
CC   protein, this plasmid was cut with XmmI, amplified by PCR and the
CC   amplified DNA cut with BamHI and EcoRI.
CC   The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC   (BRL) cut with the same enzymes to recover pTNF-BP.  This was cut
CC   with BamHI and EcoRI, and the recovered fragment inserted into
CC   pAD-CMV1 (Q06283) to give the required plasmid pADTNF-BP.
CC   See also Q06282-Q06285.
SQ   Sequence   1334 BP;     299 A;     409 C;     342 G;     284 T;

  Query Match             39.5%;  Score 514;  DB 1;  Length 1334;
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Db     333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 392
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Qy     345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
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Qy     405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db     453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
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Qy     465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db     513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
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Qy     525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db     573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 632
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Qy     585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db     633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
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Qy     645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db     693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
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Qy     705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db     753 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 812
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Qy     765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db     813 aatgttaagggcactgaggactcaggcaccacag 846
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Qy     825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    2
ID   Q49932 standard; cDNA to mRNA; 1368 BP.
AC   Q49932;
DT   29-APR-1994  (first entry)
DE   Lambda-derived TNF-R cDNA.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction; ss.
OS   Homo sapiens.
OS   Lambda-gt10-7-ctnfbp.
FH   Key             Location/Qualifiers
FT   CDS             1..1366
FT   /*tag= a
FT   /product= hTNF-R
FT   sig_peptide     1..120
FT   /*tag= b
FT   mat_peptide     121..1363
FT   /*tag= c
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   P-PSDB; R42059.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.

CC   The sequences given in Q49931-32 encode human tumour necrosis factor
CC   receptor (TNF-R) and the sequences in Q49933-34 encode human
CC   interleukin-1 receptor (IL-1R).  These sequences were used in the
CC   production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence   1368 BP;    292 A;    424 C;    376 G;    276 T;

  Query Match           39.5%;  Score 514;  DB 8;  Length 1368;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     121 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 180
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Qy     345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db     181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 240
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Qy     405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db     241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
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Qy     465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db     301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
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Qy     525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db     361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 420
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Qy     585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db     421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
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Qy     645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db     481 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 540
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Db     541 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 600
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Db     601 aatgttaagggcactgaggactcaggcaccacag 634
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Qy     825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    3
ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-NOV-1992  (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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FT   /note= "3"
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FT   /*tag= c
FT   /codon= seq:"TGG", aa:Thr
FT   mat_peptide     1258..1260
FT   /*tag= d
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FT   mat_peptide     1433..1435
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FT   /codon= Seq:"GAC", aa:Asn
FT   sig_peptide     156..274
FT   /*tag= f
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24000
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Claim 4; Fig 1; 43pp; English.
CC   This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC   library in gt10 was screened with probe Q29236. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in prTNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain. PCR with primers Q29237,8 generated a 300bp
CC   restriction fragment which was cloned into prTNFR, giving pTNFRecd.
CC   DNA sequencing confirmed this contained the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   2062 BP;    429 A;    618 C;    572 G;    443 T;

  Query Match           39.5%;  Score 514;  DB 4;  Length 2062;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
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Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
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Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
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Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    755 aatgttaagggcactgaggactcaggcaccacag 788
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    4
ID   Q20973 standard; DNA; 2062 BP.
AC   Q20973;
DT   11-MAY-1992  (first entry)
DE   TNF-alpha binding protein gene.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             155..1522
FT   /*tag= a
FT   sig_peptide     155..274
FT   /*tag= b
FT   mat_peptide     275..1522
FT   /*tag= c
FT   misc_feature    473..532
FT   /*tag= d
FT   /note= "homologous to probe Q20974"
FT   misc_feature    242..751
FT   /*tag= e
FT   /note= "encodes the extracellular domain of human
FT   TNF alpha receptor"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding tumour necrosis factor alpha
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence   2062 BP;    429 A;    616 C;    573 G;    444 T;

  Query Match           39.5%;  Score 514;  DB 3;  Length 2062;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    395 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524
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Db    455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    575 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    635 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    695 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    755 aatgttaagggcactgaggactcaggcaccacag 788
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
```

```
RESULT    5
ID   Q10883 standard; cDNA; 2088 BP.
AC   Q10883;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
KW   Tumour necrosis factor; inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             171..1536
FT   /*tag= a
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   P-PSDB; R10986.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.  The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also Q10878, Q10884 and Q10907.
SQ   Sequence   2088 BP;    439 A;    626 C;    578 G;    445 T;

  Query Match           39.5%;  Score 514;  DB 2;  Length 2088;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    289 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    349 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    409 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524
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Db    469 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    529 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    589 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    649 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    709 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    769 aatgttaagggcactgaggactcaggcaccacag 802
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
```

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RESULT    6
ID   Q10955 standard; cDNA; 2111 BP.
AC   Q10955;
DT   24-MAY-1991  (first entry)
DE   Encodes human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   sig_peptide     187..273
FT   /*tag= a
FT   mat_peptide     274..1551
FT   /*tag= b
FT   /product= 55kD TNF-BP
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   P-PSDB; R11082.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 4; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   2111 BP;    445 A;    628 C;    588 G;    450 T;

  Query Match           39.5%;  Score 514;  DB 2;  Length 2111;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    307 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
```

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Db    367 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    427 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    487 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    547 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    607 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    667 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    727 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    787 aatgttaagggcactgaggactcaggcaccacag 820
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
```

RESULT 7
ID Q90513 standard; DNA; 2175 BP.
AC Q90513;
DT 19-JAN-1996 (first entry)
DE p55 TNF-R gene.
KW p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW phorbol myristate acetate; PMA; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 256..1623
FT /*tag= a
FT /product= p55 TNF-R
FT misc_signal 2143..2149
FT /*tag= b
FT /note= "possible poly-A signal"
PN AU9475742-A.
PD 04-MAY-1995.
PF 11-OCT-1994; 075742.
PR 12-OCT-1993; IL-107268.
PA (YEDA) YEDA RES & DEV CO LTD.
PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
DR WPI; 95-194342/26.
DR P-PSDB; R75084.
PT New protease capable of cleaving soluble tumour necrosis factor
PT (TNF) receptor - from cell-bound TNF- receptor, useful for
PT antagonising deleterious effects of TNF.
PS Disclosure; Fig 1; 40pp; English.
CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC Expression of this receptor is regulated by shedding of the extracellular
CC receptor fragment. The p55 TNF-R can be shed in response to different
CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC type. The only region of the receptor whose structure affects the
CC shedding response is the spacer region (see R75012) in the extracellular
CC domain. This region is located close to a site of cleavage of the
CC molecule, and links the Cys rich module to the transmembrane domain. The
CC spacer region of the encoded protein was used to create the chimeras
CC between human p55 TNF-R and murine epidermal growth factor receptor
CC (EGF-R) that are represented by R75007-11. This spacer region was
CC subjected to deletion mutations (R75013-25) and substitutions
CC (R75026-47). Of the spacer region, the most important residues are
CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC important of these. The shedding of the receptor is independent of the
CC side chain identity of these residues, with the exception of a limited
CC dependence on the identity of Val 173. Mutations which alter the
CC conformation of the protein adversely effect the shedding process. The
CC mutations shown in R75013-47 were introduced in order to create an
CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC be used for enhancing TNF function.
SQ Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;

Query Match 39.5%; Score 514; DB 15; Length 2175;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    856 aatgttaagggcactgaggactcaggcaccacag 889
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
```

RESULT 8
ID T15931 standard; DNA; 6889 BP.
AC T15931;
DT 20-JUN-1996 (first entry)
DE DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.
KW Recombinant host cell; dihydrofolate reductase; selectable marker;
KW DHFR; ras splice donor; dicistronic vector; gene expression;
KW immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
OS Synthetic.
PN WO9604391-A1.
PD 15-FEB-1996.
PF 28-JUL-1995; U09576.
PR 05-AUG-1994; US-286740.
PA (GETH) GENENTECH INC.
PI Crowley CW;
DR WPI; 96-129407/13.
PT Improved process for the selection of recombinant host cells
PT expressing high level of a desired product - uses eukaryotic host
PT cells contg. a DNA construct comprising a selectable gene

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PS   Example 2; Page 36-42; 137pp; English.
CC   A dicistronic vector (T15930) comprises a regulatory region
CC   derived from the cytomegalovirus immediate-early gene, a
CC   selectable dihydrofolate reductase gene positioned within an
CC   intron having a 5' wild-type ras splice donor site, a downstream
CC   sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
CC   tumour necrosis factor, and a poly-A sequence.  Transfection of CHO
CC   DHFR- cells and subsequent methotrexate amplification and growth of
CC   the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC   ug/ml (15-fold higher compared to conventional vector amplified
CC   pools).
SQ   Sequence   6889 BP;    1729 A;    1826 C;    1681 G;    1653 T;

  Query Match           39.5%;  Score 514;  DB 18;  Length 6889;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   514;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1725 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 1784
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   1785 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 1844
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   1845 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 1904
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 1964
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   1965 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 2024
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 2084
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 2144
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 2204
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db   2205 aatgttaagggcactgaggactcaggcaccacag 2238
         |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT    9
ID   Q06285 standard; DNA; 2141 BP.
AC   Q06285;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   lambdaTNF-R2; raTNF-R8; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             213..1577
FT   /*tag=  a
FT   /label=huTNF-R
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   P-PSDB; R07451.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).
CC   See also Q06282-Q06285.
SQ   Sequence   2141 BP;    455 A;    633 C;    593 G;    460 T;

  Query Match           39.4%;  Score 512;  DB 1;  Length 2141;
  Best Local Similarity 99.8%;  Pred. No. 0.00e+00;
  Matches   513;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    453 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    513 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    633 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    693 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    753 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattcag 812
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    813 aatgttaagggcactgaggactcaggcaccacag 846
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT   10
ID   Q12215 standard; DNA; 2176 BP.
AC   Q12215;
DT   12-SEP-1991  (first entry)
DE   Type I TNF receptor.
KW   Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   terminator      244..246
FT   /*tag=  a
FT   /note= "in-frame termination codon"
FT   CDS             256..1620
FT   /*tag=  a
FT   /product= type I TNF receptor
FT   sig_peptide     256..318
FT   /*tag=  b
FT   mat_peptide     319..1620
FT   /*tag=  c
FT   misc_RNA        319..864
FT   /*tag=  d
```

```
FT   /label= soluble_domain
FT   /note= "may be 2 codons shorter or a few codons
FT   longer"
FT   misc_feature    376..414
FT   /*tag= e
FT   /note= "TBP-I derived sequence"
FT   misc_feature    583..627
FT   /*tag= f
FT   /note= "TBP-I derived sequence"
FT   misc_feature    850..858
FT   /*tag= g
FT   /note= "TBP-I derived sequence"
FT   misc_RNA        889..957
FT   /*tag= h
FT   /label= transmembrane_domain
FT   repeat_unit     385..504
FT   /*tag= i
FT   /number= 1
FT   repeat_unit     505..633
FT   /*tag= j
FT   /number= 2
FT   repeat_unit     634..756
FT   /*tag= k
FT   /number= 3
FT   repeat_unit     757..858
FT   /*tag= l
FT   /number= 4
FT   polyA_signal    2145..2150
FT   /*tag= m
PN   EP-433900-A.
PD   26-JUN-1991.
PF   13-DEC-1990; 124133.
PR   13-DEC-1989; IL-092697.
PR   12-JUL-1990; IL-095064.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI   Aderka D;
DR   WPI; 91-186774/26.
DR   P-PSDB; R12550.
PT   Recombinant tumour necrosis factor binding protein I - prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PT   acid encoding human type T TNF receptor or soluble domain
PS   Disclosure; Fig 1(D); 30pp; English.
CC   The Tumour Necrosis Factor Binding Protein I is the soluble form of
CC   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA.  The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also Q12212-15.
SQ   Sequence   2176 BP;    475 A;    644 C;    602 G;    455 T;

  Query Match           39.4%;  Score 512;  DB 2;  Length 2176;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   513;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgcagtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    856 aatgttaagggcactgaggactcaggcaccacag 889
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


RESULT   11
ID   Q50870 standard; DNA; 2170 BP.
AC   Q50870;
DT   13-MAY-1994  (first entry)
DE   p55 Tumour necrosis factor receptor coding sequence.
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT   /*tag= a
FT   /product= p55 Tumour necrosis factor receptor.
PN   EP-568925-A.
PD   10-NOV-1993.
PF   29-APR-1993; 106981.
PR   03-MAY-1992; IL-101769.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Brakebusch C,  Wallach D;
DR   WPI; 93-353057/45.
DR   P-PSDB; R42197.
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
PS   Claim 2; Figure 1; 17pp; English.
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor.  This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock.  They can also
CC   be used to treat overdoses of exogenous TNF.
SQ   Sequence   2170 BP;    474 A;    657 C;    584 G;    455 T;

  Query Match           39.2%;  Score 510;  DB 9;  Length 2170;
  Best Local Similarity  99.6%;  Pred. No. 0.00e+00;
  Matches   512;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    376 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    496 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524
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Db    556 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    676 ttccagtgcttcaattgcagcctctgcctcaatgcgaccgtgcacctctcctgccaggag 735
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    796 tcctgtagtaactgtaagaaaagcctgcagtgcacgaagttgtgcctaccccagattgag 855
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db    856 aatgttaagggcactgaggactcaggcaccacag 889
          |||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
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RESULT   12
ID   Q24441 standard; DNA; 608 BP.
AC   Q24441;
DT   05-NOV-1992  (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (197 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24080.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
CC   derivative, as present in pTNFRecd. This was produced as described in
CC   Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC   the cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   608 BP;    148 A;    159 C;    165 G;    136 T;

  Query Match           36.7%;  Score 478;  DB 4;  Length 608;
  Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
  Matches   479;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    129 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db    189 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db    249 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db    309 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db    369 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccttt 428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db    429 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db    489 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db    549 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagatttag 608
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy    765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824
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RESULT   13
ID   Q14800 standard; DNA; 579 BP.
AC   Q14800;
DT   11-FEB-1992  (first entry)
DE   Human chorionic gonadotropin beta subunit analogue.
KW   Glycoprotein hormone; hCGB'; fertility; immuno-castration;
KW   immuno-contragestive; vaccine; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             26..523
FT   /*tag= a
FT   mat_peptide     86..520
FT   /*tag= b
FT   sig_peptide     26..85
FT   /*tag= c
FT   polyA_site      524..579
FT   /*tag= d
FT   mutation        229
FT   /*tag= e
FT   /note="c -> g"
FT   mutation        232
FT   /*tag= f
FT   /note="c -> g"
PN   WO9116922-A.
PD   14-NOV-1991.
PF   07-MAY-1991; U03162.
PR   08-MAY-1990; US-520703.
PA   (UYNE-) UNIV MED NEW JERSEY.
PI   Campbell RK, Moyle WR;
DR   WPI; 91-353528/48.
DR   P-PSDB; R15043.
PT   New glyco-protein hormone analogues - for inducing fertility as
PT   immuno-castration agents, for suppressing reproductive system
PT   development and as immuno-contragestive vaccines.
PS   Example 3; Fig 4a; 94pp; English.
CC   The sequence is an analogue of hCG beta subunit cDNA contg. two
CC   silent mutations which eliminate restriction sites. It was prepd.
CC   from the plasmid pKMB-hCG-beta, a construct contg. the hCG beta
CC   subunit isolated from human placenta (Fiddes and Goodman) in
CC   plasmid pKMB, a derivative of pUC18 designed to facilitate cloning
CC   of glycoprotein hormones. The sequence was used as the starting
CC   construct for many mutants. (See R15061-R15125 and R15161-R15198).
SQ   Sequence   579 BP;    128 A;    205 C;    151 G;    95 T;

  Query Match           32.0%;  Score 416;  DB 3;  Length 579;
  Best Local Similarity  99.5%;  Pred. No. 6.61e-279;
  Matches   418;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    104 ccacggtgccgccccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    870 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 929

Db    164 atcaccgtcaacaccaccatctgtgccggctactgccccaccatgacccgcgtgctgcag 223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    930 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 989

Db    224 ggggtgctcccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 283
          ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    990 GGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 1049

Db    284 atccggctccctggctgcccgcgcggcgtgaaccccgtggtctcctacgccgtggctctc 343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1050 ATCCGGCTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTC 1109

Db    344 agctgtcaatgtgcactctgccgccgcagcaccactgactgcgggggtcccaaggaccac 403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1110 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1169

Db    404 cccttgacctgtgatgaccccgcttccaggactcctcttcctcaaaggcccctcccccc 463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1170 CCCTTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCC 1229

Db    464 agccttccaagcccatcccgactcccggggccctcggacaccccgatcctcccacaataa 523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1230 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGATCCTCCCACAATAA 1289
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RESULT 14
ID T03212 standard; cDNA; 836 BP.
AC T03212;
DT 26-APR-1996 (first entry)
DE Single chain gonadotropin analogue 1 coding sequence.
KW Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS Synthetic.

FH	Key	Location/Qualifiers
FT	CDS	33..830
FT	/*tag= a	
FT	/transl_except=	pos:240..242, aa:Arg
FT	sig_peptide	33..92
FT	/*tag= b	
FT	mat_peptide	93..827
FT	/*tag= c	
FT	/label= Analogue_1	
FT	/note= "nucleotides 93..527 encode amino acids	
FT	1-145 of hCG beta-subunit; nucleotides	
FT	528..551 encode a (Gly-Ser)4 linker and	
FT	nucleotides 552..827 encode amino acids	
FT	1-92 of gonadotropin alpha-subunit"	
FT	misc_feature	1..26
FT	/*tag= d	
FT	/label= sticky_end	
FT	/note= "single-strand overhang. The complementary	
FT	strand also has a single-strand overhang at	
FT	its 5'-end; the sequence of the overhang is	
FT	5'-TCCGGATTAGCTTGAGATGGATCC-3'"	

PN WO9522340-A1.
PD 24-AUG-1995.
PF 17-FEB-1995; U02067.
PR 18-FEB-1994; US-199382.
PA (SENS-) SENSI-TEST.
PI Moyle WR;
DR WPI; 95-302553/39.
DR P-PSDB; R86247.
PT Methods for altering fertility in mammals, esp. humans - e.g.
PT stimulating fertility by reducing the activity and/or levels of
PT circulating glyco:protein hormones having lutropin activity
PS Example 12; Fig 6; 102pp; English.
CC Analogue 1 (human CG-beta(1-145)-linker-human CG-alpha(1-92)) is a
CC specific example of a single chain gonadotropin having a chorionic
CC gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-
CC subunit at the C-terminus, joined by a linker of 1-16 amino acids.
CC The analogue has luteinising hormone (lutropin) activity and is
CC useful for inducing ovulation and increasing male fertility.
CC The sequences coding for analogue 1 were cloned from a human
CC placental cDNA library using strand overlap extension PCR.
SQ Sequence 836 BP; 166 A; 282 C; 222 G; 166 T;

Query Match 31.9%; Score 415; DB 17; Length 836;
Best Local Similarity 99.8%; Pred. No. 3.64e-278;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    111 ccacggtgccgccccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 170
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Qy    870 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 929

Db    171 atcaccgtcaacaccaccatctgtgccggctactgccccaccatgacccgcgtgctgcag 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    930 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 989

Db    231 ggggtcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    990 GGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 1049

Db    291 atccggctccctggctgcccgcgcggcgtgaaccccgtggtctcctacgccgtggctctc 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1050 ATCCGGCTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTC 1109

Db    351 agctgtcaatgtgcactctgccgccgcagcaccactgactgcgggggtcccaaggaccac 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1110 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1169

Db    411 cccttgacctgtgatgaccccgcttccaggactcctcttcctcaaaggcccctcccccc 470
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Qy   1170 CCCTTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCC 1229

Db    471 agccttccaagcccatcccgactcccggggccctcggacaccccgatcctccccaa 527
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy   1230 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGATCCTCCCACAA 1286
```

RESULT 15
ID T03243 standard; cDNA; 836 BP.
AC T03243;
DT 08-MAY-1996 (first entry)
DE Single chain gonadotropin analogue 1a coding sequence.
KW Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS Synthetic.

FH	Key	Location/Qualifiers
FT	CDS	33..830
FT	/*tag= a	
FT	/transl_except=	pos:240..242, aa:Arg
FT	sig_peptide	33..92
FT	/*tag= b	
FT	mat_peptide	93..827
FT	/*tag= c	
FT	/label= Analogue_1a	
FT	/note= "nucleotides 93..527 encode amino acids	
FT	1-145 of hCG beta-subunit; nucleotides	
FT	528..551 encode a (Gly-Ser)4 linker and	
FT	nucleotides 552..827 encode amino acids	
FT	1-92 of gonadotropin alpha-subunit lacking	
FT	the glycosylation sites at amino acid	
FT	positions 52 and 78"	
FT	Misc_difference 705..707	
FT	/*tag= d	
FT	/note= "wild-type Asn 52 codon has been changed to a	
FT	Gln codon to remove a glycosylation site"	
FT	Misc_difference 783..785	
FT	/*tag= e	
FT	/note= "wild-type Asn 78 codon has been changed to a	

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FT   Gln codon to remove a glycosylation site"
FT   misc_feature    1..26
FT   /*tag= f
FT   /label= sticky_end
FT   /note= "single-strand overhang. The complementary
FT   strand also has a single-strand overhang at
FT   its 5'-end; the sequence of the overhang is
FT   5'-TCCGGATTAGCTTGAGATGGATCC-3'"
PN   WO9522340-A1.
PD   24-AUG-1995.
PF   17-FEB-1995; U02067.
PR   18-FEB-1994; US-199382.
PA   (SENS-) SENSI-TEST.
PI   Moyle WR;
DR   WPI; 95-302553/39.
DR   P-PSDB; R86259.
PT   Methods for altering fertility in mammals, esp. humans - e.g.
PT   stimulating fertility by reducing the activity and/or levels of
PT   circulating glyco:protein hormones having lutropin activity
PS   Example 23; Fig 18; 102pp; English.
CC   Analogue 1a (human CG-beta(1-145)-linker-human CG-alpha(1-92)[N53Q,
CC   N78Q]) is a specific example of a single chain gonadotropin having
CC   a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a
CC   CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino
CC   acids. The analogue 1a was derived from analogue 1 by removing the
CC   two glycosylation sites from the alpha-subunit. The analogue has
CC   anti-luteinising hormone (lutropin) activity and can be used for
CC   facilitating ovulation, terminating pregnancy and reducing androgen
CC   secretion. The present sequence codes for analogue 1a.
SQ   Sequence   836 BP;    166 A;    282 C;    222 G;    166 T;

  Query Match           31.9%;  Score 415;  DB 17;  Length 836;
  Best Local Similarity  99.8%;  Pred. No. 3.64e-278;
  Matches   416;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    111 ccacggtgccgccccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    870 CCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGC 929

Db    171 atcaccgtcaacaccaccatctgtgccggctactgccccaccatgacccgcgtgctgcag 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    930 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 989

Db    231 ggggtcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    990 GGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 1049

Db    291 atccggctccctggctgcccgcgcggcgtgaaccccgtggtctcctacgccgtggctctc 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1050 ATCCGGCTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTC 1109

Db    351 agctgtcaatgtgcactctgccgccgcagcaccactgactgcgggggtcccaaggaccac 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1110 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1169

Db    411 cccttgacctgtgatgacccccgcttccaggactcctcttcctcaaaggcccctcccccc 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1170 CCCTTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCC 1229

Db    471 agccttccaagcccatcccgactcccggggccctcggacaccccgatcctcccccaa 527
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy   1230 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGATCCTCCCACAA 1286


Search completed: Wed May  6 15:08:03 1998
Job time : 173 secs.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:44:44 1998; MasPar time 1191.25 Seconds
1327.720 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-7
Description: (1-1301) from US08804166.seq
Perfect Score: 1301
N.A. Sequence: 1 CTCGAGATGGCTACAGGTAA.....CACAATAAGGATCCCTCGAG 1301
Comp: GAGCTCTACCGATGTCCATT.....GTGTTATTCCTAGGGAGCTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est8 8:em_gss 9:em_est13
Database: genbank-est
10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13
25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.285; Variance 2.123; scale 5.317

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c 1	397	30.5	601	13	N32759	yw91b05.s1 Homo sapien	0.00e+00
c 2	391	30.1	537	13	N30276	yw69d04.s1 Homo sapien	0.00e+00
c 3	387	29.7	564	13	N32604	yw95d03.s1 Homo sapien	0.00e+00
c 4	385	29.6	548	13	N30036	yw80b11.s1 Homo sapien	0.00e+00
c 5	383	29.4	593	13	N29730	yw78h03.s1 Homo sapien	0.00e+00
c 6	379	29.1	442	13	N32233	yw81f08.s1 Homo sapien	0.00e+00
c 7	379	29.1	473	13	N27302	yw71f12.s1 Homo sapien	0.00e+00
c 8	379	29.1	566	13	N30831	yw70b04.s1 Homo sapien	0.00e+00
c 9	377	29.0	563	13	N31955	yw89a07.s1 Homo sapien	0.00e+00
c 10	376	28.9	479	13	N30684	yw77h04.s1 Homo sapien	0.00e+00
c 11	373	28.7	473	25	AA400910	zt71h09.s1 Soares test	0.00e+00
c 12	371	28.5	446	13	N31616	yw84a02.s1 Homo sapien	0.00e+00
c 13	367	28.2	526	28	AA644163	af62d08.s1 Soares NhHM	0.00e+00
c 14	356	27.4	400	25	AA232905	zr46c04.s1 Soares NhHM	0.00e+00
c 15	351	27.0	419	16	H95374	yw60b03.s1 Soares plac	0.00e+00
c 16	350	26.9	531	16	W71989	zd66b03.s1 Soares feta	0.00e+00
c 17	335	25.7	403	13	N26397	yw76g11.s1 Homo sapien	0.00e+00
c 18	331	25.4	441	13	N30741	yw74b04.s1 Homo sapien	0.00e+00
c 19	322	24.8	422	11	R23214	yh28a03.s1 Homo sapien	0.00e+00
c 20	319	24.5	404	13	N30833	yw70b08.s1 Homo sapien	0.00e+00
c 21	319	24.5	515	13	N30608	yw72c07.s1 Homo sapien	0.00e+00
c 22	317	24.4	386	13	N30822	yw65h07.s1 Homo sapien	0.00e+00
c 23	315	24.2	367	11	R68815	yi43c05.s1 Homo sapien	0.00e+00
c 24	307	23.6	329	12	H12587	yj12g11.s1 Homo sapien	0.00e+00
c 25	305	23.4	367	16	H94446	yw55f02.s1 Soares plac	0.00e+00
c 26	300	23.1	352	13	H87464	yw17e05.s1 Homo sapien	0.00e+00
c 27	298	22.9	380	13	N30290	yw69f05.s1 Homo sapien	0.00e+00
28	297	22.8	526	25	AA393716	zt71h09.r1 Soares test	0.00e+00
c 29	295	22.7	427	13	N27111	yw75h12.s1 Homo sapien	0.00e+00
c 30	293	22.5	386	16	H94451	yw55g08.s1 Soares plac	0.00e+00
c 31	285	21.9	319	13	H87631	yw17e12.s1 Homo sapien	0.00e+00
c 32	280	21.5	329	13	H87156	yw15b04.s1 Homo sapien	0.00e+00
c 33	276	21.2	311	10	T47334	yb10e11.s1 Homo sapien	0.00e+00
c 34	273	21.0	284	13	H93656	yw55a11.s1 Homo sapien	0.00e+00
c 35	268	20.6	303	13	H86993	yw15b10.s1 Homo sapien	0.00e+00
c 36	259	19.9	291	10	T90191	yd38g09.s1 Homo sapien	0.00e+00
c 37	251	19.3	266	13	H93668	yw55c12.s1 Homo sapien	0.00e+00
38	245	18.8	251	19	AA330413	EST34462 Embryo, 6 wee	0.00e+00
39	239	18.4	278	10	T49170	yb09g02.r1 Homo sapien	0.00e+00
40	240	18.4	519	23	C18044	Human placenta cDNA 5'	0.00e+00
c 41	235	18.1	248	16	H95381	yw60d07.s1 Soares plac	0.00e+00
42	230	17.7	341	12	T29543	EST83815 Homo sapiens	0.00e+00
c 43	224	17.2	244	16	H94107	yw58h09.s1 Soares plac	0.00e+00
44	224	17.2	360	14	HSC32B021	H. sapiens partial cDN	0.00e+00
c 45	219	16.8	255	11	R63352	yi07h10.s1 Homo sapien	0.00e+00

ALIGNMENTS

RESULT 1
LOCUS N32759 601 bp mRNA EST 10-JAN-1996

DEFINITION yw91b05.s1 Homo sapiens cDNA clone 259569 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION N32759
NID g1153158
KEYWORDS EST.
SOURCE human clone=259569 primer=m13 -40 forward library=Soares placenta 8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 601)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

```
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 387
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .601
                      /organism="Homo sapiens"
                      /clone="259569"
     mRNA             <1. .>601
BASE COUNT      112 a    154 c    219 g    110 t      6 others
ORIGIN

  Query Match           30.5%;  Score 397;  DB 13;  Length 601;
  Best Local Similarity  97.9%;  Pred. No. 0.00e+00;
  Matches   411;  Conservative    0;  Mismatches   8;  Indels   1;  Gaps   1;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
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Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGCAGCCAAGGGAGCCGGAT 255
           |||||||||||||||||||||||||||||||||||||||    | ||||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCCC 315
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     316 TTGCAGCACGCGGGTCATGGTGGGGCAGTAGCGGGCACAGATGGTGGTGTTGACGGTGAT 375
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Cp     989 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db     376 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTGG 435
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Cp     929 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTGG 870


RESULT    2
LOCUS       N30276         537 bp    mRNA            EST       05-JAN-1996

DEFINITION  yw69d04.s1 Homo sapiens cDNA clone 257479 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30276
NID         g1148796
KEYWORDS    EST.
SOURCE      human clone=257479 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsitel=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 537)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 313
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
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                      /clone="257479"
     mRNA             <1. .>537
BASE COUNT       98 a    145 c    201 g     90 t      3 others
ORIGIN

  Query Match           30.1%;  Score 391;  DB 13;  Length 537;
  Best Local Similarity  96.2%;  Pred. No. 0.00e+00;
  Matches   426;  Conservative    0;  Mismatches  13;  Indels   4;  Gaps   4;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     196 GAGAGCCACGGCGTTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGA 254
           ||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||
Cp    1109 GAGAGCCACGGCGT-AGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGA 1051

Db     255 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCC 314
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Cp    1050 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCC 991

Db     315 CCCTGCAGCACGCGGGTCATGGTGGGGCAGTAACCGGCACAGATGGTGGTGTTGACGGTG 374
           || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Cp     990 CC-TGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTG 932

Db     375 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCANCGT 434
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Cp     931 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGT 872

Db     435 GGCNAAGCGGCTCCTTGGATGCC 457
           ||  |||  |  ||  | ||||
Cp     871 GGACCAGCACCAGCTGTGGTGCC 849


RESULT    3
LOCUS       N32604         564 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw95d03.s1 Homo sapiens cDNA clone 259973 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32604
NID         g1153003
KEYWORDS    EST.
SOURCE      human clone=259973 primer=m13 -40 forward library=Soares placenta
```

```
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 364
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .564
                     /organism="Homo sapiens"
                     /clone="259973"
     mRNA            <1. .>564
BASE COUNT      103 a    148 c    206 g     99 t      8 others
ORIGIN

  Query Match           29.7%;  Score 387;  DB 13;  Length 564;
  Best Local Similarity  97.2%;  Pred. No. 0.00e+00;
  Matches   413;  Conservative    0;  Mismatches   9;  Indels   3;  Gaps   3;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 76
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGCAGCCAAGGGAGCCGGAT 255
           ||||||||||||||||||||||||||||||||||||||||    | ||||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCCC 315
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     316 CTTGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGA 374
           || ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Cp     989 CT-GCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 931

Db     375 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Cp     930 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 871

Db     435 GCCNA 439
           | | |
Cp     870 GACCA 866


RESULT    4
LOCUS       N30036        548 bp    mRNA            EST       05-JAN-1996

DEFINITION  yw80b11.s1 Homo sapiens cDNA clone 258525 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30036
NID         g1148556
KEYWORDS    EST.
SOURCE      human clone=258525 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 548)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 333
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .548
                     /organism="Homo sapiens"
                     /clone="258525"
     mRNA            <1. .>548
BASE COUNT       99 a    143 c    206 g     93 t      7 others
ORIGIN

  Query Match           29.6%;  Score 385;  DB 13;  Length 548;
  Best Local Similarity  97.6%;  Pred. No. 0.00e+00;
  Matches   413;  Conservative    0;  Mismatches   6;  Indels   4;  Gaps   4;

Db      18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      78 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     138 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 196
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
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Cp   1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db    197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGCAAGCCATGGGAGCCGGA 256
          ||||||||||||||||||||||||||||||||||||||||||||  ||||| ||||||||||
Cp   1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCA-GGGAGCCGGA 1051

Db    257 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGACCN 316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Cp   1050 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCC 991

Db    317 CCTTGCAAGCACGCGGGTCATGGTGGGGCAGTAGCGGGCACAGATGGTGGTGTTGACGGT 376
          ||| ||| |||||||||||||||||||||||||| ||||||||||||||||||||||||
Cp    990 CCT-GCA-GCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGT 933

Db    377 GATGNACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 436
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    932 GATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 873

Db    437 TGG 439
          |||
Cp    872 TGG 870
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RESULT    5
LOCUS       N29730        593 bp    mRNA            EST       05-JAN-1996

DEFINITION  yw78h03.s1 Homo sapiens cDNA clone 258389 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N29730
NID         g1148250
KEYWORDS    EST.
SOURCE      human clone=258389 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 368
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .593
                      /organism="Homo sapiens"
                      /clone="258389"
     mRNA             <1. .>593
BASE COUNT      109 a    151 c    216 g    111 t      6 others
```

```
ORIGIN

  Query Match          29.4%;  Score 383;  DB 13;  Length 593;
  Best Local Similarity  95.3%;  Pred. No. 0.00e+00;
  Matches   422;  Conservative    0;  Mismatches  17;  Indels   4;  Gaps   4;

Db      18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      78 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     138 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 196
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGNGG-CAGCCAGGGAGCCGGAT 255
           |||||||||||||||||||||||||||||||||||||||||| || |||||||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGCAAGACCACC 315
           |||||||||||||||||||||||||||||||||||||||||||| |  ||  | ||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     316 CTGCAGCACGCGGGTCATGGTTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 375
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Cp     989 CTGCAGCACGCGGGTCATGGT-GGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 931

Db     376 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCANGGTTGGCATTGATGGGGCGGCACCGT 435
           |||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||
Cp     930 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGT-GGCATTGATGGGGCGGCACCGT 872

Db     436 GGCCAAGCGGCTCCTTGGATGCC 458
           || | ||| | || | ||||
Cp     871 GGACCAGCACCAGCTGTGGTGCC 849
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```
RESULT    6
LOCUS       N32233        442 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw81f08.s1 Homo sapiens cDNA clone 258663 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32233
NID         g1152632
KEYWORDS    EST.
SOURCE      human clone=258663 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
```

```
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 364
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .442
                      /organism="Homo sapiens"
                      /clone="258663"
     mRNA             <1. .>442
BASE COUNT       85 a    110 c    174 g     68 t      5 others
ORIGIN

  Query Match           29.1%;  Score 379;  DB 13;  Length 442;
  Best Local Similarity  94.6%;  Pred. No. 0.00e+00;
  Matches   402;  Conservative    0;  Mismatches  22;  Indels   1;  Gaps   1;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 76
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACCCCGCAAGTCAGTTGGTGCTGCGGCGGCAGAGTGCACATTGACAGC 196
           |||||||||||||||    ||||||| ||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGT-GGTGCTGCGGCGGCAGAGTGCACATTGACAGC 1111

Db     197 TGAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCNCGGCAGCCANGGGAGCCGGA 256
           |||||||||||||||||||||||||||||||||||| |||    |  ||||||||||
Cp    1110 TGAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGA 1051

Db     257 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGNCAAGACCAC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||    ||  | |
Cp    1050 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCC 991

Db     317 CCTGCAGCACGCGGGTCATGGTGGGGCAGTAACCGGCACAGATGGTGGTGTTGACGGTNA 376
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||| |
Cp     990 CCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGA 931

Db     377 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCANCGTG 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Cp     930 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 871

Db     437 GCCCA 441
           | |||
Cp     870 GACCA 866


RESULT    7
LOCUS       N27302        473 bp    mRNA            EST       29-DEC-1995

DEFINITION  yw71f12.s1 Homo sapiens cDNA clone 257711 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N27302
NID         g1141650
KEYWORDS    EST.
SOURCE      human clone=257711 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 225
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES              Location/Qualifiers
     source           1. .473
                      /organism="Homo sapiens"
                      /clone="257711"
     mRNA             <1. .>473
BASE COUNT       87 a    122 c    182 g     76 t      6 others
ORIGIN

  Query Match           29.1%;  Score 379;  DB 13;  Length 473;
  Best Local Similarity  95.5%;  Pred. No. 0.00e+00;
  Matches   402;  Conservative    0;  Mismatches  17;  Indels   2;  Gaps   2;

Db      18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 77
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      78 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     138 GTGGTCCTTGGGACCCCGCCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 197
           ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     198 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGANCCGGAT 256
           |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     257 GGACTCGAANCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGACAAGACCACC 316
           |||||||| ||||||||||||||||||||||||||||||||||||    ||  | ||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     317 TTGCAGCACGCGGGTCATGGTGGGGCAGTANCCGGGCACAGATGGTGGTGTTNACGGTGA 376
           |||||||||||||||||||||||||||||| |||| |||||||||||||||| |||||||
Cp     989 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGG-CACAGATGGTGGTGTTGACGGTGA 931

Db     377 TGCACACGGGGCAGCCCNCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTN 436
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Cp     930 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 871

Db     437 G 437
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Cp     870 G 870


RESULT    8
LOCUS       N30831        566 bp    mRNA            EST       05-JAN-1996
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```
DEFINITION  yw70b04.s1 Homo sapiens cDNA clone 257551 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30831
NID         g1149351
KEYWORDS    EST.
SOURCE      human clone=257551 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 566)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 400
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .566
                     /organism="Homo sapiens"
                     /clone="257551"
     mRNA            <1. .>566
BASE COUNT      103 a    148 c    209 g    100 t      6 others
ORIGIN

  Query Match           29.1%;  Score 379;  DB 13;  Length 566;
  Best Local Similarity  96.7%;  Pred. No. 0.00e+00;
  Matches   408;  Conservative    0;  Mismatches   11;  Indels    3;  Gaps    3;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGG-CCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     196 GAGAGCCACGGCTTAGGAGACCACGGGGTTCACGCCGCGCGGCAAGCCANGGGAGCCGGA 255
           |||||||||||| |||||||||||||||||||||||||||  ||||| ||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCA-GGGAGCCGGA 1051

Db     256 TGGACTCGAAGCGCAAATCGCGGGTAGTTGCACACCACCTGAGGCAGGGCGGCCAGACCC 315
           |||||||||||||| ||||||| |||||||||||||||||||||| | |||  ||
Cp    1050 TGGACTCGAAGCGCACATCGCGG-TAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACC 992

Db     316 CCCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCGGTCACAGATGGTGGTGTTGACGGTG 375
           |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Cp     991 CCCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTG 932

Db     376 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGT 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     931 ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGT 872

Db     436 GG 437
           ||
Cp     871 GG 870


RESULT    9
LOCUS       N31955        563 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw89a07.s1 Homo sapiens cDNA clone 259380 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N31955
NID         g1152354
KEYWORDS    EST.
SOURCE      human clone=259380 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 335
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Homo sapiens"
                     /clone="259380"
     mRNA            <1. .>563
BASE COUNT      101 a    148 c    208 g    103 t      3 others
ORIGIN

  Query Match           29.0%;  Score 377;  DB 13;  Length 563;
  Best Local Similarity  97.4%;  Pred. No. 0.00e+00;
  Matches   418;  Conservative    0;  Mismatches    5;  Indels    6;  Gaps    6;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230
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```
Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTTGGTGCTGCGGCGGCAGAGTGCACATTGACAGC 195
           |||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGT-GGTGCTGCGGCGGCAGAGTGCACATTGACAGC 1111

Db     196 TGAGAGCCACGGCGTTAGGAGACCACGGGGTTCACGCCGCGCGGCAAGCCANGGGAGCCG 255
           |||||||||||||| ||||||||||||||||||||||||||||  ||||| ||||||||
Cp    1110 TGAGAGCCACGGCGT-AGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCA-GGGAGCCG 1053

Db     256 GATGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGC-GGCAAGAC 314
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||| |||
Cp    1052 GATGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGAC 993

Db     315 CCC-TGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGT 373
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     992 CCCCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGT 933

Db     374 GATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     932 GATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCG 873

Db     434 TGGCCAAGC 442
           ||| | |||
Cp     872 TGGACCAGC 864
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RESULT 10
LOCUS N30684 479 bp mRNA EST 05-JAN-1996

DEFINITION yw77h04.s1 Homo sapiens cDNA clone 258295 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION N30684
NID g1149204
KEYWORDS EST.
SOURCE human clone=258295 primer=ml3 -40 forward library=Soares placenta 8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 333
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES Location/Qualifiers
source 1. .479
/organism="Homo sapiens"
/clone="258295"
mRNA <1. .>479
BASE COUNT 86 a 122 c 184 g 79 t 8 others
ORIGIN

Query Match 28.9%; Score 376; DB 13; Length 479;
Best Local Similarity 96.0%; Pred. No. 0.00e+00;
Matches 403; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

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Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     196 GAGAGCCACGGCNTAGGAGACCACGGGGTTCACGCCGCGCGGCAGCCANGGGAGCCGGAT 255
           |||||||||||| |||||||||||||||||||||||||||||    |  ||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     256 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGC-GGCAGACCCCC 314
           |||||||||||||||||||||||||||||||||||||||||||||||| |||||  ||||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     315 TTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTNACGGTGAT 374
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Cp     989 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db     375 GCACACGGGGCAGCCCTCCTTCTCCACAGCCANGGGTGGNATTGATGGGGCGGCACNTTG 434
           |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||  ||
Cp     929 GCACACGGGGCAGCCCTCCTTCTCCACAGCCA-GGGTGGCATTGATGGGGCGGCACCGTG 871
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RESULT 11
LOCUS AA400910 473 bp mRNA EST 12-AUG-1997

DEFINITION zt71h09.s1 Soares testis NHT Homo sapiens cDNA clone 727841 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION AA400910
NID g2054783
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 640 Std Error: 0.00

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          Seq primer: -41m13 fwd. ET from Amersham
          High quality sequence stop: 392.
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Homo sapiens"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with  a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo."
                     /db_xref="taxon:9606"
                     /clone="727841"
                     /clone_lib="Soares testis NHT"
                     /sex="male"
                     /lab_host="DH10B"
     mRNA            complement(<1. .>473)
                     /db_xref="GDB:5924752"
BASE COUNT       84 a    120 c    190 g     78 t      1 others
ORIGIN

  Query Match           28.7%;  Score 373;  DB 25;  Length 473;
  Best Local Similarity  97.8%;  Pred. No. 0.00e+00;
  Matches   406;  Conservative    0;  Mismatches   4;  Indels   5;  Gaps   5;

Db      20 TTATTGTGGGAGGATCGGGGTGTCTGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 79
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      80 GGGGGGAGGGGCCTTTGAGGAAGAGGAGGCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 139
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     140 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 198
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     199 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGAT 257
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     258 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGNCAG-ACCCC 316
           |||||||||||||||||||||||||||||||||||||||||||| | ||| |||||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     317 -TGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGAT 374
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Cp     989 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db     375 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCAC 429
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     929 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCAC 875


RESULT   12
LOCUS       N31616        446 bp    mRNA            EST       10-JAN-1996

DEFINITION  yw84a02.s1 Homo sapiens cDNA clone 258890 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N31616
NID         g1152015
KEYWORDS    EST.
SOURCE      human clone=258890 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 446)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 329
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1. .446
                     /organism="Homo sapiens"
                     /clone="258890"
     mRNA            <1. .>446
BASE COUNT       82 a    108 c    170 g     71 t     15 others
ORIGIN

  Query Match           28.5%;  Score 371;  DB 13;  Length 446;
  Best Local Similarity  94.8%;  Pred. No. 0.00e+00;
  Matches   399;  Conservative    0;  Mismatches  18;  Indels   4;  Gaps   4;

Db      17 TTANTGTGGGANGATNGGGGTTTNCGANGGCCCCGGGANTNNNNATGGACTTGGNAGGCT 76
           ||| ||||||| ||| ||||| | ||| |||||||||| |    |||| ||||| |||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGGGGCCTTTNAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTNACAGCT 195
           |||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGAT 254
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     255 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAG-ACCCC 313
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     314 TTGCAGCACGCGGGTCATGGTGGGGCAGTAACCGGCACAGATGGTGGTGTTGACGGTGAT 373
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Cp     989 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db     374 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTTGATGGNGCGGCACCGTG 433
           |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||
Cp     929 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATT-GATGGGGCGGCACCGTG 871

Db     434 G 434
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Cp     870 G 870
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RESULT   13
LOCUS       AA644163      526 bp    mRNA            EST       27-OCT-1997

DEFINITION  af62d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 1046607 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.
ACCESSION   AA644163
NID         g2569381
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 335.
FEATURES             Location/Qualifiers
     source          1. .526
                     /organism="Homo sapiens"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
                     /db_xref="taxon:9606"
                     /clone="1046607"
                     /clone_lib="Soares NhHMPu S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
BASE COUNT      100 a    140 c    201 g     85 t
ORIGIN

  Query Match           28.2%;  Score 367;  DB 28;  Length 526;
  Best Local Similarity  97.1%;  Pred. No. 0.00e+00;
  Matches   409;  Conservative    0;  Mismatches   6;  Indels   6;  Gaps   6;

Db      16 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCT 75
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Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      76 GGCAGGAGGGGCCTTTAAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 135
           ||  ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     136 GTGGTCCTTGGGACCCCGACAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 195
           ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     196 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGG-CAGCCAGGGAGCCGGAT 254
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     255 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGC-GGCAGGACCCC 313
           ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     314 -TGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGAT 371
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Cp     989 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db     372 GGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGG-ACCGTG 430
           | ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Cp     929 G-CACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCACCGTG 871

Db     431 G 431
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Cp     870 G 870


RESULT   14
LOCUS       AA232905      400 bp    mRNA            EST       06-AUG-1997

DEFINITION  zr46c04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666438 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.
ACCESSION   AA232905
NID         g1855917
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 834   Std Error: 0.00
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 361.
FEATURES             Location/Qualifiers
     source          1. .400
                     /organism="Homo sapiens"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
                     /db_xref="taxon:9606"
                     /clone="666438"
                     /clone_lib="Soares NhHMPu S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
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                     /db_xref="GDB:5428470"
BASE COUNT       74 a     98 c    165 g     63 t
ORIGIN

  Query Match           27.4%;  Score 356;  DB 25;  Length 400;
  Best Local Similarity  97.4%;  Pred. No. 0.00e+00;
  Matches   376;  Conservative    0;  Mismatches   8;  Indels   2;  Gaps   2;

Db      17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCT 1230

Db      77 GGGGGGAGTGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 136
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 1170

Db     137 GTGGTCCTTGGGACACCCGCAGTCAGTGGTGCTGCGGCGGCAGGAGGCACATTGACAGCT 196
           |||||||||||||| |||||||||||||||||||||||||||   ||||||||||||||
Cp    1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db     197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db     257 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCGGTCAG-AGCCC 315
           |||||||||||||||||||||||||||||||||||||||||||| | ||| | |||
Cp    1049 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGGACCCC 990

Db     316 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGC-GGCACAGATGGTGGTGTTGACGGTGAT 374
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Cp     989 CTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db     375 GCACACGGGGCAGCCCTCCTTCTCCA 400
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Cp     929 GCACACGGGGCAGCCCTCCTTCTCCA 904


RESULT   15
LOCUS       H95374         419 bp    mRNA            EST       25-NOV-1996

DEFINITION  yw60b03.s1 Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA
            clone 256589 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN
            PRECURSOR (HUMAN);.
ACCESSION   H95374
NID         g1103007
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 297
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1014    Std Error: 0.00
            Seq primer: Promega -21m13.

FEATURES             Location/Qualifiers
     source          1. .419
                     /organism="Homo sapiens"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
                     /db_xref="taxon:9606"
                     /clone="256589"
                     /clone_lib="Soares placenta 8to9weeks 2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
     mRNA            complement(<1. .>419)
BASE COUNT       73 a    109 c    168 g     63 t      6 others
ORIGIN

  Query Match           27.0%;  Score 351;  DB 16;  Length 419;
  Best Local Similarity  95.6%;  Pred. No. 0.00e+00;
  Matches   390;  Conservative    0;  Mismatches  13;  Indels   5;  Gaps   5;

Db       1 CCGAGGGCCCCGGGAGTCGGGATGGACTTGGAAGGCTGGGGGGAGGGGCCTTTGAGGAAG 60
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Cp    1266 CCGAGGGCCCCGGGAGTCGGGATGGGCTTGGAAGGCTGGGGGGAGGGGCCTTTGAGGAAG 1207

Db      61 AGGAGGCCTGGAAGCGGGGGTCATCACAGGTCAAGGGGTGGTCCTTGGGACCCCGGCAGT 120
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||
Cp    1206 AGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGGGTGGTCCTTGGGACCCCCGCAGT 1147

Db     121 CAGTGGTGCTGCGGCGGCNGAGTGCACATTGACAGCTGAGAGCCACGGCGTAGGAGACCA 180
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Cp    1146 CAGTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCTGAGAGCCACGGCGTAGGAGACCA 1087

Db     181 CGGGGTTCACGCCGCGNGGCCAGCCAGGGAGCCGGATGGACTCGAAGCGCACATCGCGGT 240
           |||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Cp    1086 CGGGGTTCACGCCGCGCGGGCAGCCAGGGAGCCGGATGGACTCGAAGCGCACATCGCGGT 1027

Db     241 TAGTTGCACACCACCTGAGGCAGGGCCGCCAGGACNCCCCTGCAGCACGCGGGTTCATGG 300
           ||||||||||||||||||||||||| |||||| |||||||||||||||| |||||
Cp    1026 -AGTTGCACACCACCTGAGGCAGGGCCGGCAGGAC-CCCCTGCAGCACGCGGGT-CATGG 970

Db     301 TGGGGCAGTAGCGGNCACAGATGGTGGTGTTGANGGTGATGCACACGGGGCAGCCCTCCT 360
           |||||||||||| | |||||||||||||||||| ||||||||||||||||||||||||||
Cp     969 TGGGGCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGATGCACACGGGGCAGCCCTCCT 910

Db     361 TNCTCCACAGCCAGGGTGGCTTTGATTGGGGCGGCACCGTGGCCAAGC 408
           | |||||||||||||||| ||||| |||||||||||||| | |||
Cp     909 T-CTCCACAGCCAGGGTGGCATTGAT-GGGGCGGCACCGTGGACCAGC 864


Search completed: Wed May  6 15:04:47 1998
Job time : 1203 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:06:59 1998; MasPar time 10.23 Seconds
491.010 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-8
Description: (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 32.744; Variance 136.204; scale 0.240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	2541	100.0	336	26	W33360	TBP(20-190)/hCG-beta	2.22e-245
2	2022	79.6	307	26	W33358	TBP(20-161)/hCG-beta	7.11e-192
3	1505	59.2	285	26	W33359	TBP(20-190)/hCG-alpha	8.93e-139
4	1322	52.0	371	2	R07449	Tumour Necrosis Facto	4.69e-120
5	1321	52.0	451	13	R70107	TNF-R-GBP 130 fusion	5.93e-120
6	1322	52.0	455	4	R24000	TNF-alpha 55kD recept	4.69e-120
7	1322	52.0	455	14	R75084	p55 TNF-R.	4.69e-120
8	1322	52.0	455	4	R20787	TNF-alpha binding pro	4.69e-120
9	1322	52.0	455	8	R42059	Lambda derived TNF-R.	4.69e-120
10	1322	52.0	455	2	R10986	30kD TNF inhibitor pr	4.69e-120
11	1322	52.0	455	2	R11082	Human 55kD TNF-bindin	4.69e-120
12	1321	52.0	900	13	R70103	TNF-R-GBP 130 fusion	5.93e-120
13	1319	51.9	309	13	R70108	TNF-R-GBPH fusion pro	9.50e-120
14	1319	51.9	455	2	R07451	Human Tumour Necrosis	9.50e-120
15	1319	51.9	547	13	R70104	TNF-R-GBPH fusion pro	9.50e-120
16	1319	51.9	1604	13	R70105	TNF-R-EBA 175 fusion	9.50e-120
17	1317	51.8	1245	13	R70106	TNF-R-Pl. vivax Duffy	1.52e-119
18	1313	51.7	433	8	R51032	Mutant p55 tumour nec	3.89e-119
19	1313	51.7	443	8	R51033	Mutant p55 tumour nec	3.89e-119
20	1313	51.7	455	8	R42197	p55 Tumour necrosis f	3.89e-119
21	1313	51.7	455	8	R51034	Mutant p55 tumour nec	3.89e-119
22	1308	51.5	455	3	R12550	Type I TNF receptor.	1.26e-118
23	1291	50.8	256	26	W33357	TBP(20-161)/hCG-alpha	6.87e-117
24	1263	49.7	161	5	R27496	Native 30 kD TNF inhi	4.96e-114
25	1263	49.7	884	13	R70109	TNF-R-GBP 130 fusion	4.96e-114
26	1252	49.3	199	4	R24080	Truncated TNF-alpha 5	6.57e-113
27	1030	40.5	165	3	R15043	Human chorionic gonad	2.60e-90
28	1025	40.3	145	6	R30999	Human chorionic gonad	8.37e-90
29	1022	40.2	145	3	R15174	hCG histidine substit	1.69e-89
30	1021	40.2	145	3	R15171	hCG methionine substi	2.13e-89
31	1021	40.2	145	3	R15120	hCG/hLH chimera, A5.	2.13e-89
32	1021	40.2	265	15	R86247	Single chain gonadotr	2.13e-89
33	1021	40.2	265	15	R86259	Partially deglycosyla	2.13e-89
34	1020	40.1	145	25	W31200	Human chorionic gonad	2.69e-89
35	1020	40.1	145	3	R15117	hCG/hLH chimera, A3a.	2.69e-89
36	1020	40.1	145	3	R15169	hCG methionine substi	2.69e-89
37	1018	40.1	145	3	R15173	hCG histidine substit	4.30e-89
38	1016	40.0	181	15	R86258	Human CG beta-subunit	6.86e-89
39	1015	39.9	145	24	W27681	Chorionic gonadotroph	8.67e-89
40	1015	39.9	145	3	R15177	hCG histidine substit	8.67e-89
41	1014	39.9	145	24	W27688	Chorionic gonadotroph	1.09e-88
42	1013	39.9	145	3	R15103	hCG/bLH chimera, D7.	1.38e-88
43	1013	39.9	145	3	R15170	hCG methionine substi	1.38e-88
44	1013	39.9	145	24	W27687	Chorionic gonadotroph	1.38e-88
45	1013	39.9	145	24	W27682	Chorionic gonadotroph	1.38e-88

ALIGNMENTS

RESULT 1
ID W33360 standard; Protein; 336 AA.
AC W33360;
DT 19-MAR-1998 (first entry)
DE TBP(20-190)/hCG-beta fusion protein.
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW beta subunit; hCG-beta.
OS Homo sapiens.
PN WO9730161-A1.
PD 21-AUG-1997.
PF 20-FEB-1997; U02315.
PR 20-FEB-1996; US-011936.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PI Campbell RK, Chappel SC, Jameson BA;
DR WPI; 97-425036/39.
DR N-PSDB; T94022.
PT Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation
PS Example; Pages 39-40; 60pp; English.
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein hormone capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC (hCG-beta) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed.
SQ Sequence 336 AA;

Query Match 100.0%; Score 2541; DB 26; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.22e-245;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db     61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db     121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscsnckkslectklclpq 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ 180

Db     181 ienvkgtedsgttagagprcrpinatlavekegcpvcitvntticagycptmtrvlqgvl 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     181 IENVKGTEDSGTTAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVL 240

Db     241 palpqvvcnyrdvrfesirlpgcprgvnpvvsyavalscqcalcrrsttdcggpkdhplt 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     241 PALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLT 300

Db     301 cddprfqdsssskapppslpspsrlpgpsdtpilpq 336
           ||||||||||||||||||||||||||||||||||||
Qy     301 CDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 336


RESULT    2
ID   W33358 standard; Protein; 307 AA.
AC   W33358;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             279..1202
FT                   /*tag= a
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94008.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 34-35; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   307 AA;

  Query Match           79.6%;  Score 2022;  DB 26;  Length 307;
  Best Local Similarity  91.4%;  Pred. No. 7.11e-192;
  Matches   307;  Conservative    0;  Mismatches   0;  Indels  29;  Gaps   1;

Db       1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db      61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db     121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvsc---------------- 164
           ||||||||||||||||||||||||||||||||||||||||||||
Qy     121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ 180

Db     165 ------------agagprcrpinatlavekegcpvcitvntticagycptmtrvlqgvl 211
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     181 IENVKGTEDSGTTAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVL 240

Db     212 palpqvvcnyrdvrfesirlpgcprgvnpvvsyavalscqcalcrrsttdcggpkdhplt 271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     241 PALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLT 300

Db     272 cddprfqdsssskapppslpspsrlpgpsdtpilpq 307
           ||||||||||||||||||||||||||||||||||||
Qy     301 CDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 336


RESULT    3
ID   W33359 standard; Protein; 285 AA.
AC   W33359;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94021.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 37-38; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   285 AA;

  Query Match           59.2%;  Score 1505;  DB 26;  Length 285;
  Best Local Similarity  98.0%;  Pred. No. 8.93e-139;
  Matches   196;  Conservative    2;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 srtslllafgllclpwlqegsadsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqd 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db      61 tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Db     121 nlfqcfnctlclngtvhlscqekqntvctchagfflrenecvscsnckkslectklslpq 180
           ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy     121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ 180

Db     181 ienvkgtedsgttagaapgc 200
           ||||||||||||||:| |
Qy     181 IENVKGTEDSGTTAGAGPRC 200


RESULT    4
ID   R07449 standard; protein; 371 AA.
AC   R07449;
DT   29-JAN-1991  (first entry)
DE   Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock.
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OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06282.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of
CC   e.g. COS7 cells.  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   371 AA;

  Query Match           52.0%;  Score 1322;  DB 2;  Length 371;
  Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    5
ID   R70107 standard; Protein; 451 AA.
AC   R70107;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 53-54; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence   451 AA;

  Query Match           52.0%;  Score 1321;  DB 13;  Length 451;
  Best Local Similarity 99.4%;  Pred. No. 5.93e-120;
  Matches   171;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtna 191
        |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTA 194


RESULT    6
ID   R24000 standard; Protein; 455 AA.
AC   R24000;
DT   05-NOV-1992  (first entry)
DE   TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /label= signal peptide
FT   modified_site   54..56
FT                   /label= N linked glycosylation site
FT                   /note= "potential"
FT   modified_site   145..147
FT                   /label= N linked glycosylation site
FT                   /note= "potential "
FT   modified_site   151..153
FT                   /label= N linked glycosylation site
FT                   /note= "potential"
FT   domain          212..234
FT                   /label= transmembrane domain
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   N-PSDB; Q24440.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 1; 43pp; English.
CC   This sequence was deduced from human TNF-alpha cDNA isolated as in
CC   Q24440. The first 35 amino acids are generally quite hydrophobic
CC   and probably represent a signal sequence. Residues 35-40  are highly
CC   charged (DREKR) and this is not normally found in secretory
CC   signal sequences. It is possible the receptor is processed by
CC   proteolysis after residue 40 which contains a dibasic cleavage site
CC   (KR). Hydropathy analysis of this sequence predicts a single
CC   transmembrane domain of 23 amino acids, dividing the sequence into
CC   an extracellular domain of 171 residues and a cytoplasmic domain of
CC   221 residues. The sequence contains a large number of cysteine
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CC   residues, the arrangement of which is similar to that of other cell
CC   surface proteins, suggesting the TNF-alpha receptor is structurally
CC   related to a family of receptors.
CC   NOTE:- Residues 371,2 given in the sequence as T,L, are encoded by
CC   TGG (W) and AAG (K).
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   455 AA;

  Query Match           52.0%;  Score 1322;  DB 4;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    7
ID   R75084 standard; Protein; 455 AA.
AC   R75084;
DT   19-JAN-1996  (first entry)
DE   p55 TNF-R.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         41..53
FT                   /note= "N terminus of soluble p55 TNF-R"
FT   modified_site   54..56
FT                   /note= "glycosylation site"
FT   modified_site   145..147
FT                   /note= "glycosylation site"
FT   modified_site   161..163
FT                   /note= "glycosylation site"
FT   peptide         193..210
FT                   /note= "peptide used in creation of chimeras"
FT   region          198..210
FT                   /note= "spacer region"
FT   misc_difference 201
FT                   /note= "major C terminus for soluble p55 TNF-R"
FT   misc_difference 202
FT                   /note= "essential for shedding reaction"
FT   misc_difference 203
FT                   /note= "minor C terminus for soluble p55 TNF-R"
FT   region          212..234
FT                   /note= "transmembrane region"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
DR   WPI; 95-194342/26.
DR   N-PSDB; Q90513.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor  - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R).
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment.  The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type.  The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain.  This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain.  The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11.  This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.
CC   The mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3.  These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence   455 AA;

  Query Match           52.0%;  Score 1322;  DB 14;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    8
ID   R20787 standard; Protein; 455 AA.
AC   R20787;
DT   11-MAY-1992  (first entry)
DE   TNF-alpha binding protein.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "signal peptide"
FT   peptide         41..455
FT                   /note= "mature peptide"
FT   domain          30..199
FT                   /note= "extracellular domain"
FT   domain          212..234
FT                   /note= "transmembrane domain"
FT   modified_site   145..147
FT                   /note= "potential N-glycosylation site"
FT   modified_site   151..153
FT                   /note= "potential N-glycosylation site"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   N-PSDB; Q20973.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
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CC   can therefore be used therapeutically to treat disorders such as
CC   cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC   arthritis.
SQ   Sequence   455 AA;

  Query Match           52.0%;  Score 1322;  DB 4;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    9
ID   R42059 standard; Protein; 455 AA.
AC   R42059;
DT   29-APR-1994  (first entry)
DE   Lambda derived TNF-R.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction.
OS   Homo sapiens.
OS   Lambda-gt10-7ctnfbp.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "Signal peptide"
FT   protein         41..455
FT                   /note= "Mature hTNF-R"
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   N-PSDB; Q49932.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.
CC   The sequences given in R42058-59 repressent human tumour necrosis
CC   factor receptor (TNF-R) and the sequences in R42060-61 represent
CC   human interleukin-1 receptor (IL-1R).  These sequences were used in
CC   the production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence   455 AA;

  Query Match           52.0%;  Score 1322;  DB 8;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT   10
ID   R10986 standard; Protein; 455 AA.
AC   R10986;
DT   13-MAY-1991  (first entry)
DE   30kD TNF inhibitor precursor.
KW   Tumour necrosis factor; inhibitor.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cleavage_site   40..41
FT                   note=" cleavage gives active protein "
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   N-PSDB; Q10883.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC   from which the sequence was deduced was isolated from a cDNA
CC   library prepd. from RNA form U937 cells treated with PMA/PHA.
CC   The whole gene can be inserted into expression vectors for prepn.
CC   of TNF inhibitor for use in the treatment of inflammatory and
CC   degenerative diseases.  The active protein is claimed (Claim 8).
CC   See also R10984 and R11001.
SQ   Sequence   455 AA;

  Query Match           52.0%;  Score 1322;  DB 2;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT   11
ID   R11082 standard; Protein; 455 AA.
AC   R11082;
DT   24-MAY-1991  (first entry)
DE   Human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
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FH   Key             Location/Qualifiers
FT   modified_site   54
FT                   /label= putative N-glycosylation site
FT   modified_site   145
FT                   /label= putative N-glycosylation site
FT   modified_site   151
FT                   /label= putative N-glycosylation site
FT   modified_site   270
FT                   /label= putative N-glycosylation site
FT   region          212..230
FT                   /label= transmembrane region
FT   peptide         1..28
FT                   /label= signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   455 AA;

  Query Match           52.0%;  Score 1322;  DB 2;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT   12
ID   R70103 standard; Protein; 900 AA.
AC   R70103;
DT   02-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 46-47; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70103 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence   900 AA;

  Query Match           52.0%;  Score 1321;  DB 13;  Length 900;
  Best Local Similarity 99.4%;  Pred. No. 5.93e-120;
  Matches   171;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtna 191
        |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTA 194


RESULT   13
ID   R70108 standard; Protein; 309 AA.
AC   R70108;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
FH   Key             Location/Qualifiers
FT   misc_difference 230..269
FT                   /label= repeat_region
FT                   /note= "can be repeated n times, where n is a real
FT                   number"
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 54-55; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
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CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The
CC   use of cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   309 AA;

  Query Match           51.9%;  Score 1319;  DB 13;  Length 309;
  Best Local Similarity  99.4%;  Pred. No. 9.50e-120;
  Matches   170;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
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Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
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Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts 190
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Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT   14
ID   R07451 standard; protein; 455 AA.
AC   R07451;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06285.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   455 AA;

  Query Match           51.9%;  Score 1319;  DB 2;  Length 455;
  Best Local Similarity  99.4%;  Pred. No. 9.50e-120;
  Matches   170;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 kqntvctchagfflrenecvscsnckkslectklclpqiqnvkgtedsgtt 211
        ||||||||||||||||||||||||||||||||||||||||||:||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT   15
ID   R70104 standard; Protein; 547 AA.
AC   R70104;
DT   02-NOV-1995  (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 47-48; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70104 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The use of
CC   cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   547 AA;

  Query Match           51.9%;  Score 1319;  DB 13;  Length 547;
  Best Local Similarity  99.4%;  Pred. No. 9.50e-120;
  Matches   170;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db     20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
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Db     80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
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Db    140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts 190
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Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


Search completed: Wed May  6 09:09:10 1998
Job time : 131 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:05:45 1998; MasPar time 14.61 Seconds
839.893 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-8
Description: (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 42.414; Variance 82.038; scale 0.517

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1322	52.0	455	1	GQHUT1	tumor necrosis factor	9.45e-253
2	1257	49.5	160	5	1EXTA	tumor necrosis factor	1.30e-238
3	1238	48.7	158	5	1EXTB	tumor necrosis factor	1.74e-234
4	1121	44.1	142	5	1NCFB	tumor necrosis factor	4.07e-209
5	1105	43.5	139	5	1TNRR	tumor necrosis factor	1.18e-205
6	1098	43.2	140	5	1NCFA	tumor necrosis factor	3.86e-204
7	1030	40.5	145	2	I37412	beta-gonadotropin - h	1.88e-189
8	1030	40.5	165	1	KTHUB	choriogonadotropin be	1.88e-189
9	1028	40.5	461	2	JC4302	tumor necrosis factor	5.08e-189
10	1024	40.3	145	2	I37231	beta-gonadotropin - h	3.70e-188
11	960	37.8	454	1	GQMST1	tumor necrosis factor	2.26e-174
12	960	37.8	454	2	I57826	tumor necrosis factor	2.26e-174
13	944	37.2	461	1	GQRTT1	tumor necrosis factor	6.21e-171
14	857	33.7	165	1	KTBAB	choriogonadotropin be	2.82e-152
15	803	31.6	110	5	1XULB	chorionic gonadotropi	9.67e-141
16	803	31.6	110	5	1HCNB	Human chorionic gonad	9.67e-141
17	803	31.6	110	5	1HRPB	chorionic gonadotropi	9.67e-141
18	740	29.1	121	2	I37994	beta-LH - human (frag	2.46e-127
19	709	27.9	115	1	UTHUB	lutropin beta chain -	9.18e-121
20	614	24.2	141	1	UTBOB	lutropin beta chain p	9.77e-101
21	614	24.2	141	2	I46949	luteinizing hormone b	9.77e-101
22	613	24.1	169	1	KTHOB	choriogonadotropin be	1.58e-100
23	596	23.5	119	2	A61465	lutropin beta chain -	5.78e-97
24	598	23.5	141	1	UTPGB	lutropin beta chain p	2.20e-97
25	597	23.5	141	1	UTRTB	lutropin beta chain p	3.57e-97
26	595	23.4	118	2	PN0139	lutropin beta chain -	9.36e-97
27	594	23.4	141	1	UTSHB	lutropin beta chain p	1.52e-96
28	587	23.1	138	2	S00512	lutropin beta chain p	4.42e-95
29	585	23.0	118	2	PN0141	lutropin beta chain -	1.16e-94
30	582	22.9	141	2	JC4527	luteinizing hormone b	4.90e-94
31	430	16.9	144	1	UTCAB	gonadotropin beta cha	1.20e-62
32	427	16.8	141	2	B60626	gonadotropin beta cha	4.90e-62
33	426	16.8	146	2	S16763	gonadotropin beta cha	7.82e-62
34	420	16.5	119	2	S09344	gonadotropin II beta	1.29e-60
35	416	16.4	142	2	C36179	gonadotropin II beta	8.39e-60
36	411	16.2	142	2	I51232	gonadotropin II beta	8.65e-59
37	407	16.0	113	2	S07092	gonadotropin beta cha	5.58e-58
38	405	15.9	112	2	S21196	lutropin beta chain -	1.42e-57
39	403	15.9	140	2	A48166	gonadotropin II beta	3.59e-57
40	398	15.7	142	2	A25800	gonadotropin beta cha	3.68e-56
41	388	15.3	142	2	I50143	gonadotropin II beta	3.81e-54
42	368	14.5	158	2	A61091	lutropin beta chain p	3.92e-50
43	366	14.4	166	2	I51242	luteinizing hormone b	9.84e-50
44	361	14.2	147	2	I50994	gonadotropin II beta	9.80e-49
45	352	13.9	159	2	I51373	luteinizing hormone b	6.08e-47

ALIGNMENTS

RESULT 1
ENTRY GQHUT1 #type complete

TITLE tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAM
CONTAINS tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-Oct-1997
ACCESSIONS A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE A38208
#authors Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
#journal Genomics (1992) 13:219-224
#title Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to chromosome 12p13.
#accession A38208
##molecule_type DNA
##residues 1-455 ##label FUC
##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748; PID:g339750
REFERENCE A34899
#authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.
#journal Cell (1990) 61:351-359
#title Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.
#cross-references MUID:90235284
#accession A34899
##molecule_type mRNA
##residues 1-455 ##label LOE
##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
##experimental_source placenta
##note part of this sequence, including the amino end of the mature protein, confirmed by protein sequencing
REFERENCE A34900
#authors Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab, H.; Kohr, W.J.; Goeddel, D.V.
#journal Cell (1990) 61:361-370
#title Molecular cloning and expression of a receptor for human tumor necrosis factor.
#cross-references MUID:90235285
#accession A34900
##molecule_type mRNA
##residues 1-455 ##label SCH
##cross-references GB:M33294; NID:g339744; PID:g339745

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REFERENCE        A36555
  #authors       Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                   Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                   Stratowa, C.; Adolf, G.R.
  #journal       DNA Cell Biol. (1990) 9:705-715
  #title         Molecular cloning and expression of human and rat tumor
                   necrosis factor receptor chain (p60) and its soluble
                   derivative, tumor necrosis factor-binding protein.
  #cross-references MUID:91090841
  #accession     A36555
    ##molecule_type mRNA
    ##residues      1-455 ##label HIM
    ##cross-references GB:M63121; NID:g339755; PID:g339756
  #accession     C36555
    ##molecule_type protein
    ##residues      30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
                     107-128;162-167,'X',169-201 ##label HI2
    ##note          the purified protein, called tumor necrosis factor
                     binding protein, is a soluble derivative of the
                     receptor
REFERENCE        A38281
  #authors       Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
                   M.
  #journal       Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
  #title         Cloning of human tumor necrosis factor (TNF) receptor cDNA
                   and expression of recombinant soluble TNF-binding protein.
  #cross-references MUID:91017509
  #accession     A38281
    ##molecule_type mRNA
    ##residues      1-455 ##label GRA
    ##cross-references GB:M37764
    ##note          the authors translated the codon TGG for residue 371 as
                     Thr, AAG for residue 372 as Leu, and GAC for residue
                     427 as Asn
REFERENCE        S12057
  #authors       Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
                   R.; Aderka, D.; Holtmann, H.; Wallach, D.
  #journal       EMBO J. (1990) 9:3269-3278
  #title         Soluble forms of tumor necrosis factor receptors (TNF-Rs).
                   The cDNA for the type I TNF-R, cloned using amino acid
                   sequence data of its soluble form, encodes both the cell
                   surface and a soluble form of the receptor.
  #cross-references MUID:91006021
  #accession     S12057
    ##molecule_type mRNA
    ##residues      1-455 ##label NOP
    ##cross-references EMBL:X55313; NID:g37223; PID:g37224
    ##note          parts of soluble TNF binding protein 1, including its
                     amino and carboxyl ends, were confirmed by protein
                     sequencing
REFERENCE        JT0758
  #authors       Kemper, O.; Wallach, D.
  #journal       Gene (1993) 134:209-216
  #title         Cloning and partial characterization of the promoter for the
                   human p55 tumor necrosis factor (TNF) receptor.
  #accession     JT0758
    ##molecule_type DNA
    ##residues      1-13 ##label KEM
REFERENCE        A60231
  #authors       Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
                   J.M.
  #journal       Eur. J. Immunol. (1990) 20:1167-1174
  #title         Tumor necrosis factor inhibitor: purification, NH-2-terminal
                   amino acid sequence and evidence for anti-inflammatory and
                   immunomodulatory activities.
  #cross-references MUID:90292116
  #accession     A60231
    ##molecule_type protein
    ##residues      41-43,'X',45-53,'X',55-57 ##label SEC
REFERENCE        A38258
  #authors       Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
                   J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
                   R.S.; Granger, G.A.
  #journal       Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
  #title         Purification and characterization of an inhibitor (soluble
                   tumor necrosis factor receptor) for tumor necrosis factor
                   and lymphotoxin obtained from the serum ultrafiltrates of
                   human cancer patients.
  #cross-references MUID:91062364
  #accession     A38258
    ##molecule_type protein
    ##residues      41-60 ##label GAT
    ##experimental_source cancer patient serum
REFERENCE        A60594
  #authors       Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
                   Grubb, A.; Adolf, G.
  #journal       Eur. J. Haematol. (1989) 42:270-275
  #title         Isolation and characterization of a tumor necrosis factor
                   binding protein from urine.
  #accession     A60594
    ##molecule_type protein
    ##residues      41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
    ##experimental_source renal failure patient urine
REFERENCE        A35010
  #authors       Engelmann, H.; Novick, D.; Wallach, D.
  #journal       J. Biol. Chem. (1990) 265:1531-1536
  #title         Two tumor necrosis factor-binding proteins purified from
                   human urine. Evidence for immunological cross-reactivity
                   with cell surface tumor necrosis factor receptors.
  #cross-references MUID:90110215
  #accession     A35010
    ##molecule_type protein
    ##residues      41-45 ##label ENG
    ##experimental_source normal urine
REFERENCE        JC2404
  #authors       Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
  #journal       Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
  #title         Amino acid sequence of natural tumor necrosis factor alpha
                   inhibitor purified from human urine.
  #accession     JC2404
    ##molecule_type protein
    ##residues      41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
                     ##label KAJ
    ##experimental_source urine
COMMENT      This protein is one of two known receptors for both TNF-alpha
               (cachectin) and TNF-beta (lymphotoxin).
GENETICS
  #gene          GDB:TNFR1
    ##cross-references GDB:125913; OMIM:191190
  #map_position 12p13.2-12p13.2
  #introns       13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION   #superfamily tumor necrosis factor receptor type 1; NGF
                   receptor repeat homology
KEYWORDS         duplication; glycoprotein; receptor; transmembrane protein
FEATURE
  1-21               #domain signal sequence #status predicted #label SIG\
  22-455             #product tumor necrosis factor receptor type 1 #status
                       predicted #label MAT\
  30-211             #domain extracellular #status predicted #label EXT\
  41-201             #product TNF binding protein 1 (tumor necrosis factor
                       alpha inhibitor) #status experimental #label TBP1\
  44-82              #domain NGF receptor repeat homology #label NG1\
  84-126             #domain NGF receptor repeat homology #label NG2\
  127-167            #domain NGF receptor repeat homology #label NG3\
  168-196            #domain NGF receptor repeat homology #label NG4\
  212-234            #domain transmembrane #status predicted #label MEM\
  235-455            #domain intracellular #status predicted #label INT\
  54,145,151         #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
SUMMARY          #length 455  #molecular-weight 50494  #checksum 153

  Query Match           52.0%;  Score 1322;  DB 1;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 9.45e-253;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    2
ENTRY             1EXTA      #type complete

TITLE             tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE         extracellular domain of the 55kda tumor necrosis factor
                    receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, the construct contains
                    residues 12 to 172 of the mature sequence of the entire
                    receptor. residue 11 is mutated to met as a result of the
                    expression system
REFERENCE         A65560
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, July 1996
   #cross-references PDB:1EXT
REFERENCE         TN026248
   #authors       Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
   #journal       J. Biol. Chem. (1995) 270:13303
   #title         Crystallographic evidence for dimerization of unliganded
                    tumor necrosis factor receptor.
REFERENCE         TN026249
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 1.85 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   66-68               #region helix (right hand 3-10)\
   141-143             #region helix (right hand 3-10)\
   151-154             #region helix (right hand alpha)\
   7-9,17-19           #region beta sheet\
   131-134,137-140     #region beta sheet\
   25-29,39-42         #region beta sheet\
   71-74,83-85         #region beta sheet\
   90-96,99-104        #region beta sheet\
   111-115,124-127     #region beta sheet\
   3-17                #disulfide_bonds\
   18-31               #disulfide_bonds\
   21-40               #disulfide_bonds\
   43-58               #disulfide_bonds\
   61-76               #disulfide_bonds\
   64-84               #disulfide_bonds\
   86-102              #disulfide_bonds\
   105-117             #disulfide_bonds\
   108-125             #disulfide_bonds\
   127-138             #disulfide_bonds\
   141-154             #disulfide_bonds\
   144-150             #disulfide_bonds
SUMMARY           #length 160  #molecular-weight 18065  #checksum 2297
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Db       1 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      24 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 83

Db      61 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      84 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 143

Db     121 QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN 160
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Qy     144 QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN 183


RESULT    3
ENTRY             1EXTB      #type complete

TITLE             tumor necrosis factor receptor extracellular domain, chain B
PDB_TITLE         extracellular domain of the 55kda tumor necrosis factor
                    receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, the construct contains
                    residues 12 to 172 of the mature sequence of the entire
                    receptor. residue 11 is mutated to met as a result of the
                    expression system
REFERENCE         A65560
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, July 1996
   #cross-references PDB:1EXT
REFERENCE         TN026251
   #authors       Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
   #journal       J. Biol. Chem. (1995) 270:13303
   #title         Crystallographic evidence for dimerization of unliganded
                    tumor necrosis factor receptor.
REFERENCE         TN026252
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 1.85 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   68-70               #region helix (right hand 3-10)\
   143-145             #region helix (right hand 3-10)\
   9-11,19-21          #region beta sheet\
   133-136,139-142     #region beta sheet\
   27-31,41-44         #region beta sheet\
   73-76,85-87         #region beta sheet\
   92-98,101-106       #region beta sheet\
   113-117,126-129     #region beta sheet\
   5-19                #disulfide_bonds\
   20-33               #disulfide_bonds\
   23-42               #disulfide_bonds\
   45-60               #disulfide_bonds\
   63-78               #disulfide_bonds\
   66-86               #disulfide_bonds\
   88-104              #disulfide_bonds\
   107-119             #disulfide_bonds\
   110-127             #disulfide_bonds\
   129-140             #disulfide_bonds\
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   143-156           #disulfide_bonds\
   146-152           #disulfide_bonds
SUMMARY          #length 158  #molecular-weight 17827  #checksum 5022

  Query Match           48.7%;  Score 1238;  DB 5;  Length 158;
  Best Local Similarity 100.0%;  Pred. No. 1.74e-234;
  Matches   157;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 158
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Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 179


RESULT    4
ENTRY             1NCFB      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain B - hu
ALTERNATE_NAMES   stnfr1; type i receptor
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029041
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   2-16                #disulfide_bonds\
   17-30               #disulfide_bonds\
   20-39               #disulfide_bonds\
   42-57               #disulfide_bonds\
   60-75               #disulfide_bonds\
   63-83               #disulfide_bonds\
   85-101              #disulfide_bonds\
   104-116             #disulfide_bonds\
   107-124             #disulfide_bonds\
   126-137             #disulfide_bonds
SUMMARY          #length 142  #molecular-weight 16046  #checksum 1225

  Query Match           44.1%;  Score 1121;  DB 5;  Length 142;
  Best Local Similarity 100.0%;  Pred. No. 4.07e-209;
  Matches   142;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
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Qy     25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db     61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db    121 NTVCTCHAGFFLRENECVSCSN 142
          ||||||||||||||||||||||
Qy    145 NTVCTCHAGFFLRENECVSCSN 166


RESULT    5
ENTRY             1TNRR      #type complete

TITLE             tumor necrosis factor receptor type 1 (P55 extracellular
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          recombinant form expressed in Baculovirus SF9
REFERENCE         A52442
   #authors       Banner, D.W.
   #submission    submitted to the Brookhaven Protein Data Bank, May 1994
   #cross-references PDB:1TNR
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
REFERENCE         TN034093
   #authors       D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
                    Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
                    Lesslauer, W.
   #journal       J. Mol. Biol. (1993) 229:555
   #title         Crystallization and preliminary analysis of tnf-beta and a
                    tnf-beta-55 kd tnf receptor complex.
COMMENT     Resolution: 2.85 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS          Complex(lymphokineRECEPTOR)
FEATURE
   1-15                #disulfide_bonds\
   16-29               #disulfide_bonds\
   19-38               #disulfide_bonds\
   41-56               #disulfide_bonds\
   59-74               #disulfide_bonds\
   62-82               #disulfide_bonds\
   84-100              #disulfide_bonds\
   103-115             #disulfide_bonds\
   106-123             #disulfide_bonds\
   125-136             #disulfide_bonds
SUMMARY          #length 139  #molecular-weight 15746  #checksum 5235

  Query Match           43.5%;  Score 1105;  DB 5;  Length 139;
  Best Local Similarity 100.0%;  Pred. No. 1.18e-205;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db     61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db    121 TVCTCHAGFFLRENECVSC 139
          |||||||||||||||||||
Qy    146 TVCTCHAGFFLRENECVSC 164


RESULT    6
ENTRY             1NCFA      #type complete

TITLE             tumor necrosis factor receptor 55 kd extracellular domain
                    contains residues 12 172 of the mature receptor sequence,
                    chain A - hu
ALTERNATE_NAMES   stnfr1; type i receptor
```

```
ORGANISM          #formal_name Homo sapiens #common_name man
   #note          expressed in Escherichia coli, residue 11 is mutated to met
                    as a result of the expression system
REFERENCE         A66195
   #authors       Naismith, J.H.; Sprang, S.R.
   #submission    submitted to the Brookhaven Protein Data Bank, October 1994
   #cross-references PDB:1NCF
REFERENCE         TN029039
   #authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                    K.; Naismith, J.H.; Sprang, S.R.
   #journal       J. Mol. Biol. (1994) 239:332
   #title         Two crystal forms of the extracellular domain of type i tumor
                    necrosis factor receptor.
REFERENCE         A40737
   #authors       Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #journal       Cell (1993) 73:431-445
   #title         Crystal structure of the soluble human 55 kd TNF
                    receptor-human TNFbeta complex: implications for TNF
                    receptor activation.
COMMENT     Resolution: 2.25 angstroms
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
   5-19                #disulfide_bonds\
   20-33               #disulfide_bonds\
   23-42               #disulfide_bonds\
   45-60               #disulfide_bonds\
   63-78               #disulfide_bonds\
   66-86               #disulfide_bonds\
   88-104              #disulfide_bonds\
   107-119             #disulfide_bonds\
   110-127             #disulfide_bonds\
   129-140             #disulfide_bonds
SUMMARY           #length 140  #molecular-weight 15889  #checksum 6622

  Query Match           43.2%;  Score 1098;  DB 5;  Length 140;
  Best Local Similarity 100.0%;  Pred. No. 3.86e-204;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENEC 140
          ||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENEC 161


RESULT    7
ENTRY             I37412      #type fragment

TITLE             beta-gonadotropin - human (fragment)ORGANISM         #formal_name Homo
DATE              21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
                    09-May-1997
ACCESSIONS        I37412
REFERENCE         I37231
   #authors       Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
   #journal       Nature (1984) 307:37-40
   #title         Evolution of the genes for the beta subunits of human
                    chorionic gonadotropin and luteinizing hormone.
   #cross-references MUID:84093590
   #accession     I37412
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-145 ##label RES
      ##cross-references EMBL:X00265; NID:g31719
GENETICS
   #introns       41/3
CLASSIFICATION    #superfamily pituitary glycoprotein hormone beta chain
SUMMARY           #length 145  #checksum 2358

  Query Match           40.5%;  Score 1030;  DB 2;  Length 145;
  Best Local Similarity 100.0%;  Pred. No. 1.88e-189;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    127 SLPSPSRLPGPSDTPILPQ 145
          |||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT    8
ENTRY             KTHUB       #type complete

TITLE             choriogonadotropin beta chain precursor - humanALTERNATE_NAMES  chor
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change
                    20-Mar-1998
ACCESSIONS        A93230; I69972; I55224; I55250; I70007; I70008; A92303;
                    A92181; A92142; PC1016; A61097; B56873; A01502
REFERENCE         A93230
   #authors       Fiddes, J.C.; Goodman, H.M.
   #journal       Nature (1980) 286:684-687
   #title         The cDNA for the beta-subunit of human chorionic gonadotropin
                    suggests evolution of a gene by readthrough into the
                    3'-untranslated region.
   #cross-references MUID:81012134
   #accession     A93230
      ##molecule_type mRNA
      ##residues       1-165 ##label FID
      ##cross-references GB:J00117; GB:M38559; GB:M54963; NID:g180436;
                          PID:g180437
REFERENCE         I55224
   #authors       Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, H.;
                    Boothby, M.R.; Boime, I.
   #journal       J. Biol. Chem. (1983) 258:11492-11499
   #title         The beta subunit of human chorionic gonadotropin is encoded
                    by multiple genes.
   #cross-references MUID:84008141
   #accession     I69972
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-165 ##label POL
      ##cross-references GB:K03189; NID:g180450; PID:g180453
      ##note           clone CG-beta-e
   #accession     I55224
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-23,'M',25-136,'A',138-165 ##label PO2
      ##cross-references GB:K03183; NID:g180442; PID:g180444
      ##note           clone CG-beta-a
REFERENCE         I55250
   #authors       Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
   #journal       J. Biol. Chem. (1986) 261:5907-5916
   #title         A map of the hCG beta-LH beta gene cluster.
   #cross-references MUID:86195987
   #accession     I55250
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-5 ##label PO3
      ##cross-references GB:M13504; NID:g180419; PID:g463088
      ##note           CG-beta-3 gene
   #accession     I70007
```

```
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-5 ##label PO4
      ##cross-references GB:M13505; NID:g180429; PID:g463089
      ##note          CG-beta-6 gene
   #accession    I70008
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-5 ##label RE5
      ##cross-references GB:M13503; NID:g180432; PID:g463090
      ##note          CG-beta-7 gene
REFERENCE        A92303
   #authors      Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
   #journal      J. Biol. Chem. (1981) 256:1816-1823
   #title        The amino acid sequences of the prepeptides contained in the
                  alpha and beta subunits of human choriogonadotropin.
   #cross-references MUID:81117268
   #accession    A92303
      ##molecule_type protein
      ##residues      1-20 ##label BIR
      ##note          the identity of the residue at position 19 could not be
                       determined
REFERENCE        A92181
   #authors      Morgan, F.J.; Birken, S.; Canfield, R.E.
   #journal      J. Biol. Chem. (1975) 250:5247-5258
   #title        The amino acid sequence of human chorionic gonadotropin. The
                  alpha subunit and beta subunit.
   #cross-references MUID:75211304
   #accession    A92181
      ##molecule_type protein
      ##residues      21-165 ##label MOR
REFERENCE        A92142
   #authors      Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
   #journal      J. Biol. Chem. (1973) 248:6810-6827
   #cross-references MUID:74011267
   #accession    A92142
      ##molecule_type protein
      ##residues      21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
                       ##label CAR
REFERENCE        PC1016
   #authors      Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.;
                  Wang, Y.
   #journal      Chinese Biochem. J. (1990) 6:558-562
   #title        The immunological characteristics of the enzymatic fragments
                  of human chorionic gonadotropin beta-subunit.
   #accession    PC1016
      ##molecule_type protein
      ##residues      21-165 ##label SHI
      ##note          article in Chinese with English abstract
REFERENCE        A61097
   #authors      Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.;
                  Agosto, G.M.; Krichevsky, A.; Vaitukaitis, J.L.; Canfield,
                  R.E.
   #journal      Endocrinology (1988) 123:572-583
   #title        Structure of the human chorionic gonadotropin beta-subunit
                  fragment from pregnancy urine.
   #accession    A61097
      ##molecule_type protein
      ##residues      26-32,'X',34-49,'X',51-60;75-112 ##label BI2
      ##note          this material from pregancy urine lacks sialic acid in
                       its carbohydrate and has been processed further from
                       the mature form into two chains linked by disulfide
                       bonds
REFERENCE        A56873
   #authors      Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
   #journal      Br. J. Cancer (1993) 67:686-692
   #title        Characterisation of UGP and its relationship with beta-core
                  fragment.
   #cross-references MUID:93229246
   #accession    B56873
      ##molecule_type protein
      ##residues      26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',
                       78-91,'G',93-102 ##label KAR
      ##experimental_source urine
      ##note          sequence modified after extraction from NCBI backbone
      ##note          this material was designated urinary gonadotrophin
                       peptide (peak 2)
REFERENCE        A44674
   #authors      Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                  J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                  N.W.
   #journal      Nature (1994) 369:455-461
   #title        Crystal structure of human chorionic gonadotropin.
   #contents     annotation; X-ray crystallography, 3.0 angstroms; correction
                  of disulfide bonds
GENETICS
   #gene         GDB:CGB
      ##cross-references GDB:119055; OMIM:118860
   #map_position 19q13.3-19q13.3
   #introns      5/3; 61/3
   #note         the choriogonadotropin beta chain locus contains six genes
                  (or pseudogenes)
CLASSIFICATION   #superfamily pituitary glycoprotein hormone beta chain
KEYWORDS         glycoprotein; hormone; pituitary
FEATURE
   1-20              #domain signal sequence #status experimental #label SIG\
   21-165            #product choriogonadotropin beta chain #status
                       experimental #label MAT\
   29-77,43-92,46-130,
   54-108,58-110,
   113-120           #disulfide_bonds #status experimental\
   33,50             #binding_site carbohydrate (Asn) (covalent) #status
                       experimental\
   138,150           #binding_site carbohydrate (Ser) (covalent) #status
                       predicted\
   141,147,152,158   #binding_site carbohydrate (Ser) (covalent) #status
                       experimental
SUMMARY          #length 165  #molecular-weight 17739  #checksum 6523

  Query Match           40.5%;  Score 1030;  DB 1;  Length 165;
  Best Local Similarity 100.0%;  Pred. No. 1.88e-189;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     27 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 146
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    147 SLPSPSRLPGPSDTPILPQ 165
        ||||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT    9
ENTRY            JC4302     #type complete

TITLE            tumor necrosis factor receptor p55 - pigORGANISM         #formal_nam
DATE             29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                   12-Dec-1997
ACCESSIONS       JC4302; PC4093
REFERENCE        JC4302
   #authors      Suter, B.; Pauli, U.
   #journal      Gene (1995) 163:263-266
   #title        Cloning of the cDNA encoding the porcine p55 tumor necrosis
                  factor receptor.
   #accession    JC4302
      ##molecule_type mRNA
      ##residues      1-461 ##label SUT
      ##cross-references GB:U19994; NID:g1141752; PID:g1141753
   #accession    PC4093
      ##molecule_type protein
      ##residues      1-7 ##label SU2
      ##experimental_source kidney cell line 15
```

```
GENETICS
   #gene          tnfr
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
   1-29                #domain signal sequence #status predicted #label SIG\
   30-461              #product tumor necrosis factor receptor p55 #status
                         predicted #label MAT\
   44-194              #domain extracellular cysteine rich #status predicted
                         #label EXT\
   44-82               #domain NGF receptor repeat homology #label NG1\
   211-231             #domain transmembrane #status predicted #label TMM\
   361-447             #domain signal transduction #status predicted #label
                         SIT\
   54,145,151          #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
SUMMARY           #length 461  #molecular-weight 50696  #checksum 8079

  Query Match            40.5%;  Score 1028;  DB 2;  Length 461;
  Best Local Similarity  73.1%;  Pred. No. 5.08e-189;
  Matches   125;  Conservative   24;  Mismatches  21;  Indels   1;  Gaps   1;

Db      41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
           :|:|||||| |||| |||||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
           |||||| ||:|||||:|||||||||||||||| |||| ||||:||||| ||||:|:|| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPATSETRNDFQDTGTT 210
           ||:|:| ||:|||||::||||| |||:: :| :|| :  |  :  :|:|||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT   10
ENTRY             I37231     #type fragment

TITLE             beta-gonadotropin - human (fragment)ORGANISM         #formal_name Homo
DATE              21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
                    09-May-1997
ACCESSIONS        I37231
REFERENCE         I37231
   #authors       Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
   #journal       Nature (1984) 307:37-40
   #title         Evolution of the genes for the beta subunits of human
                    chorionic gonadotropin and luteinizing hormone.
   #cross-references MUID:84093590
   #accession     I37231
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-145 ##label RES
      ##cross-references EMBL:X00266; NID:g29907
GENETICS
   #introns       41/3
CLASSIFICATION    #superfamily pituitary glycoprotein hormone beta chain
SUMMARY           #length 145  #checksum 2349

  Query Match            40.3%;  Score 1024;  DB 2;  Length 145;
  Best Local Similarity  99.3%;  Pred. No. 3.70e-188;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db       7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP 126
           ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db     127 SLPSPSRLPGPSDTPILPQ 145
           ||||||||||||||||||||
Qy     318 SLPSPSRLPGPSDTPILPQ 336


RESULT   11
ENTRY             GQMST1     #type complete

TITLE             tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAM
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    05-Sep-1997
ACCESSIONS        A38634; B40254; S16677; S19021; I54532
REFERENCE         A38634
   #authors       Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
                    G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
   #title         Cloning and expression of cDNAs for two distinct murine tumor
                    necrosis factor receptors demonstrate one receptor is
                    species specific.
   #cross-references MUID:91187885
   #accession     A38634
      ##molecule_type mRNA
      ##residues       1-454 ##label LEW
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         A40254
   #authors       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
                    C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
   #journal       Mol. Cell. Biol. (1991) 11:3020-3026
   #title         Molecular cloning and expression of the type 1 and type 2
                    murine receptors for tumor necrosis factor.
   #cross-references MUID:91246168
   #accession     B40254
      ##molecule_type mRNA
      ##residues       1-454 ##label GO2
      ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE         S16677
   #authors       Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis,
                    A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
   #journal       Eur. J. Immunol. (1991) 21:1649-1656
   #title         Cloning, expression and cross-linking analysis of the murine
                    p55 tumor necrosis factor receptor.
   #cross-references MUID:91285014
   #accession     S16677
      ##molecule_type mRNA
      ##residues       1-454 ##label BAR
      ##cross-references EMBL:X59238; NID:g53578; PID:g53579
REFERENCE         S19021
   #authors       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
   #journal       Immunogenetics (1991) 34:338-340
   #title         Molecular cloning and expression of the mouse Tnf receptor
                    type b.
   #cross-references MUID:92039815
   #accession     S19021
      ##molecule_type mRNA
      ##residues       1-454 ##label ROT
      ##cross-references EMBL:X57796; NID:g54848; PID:g54849
REFERENCE         I54532
   #authors       Bebo, B.F.
   #journal       Immunogenetics (1994) 39:450-451
   #title         Nucleotide sequence of the TNF type I receptor from a mouse
                    endothelioma cell line.
   #cross-references MUID:94245292
   #accession     I54532
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-454 ##label RES
      ##cross-references GB:L26349; NID:g430732; PID:g430733
COMMENT      This protein is one of two distantly related receptors for both
               TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                #domain signal sequence #status predicted #label SIG\
```

```
   30-454            #product tumor necrosis factor receptor type 1 #status
                       predicted #label MAT\
   30-212            #domain extracellular #status predicted #label EXT\
   44-82             #domain NGF receptor repeat homology #label NG1\
   84-126            #domain NGF receptor repeat homology #label NG2\
   127-167           #domain NGF receptor repeat homology #label NG3\
   168-204           #domain NGF receptor repeat homology #label NG4\
   213-235           #domain transmembrane #status predicted #label MEM\
   236-454           #domain intracellular #status predicted #label INT\
   54,151,202        #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
SUMMARY          #length 454  #molecular-weight 50129  #checksum 4839

  Query Match           37.8%;  Score 960;  DB 1;  Length 454;
  Best Local Similarity  68.6%;  Pred. No. 2.26e-174;
  Matches   118;  Conservative   27;  Mismatches  26;  Indels   1;  Gaps   1;

Db     41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  |||||:|||||:|  |:|||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
          ||||| |||||||||:|||:||:|||: || |||||  : ||   :||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ-IENVKGTEDSGTT 193


RESULT   12
ENTRY            I57826     #type complete

TITLE            tumor necrosis factor receptor - mouseORGANISM        #formal_name Mus
DATE             02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                   23-May-1997
ACCESSIONS       I57826
REFERENCE        I57826
   #authors      Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
                   Steinmetz, M.
   #journal      Mol. Immunol. (1993) 30:165-176
   #title        Genomic organization and promoter function of the murine
                   tumor necrosis factor receptor beta gene.
   #cross-references MUID:93156721
   #accession    I57826
      ##status       preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues     1-454 ##label RES
      ##cross-references GB:M76656; NID:g202100; PID:g202102
GENETICS
   #gene         TNFR-2
   #introns      13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION   #superfamily tumor necrosis factor receptor type 1; NGF
                   receptor repeat homology
KEYWORDS         cytokine receptor
SUMMARY          #length 454  #molecular-weight 50030  #checksum 4267

  Query Match           37.8%;  Score 960;  DB 2;  Length 454;
  Best Local Similarity  68.6%;  Pred. No. 2.26e-174;
  Matches   118;  Conservative   27;  Mismatches  26;  Indels   1;  Gaps   1;

Db     41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          ||:|||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  |||||:|||||:|  |:|||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
          ||||| |||||||||:|||:||:|||: || |||||  : ||   :||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ-IENVKGTEDSGTT 193


RESULT   13
ENTRY            GQRTT1     #type complete

TITLE            tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
DATE             30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
                   05-Sep-1997
ACCESSIONS       B36555
REFERENCE        A36555
   #authors      Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                   Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                   Stratowa, C.; Adolf, G.R.
   #journal      DNA Cell Biol. (1990) 9:705-715
   #title        Molecular cloning and expression of human and rat tumor
                   necrosis factor receptor chain (p60) and its soluble
                   derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
   #accession    B36555
      ##molecule_type mRNA
      ##residues     1-461 ##label HIM
      ##cross-references GB:M63122; NID:g207361; PID:g207362
COMMENT          This protein is one of two known receptors for both TNF-alpha
                   (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION   #superfamily tumor necrosis factor receptor type 1; NGF
                   receptor repeat homology
KEYWORDS         duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29              #domain signal sequence #status predicted #label SIG\
   30-461            #product tumor necrosis factor receptor type 1 #status
                       predicted #label MAT\
   30-211            #domain extracellular #status predicted #label EXT\
   30-201            #product tumor necrosis factor binding protein #status
                       predicted #label TBP\
   44-82             #domain NGF receptor repeat homology #label NG1\
   84-126            #domain NGF receptor repeat homology #label NG2\
   127-167           #domain NGF receptor repeat homology #label NG3\
   168-204           #domain NGF receptor repeat homology #label NG4\
   212-234           #domain transmembrane #status predicted #label MEM\
   235-461           #domain intracellular #status predicted #label INT\
   54,151,201        #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
SUMMARY          #length 461  #molecular-weight 50969  #checksum 1617

  Query Match           37.2%;  Score 944;  DB 1;  Length 461;
  Best Local Similarity  67.3%;  Pred. No. 6.21e-171;
  Matches   115;  Conservative   25;  Mismatches  31;  Indels   0;  Gaps   0;

Db     41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
          |::|||||| || |||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  ||||| |||||:|  | ||||||:|||:::| ||  ||| :|| |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTA 211
          |||||| |||||||  ||| :||:|||: || ||||| : ||   :||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT   14
ENTRY            KTBAB      #type complete

TITLE            choriogonadotropin beta chain precursor - olive baboonORGANISM
                   #common_name olive baboon
DATE             31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
                   03-May-1996
ACCESSIONS       A25808
REFERENCE        A25808
   #authors      Crawford, R.J.; Tregear, G.W.; Niall, H.D.
   #journal      Gene (1986) 46:161-169
   #title        The nucleotide sequences of baboon chorionic gonadotropin
```

```
                beta-subunit genes have diverged from the human.
   #cross-references MUID:87106851
   #accession    A25808
      ##molecule_type mRNA
      ##residues      1-165 ##label CRA
COMMENT    There are at least five copies of CG-related genes and at least two
           of these are expressed in the baboon placenta.
CLASSIFICATION   #superfamily pituitary glycoprotein hormone beta chain
KEYWORDS         glycoprotein; hormone; placenta; pregnancy maintenance
FEATURE
   1-20              #domain signal sequence #status predicted #label SIG\
   21-165            #product choriogonadotropin beta chain #status predicted
                       #label CGB\
   29-77,43-92,46-130,
   54-108,58-110,
   113-120           #disulfide_bonds #status predicted\
   33,50             #binding_site carbohydrate (Asn) (covalent) #status
                       predicted\
   140,147,152       #binding_site carbohydrate (Ser) (covalent) #status
                       predicted
SUMMARY          #length 165  #molecular-weight 17592  #checksum 4960

  Query Match           33.7%;  Score 857;  DB 1;  Length 165;
  Best Local Similarity  81.3%;  Pred. No. 2.82e-152;
  Matches   113;  Conservative   14;  Mismatches  12;  Indels   0;  Gaps   0;

Db      27 PLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES 86
           | ||||||||| |||:||||:||||||||||||||| ||||:|||::|||||||:|||||
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      87 IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSSKDPPP 146
           ||||||| ||:|:|| :|||||:||||||||:||||||||||||| :| ||||| |||
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db     147 SPPSPSRLLEPAGTPFLPQ 165
           | ||||||  |: ||:|||
Qy     318 SLPSPSRLPGPSDTPILPQ 336


RESULT   15
ENTRY            1XULB      #type complete

TITLE            chorionic gonadotropin, chain B - humanPDB_TITLE       theoretical mod
                   receptor complexed with human chorionic gonadotropin
ORGANISM         #formal_name Homo sapiens #common_name man
REFERENCE        A66957
   #authors      Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                   Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #submission   submitted to the Brookhaven Protein Data Bank, December 1996
   #cross-references PDB:1XUL
REFERENCE        TN032625
   #authors      Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
                   Wu, H.; Hendrickson, W.A.; El Tayar, N.
   #journal      Structure (London) (1996) 3:1341
   #title        Structural predictions for the ligand-binding region of
                   glycoprotein hormone receptors and the nature of
                   hormone-receptor interactions structure.
REFERENCE        TN032626
   #authors      Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
                   Hendrickson, W.A.
   #journal      Structure (London) (1994) 2:545
   #title        Structure of human chorionic gonadotropin at 2.6 a resolution
                   from mad analysis of the selenomethionyl protein.
COMMENT    Resolution: not applicable
COMMENT    Determination: theoretical model
KEYWORDS         complex; glycoprotein hormone receptor glycoprotein; hormone;
                   phosphorylation; receptor
FEATURE
   97-101,26-39,9-17  #region beta sheet\
   54-59,86-91        #region beta sheet\
   61-67,78-84        #region beta sheet\
   8-56               #disulfide_bonds\
   22-71              #disulfide_bonds\
   25-109             #disulfide_bonds\
   33-87              #disulfide_bonds\
   37-89              #disulfide_bonds\
   92-99              #disulfide_bonds
SUMMARY          #length 110  #molecular-weight 11906  #checksum 6414

  Query Match           31.6%;  Score 803;  DB 5;  Length 110;
  Best Local Similarity 100.0%;  Pred. No. 9.67e-141;
  Matches   105;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       6 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 65
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      66 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 110
           |||||||||||||||||||||||||||||||||||||||||||||
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 302


Search completed: Wed May  6 09:06:41 1998
Job time : 56 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:03:29 1998; MasPar time 9.80 Seconds
859.610 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-8
Description: (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 44.259; Variance 72.852; scale 0.608

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1322	52.0	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	6.45e-296
2	1030	40.5	165	1	CGHB_HUMAN	CHORIOGONADOTROPIN BET	1.12e-221
3	1028	40.5	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	3.59e-221
4	960	37.8	454	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	5.34e-204
5	944	37.2	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	5.76e-200
6	857	33.7	165	1	CGHB_PAPAN	CHORIOGONADOTROPIN BET	4.26e-178
7	740	29.1	141	1	LSHB_HUMAN	LUTROPIN BETA CHAIN PR	7.12e-149
8	709	27.9	164	1	CGHB_CALJA	CHORIOGONADOTROPIN BET	3.56e-141
9	630	24.8	169	1	LSHB_EQUAS	LUTROPIN/CHORIOGONADOT	1.18e-121
10	614	24.2	141	1	LSHB_BOVIN	LUTROPIN BETA CHAIN PR	1.01e-117
11	613	24.1	169	1	LSHB_HORSE	LUTROPIN/CHORIOGONADOT	1.77e-117
12	602	23.7	141	1	LSHB_SHEEP	LUTROPIN BETA CHAIN PR	8.87e-115
13	598	23.5	141	1	LSHB_PIG	LUTROPIN BETA CHAIN PR	8.48e-114
14	597	23.5	141	1	LSHB_RAT	LUTROPIN BETA CHAIN PR	1.49e-113
15	595	23.4	118	1	LSHB_BALAC	LUTROPIN BETA CHAIN (L	4.61e-113
16	587	23.1	138	1	LSHB_CANFA	LUTROPIN BETA CHAIN PR	4.19e-111
17	585	23.0	118	1	LSHB_PHYCA	LUTROPIN BETA CHAIN (L	1.29e-110
18	542	21.3	105	1	LSHB_MOUSE	LUTROPIN BETA CHAIN PR	4.00e-100
19	430	16.9	144	1	GTHB_CYPCA	GONADOTROPIN BETA CHAI	3.62e-73
20	427	16.8	141	1	GTHB_HYPMO	GONADOTROPIN BETA CHAI	1.87e-72
21	426	16.8	146	1	GTHB_CTEID	GONADOTROPIN BETA CHAI	3.23e-72
22	416	16.4	142	1	GTH2_ONCKE	GONADOTROPIN BETA-II C	7.62e-70
23	411	16.2	138	1	GTHB_CLAGA	GONADOTROPIN BETA CHAI	1.16e-68
24	411	16.2	142	1	GTH2_ONCMA	GONADOTROPIN BETA-II C	1.16e-68
25	407	16.0	113	1	GTHB_MURCI	GONADOTROPIN BETA CHAI	1.03e-67
26	405	15.9	112	1	LSHB_RANCA	LUTROPIN BETA CHAIN (L	3.05e-67
27	403	15.9	140	1	GTH2_ANGAN	GONADOTROPIN BETA-II C	9.05e-67
28	398	15.7	142	1	GTHB_ONCTS	GONADOTROPIN BETA CHAI	1.37e-65
29	388	15.3	142	1	GTH2_CORAU	GONADOTROPIN BETA-II C	3.09e-63
30	371	14.6	128	1	LSHB_STRCA	LUTROPIN BETA CHAIN (L	2.98e-59
31	366	14.4	166	1	LSHB_COTJA	LUTROPIN BETA CHAIN PR	4.38e-58
32	355	14.0	115	1	GTH2_THUOB	GONADOTROPIN BETA-II C	1.59e-55
33	352	13.9	159	1	LSHB_MELGA	LUTROPIN BETA CHAIN PR	7.92e-55
34	319	12.6	136	1	GTH2_FUNHE	GONADOTROPIN BETA-II C	3.20e-47
35	320	12.6	138	1	TSHB_CANFA	THYROTROPIN BETA CHAIN	1.89e-47
36	310	12.2	138	1	TSHB_PIG	THYROTROPIN BETA CHAIN	3.63e-45
37	309	12.2	138	1	TSHB_RAT	THYROTROPIN BETA CHAIN	6.13e-45
38	309	12.2	138	1	TSHB_BOVIN	THYROTROPIN BETA CHAIN	6.13e-45
39	308	12.1	138	1	TSHB_HUMAN	THYROTROPIN BETA CHAIN	1.03e-44
40	305	12.0	130	1	FSHB_MOUSE	FOLLITROPIN BETA CHAIN	4.98e-44
41	306	12.0	138	1	TSHB_MOUSE	THYROTROPIN BETA CHAIN	2.95e-44
42	303	11.9	130	1	FSHB_RAT	FOLLITROPIN BETA CHAIN	1.42e-43
43	297	11.7	118	1	FSHB_HORSE	FOLLITROPIN BETA CHAIN	3.24e-42
44	289	11.4	129	1	FSHB_SHEEP	FOLLITROPIN BETA CHAIN	2.07e-40
45	281	11.1	129	1	FSHB_HUMAN	FOLLITROPIN BETA CHAIN	1.30e-38

ALIGNMENTS

RESULT 1
ID TNR1_HUMAN STANDARD; PRT; 455 AA.
AC P19438;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
GN TNFR1 OR TNFAR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 90235285.
RA SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL CELL 61:361-370(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90235284.
RA LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA TABUCHI H., LESSLAUER W.;
RL CELL 61:351-359(1990).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE; 91006021.
RA NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA ADERKA D., HOLTMANN H., WALLACH D.;
RL EMBO J. 9:3269-3278(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91090841.
RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL DNA CELL BIOL. 9:705-715(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 91017509.
RA GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92250049.
RA FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;

```
RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RL   CELL 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KHONO H., SPRANG S.R.;
RL   STRUCTURE 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; X55313; G37224; -.
DR   EMBL; M33294; G339745; -.
DR   EMBL; M58286; G339754; -.
DR   EMBL; M63121; G339756; -.
DR   EMBL; M75866; G339750; -.
DR   EMBL; M75864; G339750; JOINED.
DR   EMBL; M75865; G339750; JOINED.
DR   EMBL; M60275; G339760; -.
DR   EMBL; A21522; G579600; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL        1    21
FT   CHAIN        22   455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN        41   291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN       22   211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212   234       POTENTIAL.
FT   DOMAIN      235   455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43   196       4 X TNFR-CYS.
FT   REPEAT       43    82       TNFR-CYS 1.
FT   REPEAT       83   125       TNFR-CYS 2.
FT   REPEAT      126   166       TNFR-CYS 3.
FT   REPEAT      167   196       TNFR-CYS 4.
FT   DOMAIN      356   441       DEATH DOMAIN.
FT   DISULFID     44    58
FT   DISULFID     59    72
FT   DISULFID     62    81
FT   DISULFID     84    99
FT   DISULFID    102   117
FT   DISULFID    105   125
FT   DISULFID    127   143
FT   DISULFID    146   158
FT   DISULFID    149   166
FT   DISULFID    168   179
FT   DISULFID    182   191
FT   DISULFID    185   195
FT   CARBOHYD     54    54       POTENTIAL.
FT   CARBOHYD    145   145       POTENTIAL.
FT   CARBOHYD    151   151       POTENTIAL.
FT   CONFLICT    412   412       MISSING (IN REF. 4).
FT   CONFLICT    443   446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  CE0EA06F CRC32;

  Query Match           52.0%;  Score 1322;  DB 1;  Length 455;
  Best Local Similarity 100.0%;  Pred. No. 6.45e-296;
  Matches   171;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    2
ID   CGHB_HUMAN     STANDARD;      PRT;   165 AA.
AC   P01233;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81012134.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 286:684-687(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
RN   [4]
RP   SEQUENCE OF 1-20.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 21-165.
RX   MEDLINE; 75211304.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [6]
RP   PRELIMINARY SEQUENCE OF 21-165.
RX   MEDLINE; 74011267.
RA   CARLSEN R.B., BAHL O.P., SWAMINATHAN N.;
RL   J. BIOL. CHEM. 248:6810-6827(1973).
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RN   [7]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE; 86195987.
RA   POLICASTRO P.F., DANIELS-MCQUEEN S., CARLE G., BOIME I.;
RL   J. BIOL. CHEM. 261:5907-5916(1986).
RN   [8]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81215630.
RA   MISE T., BAHL O.P.;
RL   J. BIOL. CHEM. 256:6587-6592(1981).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE; 90094415.
RA   SACCUZO BEEBE J., MOUNTJOY K., KRZESICKI R.F., PERINI F.,
RA   RUDDON R.W.;
RL   J. BIOL. CHEM. 265:312-317(1990).
RN   [10]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 92314469.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   GLYCOBIOLOGY 1:393-404(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
DR   EMBL; J00117; G180437; -.
DR   EMBL; M13504; G463088; -.
DR   EMBL; M13505; G463089; -.
DR   EMBL; M13503; G463090; -.
DR   EMBL; K03189; G180453; -.
DR   EMBL; K03187; G180453; JOINED.
DR   EMBL; K03188; G180453; JOINED.
DR   PIR; A01502; KTHUB.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   MIM; 118860; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT   SIGNAL        1     20
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77
FT   DISULFID     43     92
FT   DISULFID     46    130
FT   DISULFID     54    108
FT   DISULFID     58    110
FT   DISULFID    113    120
FT   CARBOHYD     33     33
FT   CARBOHYD     50     50
FT   CARBOHYD    141    141
FT   CARBOHYD    147    147
FT   CARBOHYD    152    152
FT   CARBOHYD    158    158
FT   VARIANT      137    137       D -> A (IN GENE 6).
SQ   SEQUENCE   165 AA;  17739 MW;  FF1D4802 CRC32;

  Query Match           40.5%;  Score 1030;  DB 1;  Length 165;
  Best Local Similarity 100.0%;  Pred. No. 1.12e-221;
  Matches   139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     27 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 146
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    147 SLPSPSRLPGPSDTPILPQ 165
        ||||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT    3
ID   TNR1_PIG       STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUTER B., PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; U19994; G1141753; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    233       POTENTIAL.
FT   DOMAIN      234    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      362    447       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD     86     86       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
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FT   CARBOHYD    151    151       POTENTIAL.
SQ   SEQUENCE   461 AA;  50696 MW;  8E2C350A CRC32;

  Query Match           40.5%;  Score 1028;  DB 1;  Length 461;
  Best Local Similarity  73.1%;  Pred. No. 3.59e-221;
  Matches   125;  Conservative   24;  Mismatches  21;  Indels   1;  Gaps   1;

Db     41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|:|||||| |||| |||||||||||||| ||| ||| |||||||::|:|||||||| :||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |||||| ||:|||||:|||||||||||||||| |||| ||||:||||| ||||:|:| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPATSETRNDFQDTGTT 210
          ||:|:| ||:|||||::||||| |||:: :| :|| :  |  :  :|:|||
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    4
ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL   MOL. CELL. BIOL. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL   EUR. J. IMMUNOL. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL   IMMUNOGENETICS 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RL   IMMUNOGENETICS 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL   MOL. IMMUNOL. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M60468; G199826; -.
DR   EMBL; M59377; G202097; -.
DR   EMBL; X59238; G53579; -.
DR   EMBL; X57796; G54849; -.
DR   EMBL; L26349; G430733; -.
DR   EMBL; M76656; G202102; -.
DR   EMBL; M88067; G202102; JOINED.
DR   EMBL; M76655; G202102; JOINED.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1TNR.
DR   MGD; MGI:98781; TNFR1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235       POTENTIAL.
FT   DOMAIN      236    454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      356    441       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    202    202       POTENTIAL.
FT   CONFLICT    394    394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  4B6EEC09 CRC32;

  Query Match           37.8%;  Score 960;  DB 1;  Length 454;
  Best Local Similarity  68.6%;  Pred. No. 5.34e-204;
  Matches   118;  Conservative   27;  Mismatches  26;  Indels   1;  Gaps   1;

Db     41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          ||:|||||||:|: |||||||||||||| :|||:||:|| ||||| |:||||:| ||:||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          ||  |||||:|||||:|  |:|||||: ||:::| ||  ||| :|| |:|||| ::| |
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
          ||||| |||||||||:|||:||:|||: || |||||  : ||   :||||:
Qy    143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ-IENVKGTEDSGTT 193


RESULT    5
ID   TNR1_RAT       STANDARD;      PRT;   461 AA.
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AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M63122; G207362; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      363    448       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CARBOHYD    201    201       POTENTIAL.
SQ   SEQUENCE   461 AA;  50969 MW;  82F68B08 CRC32;

  Query Match           37.2%;  Score 944;  DB 1;  Length 461;
  Best Local Similarity  67.3%;  Pred. No. 5.76e-200;
  Matches   115;  Conservative   25;  Mismatches  31;  Indels   0;  Gaps   0;

Db      41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
           |::|||||| || ||||||||||||||| :|||:|||:| |  |: |:||||:||:|:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
           ||  ||||| |||||:|  | ||||||:|||:::| ||  ||| :|| |:|||| ::| |
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTA 211
           |||||| ||||||| ||| :||:|||: || ||||| : ||   :||||:
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    6
ID   CGHB_PAPAN     STANDARD;      PRT;   165 AA.
AC   P07434;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   PAPIO ANUBIS (OLIVE BABOON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87106851.
RA   CRAWFORD R.J., TREGEAR G.W., NIALL H.D.;
RL   GENE 46:161-169(1986).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES AND AT LEAST
CC       TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
DR   EMBL; M14966; G176573; -.
DR   PIR; A25808; KTBAB.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       BY SIMILARITY.
FT   CARBOHYD     50     50       BY SIMILARITY.
FT   CARBOHYD    141    141       BY SIMILARITY.
FT   CARBOHYD    147    147       BY SIMILARITY.
FT   CARBOHYD    152    152       BY SIMILARITY.
SQ   SEQUENCE   165 AA;  17592 MW;  78987D30 CRC32;

  Query Match           33.7%;  Score 857;  DB 1;  Length 165;
  Best Local Similarity  81.3%;  Pred. No. 4.26e-178;
  Matches   113;  Conservative   14;  Mismatches  12;  Indels   0;  Gaps   0;

Db      27 PLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES 86
           | ||||||||| |||:||||:|||||||||||||| ||||:|||::||||||||:|||||
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      87 IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSSKDPPP 146
           ||||||| ||:|:|| :|||||:|||||||:|||||||||||||| :| ||||| |||
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db     147 SPPSPSRLLEPAGTPFLPQ 165
           | ||||||  |: ||:|||
Qy     318 SLPSPSRLPGPSDTPILPQ 336
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RESULT    7
ID   LSHB_HUMAN     STANDARD;      PRT;   141 AA.
AC   P01229;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [2]
RP   SEQUENCE OF 21-141.
RX   MEDLINE; 76062547.
RA   SAIRAM M.R., LI C.H.;
RL   BIOCHIM. BIOPHYS. ACTA 412:70-81(1975).
RN   [3]
RP   PRELIMINARY SEQUENCE OF 21-141.
RX   MEDLINE; 73090987.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 36:618-621(1973).
RN   [4]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 73221227.
RA   CLOSSET J., HENNEN G., LEQUIN R.M.;
RL   FEBS LETT. 29:97-100(1973).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91122088.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [6]
RP   STRUCTURE BY NMR OF 58-77.
RX   MEDLINE; 92357029.
RA   KEUTMANN H.T., HUA Q.-X., WEISS M.A.;
RL   MOL. ENDOCRINOL. 6:904-913(1992).
RN   [7]
RP   VARIANT ARG-74.
RX   MEDLINE; 92085985.
RA   WEISS J., AXELROD L., WHITCOMB R.W., HARRIS P.E., CROWLEY W.F.,
RA   JAMESON J.L.;
RL   NEW ENGL. J. MED. 326:179-183(1992).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PITUITARY.
CC   -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC       CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
DR   EMBL; X00264; E28368; -.
DR   EMBL; S71273; E91454; -.
DR   PIR; A01497; UTHUB.
DR   HSSP; P01233; 1HCN.
DR   MIM; 152780; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; PSEUDOHERMAPHRODITISM;
KW   DISEASE MUTATION.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50
FT   VARIANT      74     74       Q -> R (IN HYPOGONADISM; LACK OF
FT                                RECEPTOR-BINDING).
FT   CONFLICT     39     39       E -> Q (IN REF. 2).
FT   CONFLICT     76     76       MISSING (IN REF. 2).
FT   CONFLICT    132    135       HPQL -> PQH (IN REF. 2).
SQ   SEQUENCE   141 AA;  15345 MW;  A2457F6F CRC32;

  Query Match           29.1%;  Score 740;  DB 1;  Length 141;
  Best Local Similarity  84.4%;  Pred. No. 7.12e-149;
  Matches    92;  Conservative   12;  Mismatches   5;  Indels   0;  Gaps   0;

Db     27 PWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRDVRFES 86
          |:|:|||| |||||||||||||||||||||||||| ||||:|||:|||||| ||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 IRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQL 135
          |||||||||:||||::|||||:|: |||||:|||||||||||| |::
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 306


RESULT    8
ID   CGHB_CALJA     STANDARD;      PRT;   164 AA.
AC   P51500;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   CALLITHRIX JACCHUS (COMMON MARMOSET).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 96115012.
RA   SIMULA A.P., AMATO F., FAAST R., LOPATA A., BERKA J., NORMAN R.J.;
RL   BIOL. REPROD. 53:380-389(1995).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
DR   EMBL; U04447; G606607; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    164       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50       BY SIMILARITY.
FT   CARBOHYD    146    146       BY SIMILARITY.
FT   CARBOHYD    151    151       BY SIMILARITY.
SQ   SEQUENCE   164 AA;  17712 MW;  E36A4DB3 CRC32;

  Query Match           27.9%;  Score 709;  DB 1;  Length 164;
  Best Local Similarity  64.7%;  Pred. No. 3.56e-141;
  Matches    90;  Conservative   25;  Mismatches  23;  Indels   1;  Gaps   1;

Db     27 PLCRPVNAILAAEKEGCPVCVAFNTTICAGYCSSMVRVLQTILPPLPQSVCNYHELRFTS 86
          | |||:|| || |||||||:: |||||||||::| |||| :||:||| ||||:::|| |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 VRLPGCRPGVDPVVSMPVALSCRCGLCRRSYSDCGSLRNEPLGCDYSTFQDSSS-KDPPR 145
          :|||||  ||:|||| :|||||:|:||||| :|||: :: || || : |||||| | ||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317
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Db    146 NLTSPSQLLEPADPPLVPQ 164
          :| |||:|  |:| |::||
Qy    318 SLPSPSRLPGPSDTPILPQ 336


RESULT   9
ID   LSHB_EQUAS     STANDARD;      PRT;   169 AA.
AC   P19794;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS ASINUS (DONKEY).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CHOPINEAU M., COMBARNOUS Y., ALLEN W.R., STEWART F.;
RL   SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90262634.
RA   LEIGH S.E.A., STEWART F.;
RL   J. MOL. ENDOCRINOL. 4:143-150(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X80116; G510971; -.
DR   EMBL; X53669; E27544; ALT_SEQ.
DR   PIR; S15676; S15676.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       PROBABLE.
SQ   SEQUENCE   169 AA;  17943 MW;  9D4B5421 CRC32;

  Query Match           24.8%;  Score 630;  DB 1;  Length 169;
  Best Local Similarity  63.4%;  Pred. No. 1.18e-121;
  Matches    85;  Conservative   21;  Mismatches  23;  Indels   5;  Gaps   4;

Db     27 PLCRPINATLAAEKEACPICITFTTSICAGYCRSMVRVMPAALPPIPQPVCTYRELRFGS 86
          | ||||||||| |||:||:|||  |:|||||| :| ||: : ||::|| || ||::|| |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 IRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACA-P--QTSSSCKDPPS 143
          ||||||| ||:|:||::|||||:|: ||  |||||||:||||:|  |  | ||| | ||:
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    144 QPLTSTSTPTPGAS 157
           :| | |   ||:|
Qy    318 -SLPSPS-RLPGPS 329


RESULT   10
ID   LSHB_BOVIN     STANDARD;      PRT;   141 AA.
AC   P04651;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85207729.
RA   VIRGIN J.B., SILVER B.J., THOMASON A.R., NILSON J.H.;
RL   J. BIOL. CHEM. 260:7072-7077(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85182575.
RA   MAURER R.A.;
RL   J. BIOL. CHEM. 260:4684-4687(1985).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 74075724.
RA   MAGHUIN-ROGISTER G., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; M10077; G163301; -.
DR   EMBL; M11506; G163299; -.
DR   PIR; A01499; UTBOB.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33
FT   CONFLICT      1      2       MISSING (IN REF. 2).
FT   CONFLICT     74     74       Q -> E (IN REF. 3).
FT   CONFLICT    112    112       P -> S (IN REF. 2).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
FT   CONFLICT    126    126       Q -> E (IN REF. 3).
SQ   SEQUENCE   141 AA;  15202 MW;  82879D1F CRC32;

  Query Match           24.2%;  Score 614;  DB 1;  Length 141;
  Best Local Similarity  64.9%;  Pred. No. 1.01e-117;
  Matches    72;  Conservative   22;  Mismatches  17;  Indels   0;  Gaps   0;

Db     27 PLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELRFAS 86
          | |:||||||| |||:|||||  |:||||||:| |||  :||::|| || |:::|| |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 VRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137
          :|||||| ||:|:||::|||||:|: || |:||||||: :||:|| | : |
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 308


RESULT   11
ID   LSHB_HORSE     STANDARD;      PRT;   169 AA.
AC   P08751; P01234;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS CABALLUS (HORSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE; 92357035.
RA   SHERMAN G.B., WOLFE M.W., FARMERIE T.A., CLAY C.M.,
RA   THREADGILL D.S., SHARP D.C., NILSON J.H.;
RL   MOL. ENDOCRINOL. 6:951-959(1992).
RN   [2]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250476.
RA   BOUSFIELD G.R., LIU W.-K., SUGINO H., WARD D.N.;
RL   J. BIOL. CHEM. 262:8610-8620(1987).
RN   [3]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250475.
RA   SUGINO H., BOUSFIELD G.R., MOORE W.T. JR., WARD D.N.;
RL   J. BIOL. CHEM. 262:8603-8609(1987).
RN   [4]
RP   CHORIOGONADOTROPIN, PARTIAL SEQUENCE.
RA   WARD D.N., MOORE W.T. JR., BURLEIGH B.D.;
RL   J. PROTEIN CHEM. 1:263-280(1982).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 90235854.
RA   DAMM J.B.L., HARD K., KAMERLING J.P., VAN DEDEM G.W.K.,
RA   VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 189:175-183(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- PTM: AT LEAST FOUR O-GLYCOSYLATION SITES ARE PRESENT.
DR   EMBL; S41704; G252741; -.
DR   PIR; A01503; KTHOB.
DR   PIR; A29304; A29304.
DR   PIR; A29305; A29305.
DR   PIR; A41917; A41917.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       GLYCAN SHOWING A REMARKABLY STRUCTURAL
FT                                HETEROGENEITY.
SQ   SEQUENCE   169 AA;  17865 MW;  9AB1CAA3 CRC32;

  Query Match           24.1%;  Score 613;  DB 1;  Length 169;
  Best Local Similarity  62.7%;  Pred. No. 1.77e-117;
  Matches    84;  Conservative   22;  Mismatches  23;  Indels   5;  Gaps   4;

Db     27 PLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAIPQPVCTYRELRFAS 86
          | ||||||||| |||:||:|||  |:||||||:| ||: : |||:|| || ||::|| |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 IRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTDCGVFRDQPLACA-P--QASSSSKDPPS 143
          ||||||| ||:|:||::|||||:|: |:  |||||  :|:||:|  |  | ||||| ||:
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    144 QPLTSTSTPTPGAS 157
          :| | |   ||:|
Qy    318 -SLPSPS-RLPGPS 329


RESULT   12
ID   LSHB_SHEEP     STANDARD;      PRT;   141 AA.
AC   P01231;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   OVIS ARIES (SHEEP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93351742.
RA   BROWN P., MCNEILLY J.R., WALLACE R.M., MCNEILLY A.S., CLARK A.J.;
RL   MOL. CELL. ENDOCRINOL. 93:157-165(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 90245669.
RA   D'ANGELO-BERNARD G., MOUMNI M., JUTISZ M., COUNIS R.;
RL   NUCLEIC ACIDS RES. 18:2175-2175(1990).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 72211145.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., HOLCOMB G.N., WARD D.N.;
RL   J. BIOL. CHEM. 247:4365-4381(1972).
RN   [4]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 73190035.
RA   SAIRAM M.R., SAMY T.S.A., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:572-586(1972).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91006170.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; S64695; G408241; -.
DR   EMBL; X52488; G1320; -.
DR   PIR; A01500; UTSHB.
DR   PIR; S09232; S09232.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   MOD_RES      21     21       BLOCKED.
FT   CARBOHYD     33     33
FT   VARIANT     138    141       MISSING (IN SOME MOLECULES).
FT   CONFLICT     30     30       Q -> E (IN REF. 4).
FT   CONFLICT     59     59       L -> P (IN REF. 1).
FT   CONFLICT     63     63       R -> Q (IN REF. 2).
FT   CONFLICT     71     72       PM -> PPM (IN REF. 4).
FT   CONFLICT     81     81       E -> Q (IN REF. 4).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3 AND 4).
FT   CONFLICT    126    126       Q -> E (IN REF. 3 AND 4).
SQ   SEQUENCE   141 AA;  15184 MW;  BA2C0204 CRC32;

  Query Match           23.7%;  Score 602;  DB 1;  Length 141;
  Best Local Similarity  64.0%;  Pred. No. 8.87e-115;
  Matches    71;  Conservative   22;  Mismatches  18;  Indels   0;  Gaps   0;

Db     27 PLCQPINATLAAEKEACPVCITFTTSICAGYCLSMKRVLPVILPPMPQRVCTYHELRFAS 86
          | |:||||||| |||:|||||  |:|||||| :| |||  :|||::|| || |:::|| |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
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Db     87 VRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137
          :|||||| ||:|:||::|||||:|: || |:||||||: :||:|| | : |
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 308


RESULT   13
ID   LSHB_PIG       STANDARD;      PRT;   141 AA.
AC   P01232;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91063934.
RA   EZASHI T., HIRAI T., KATO T., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 5:137-146(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89306142.
RA   KATO Y., HIRAI T.;
RL   MOL. CELL. ENDOCRINOL. 62:47-53(1989).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 74075724.
RA   MAGHUIN-ROGISTER G., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; D00579; G217694; -.
DR   PIR; A30322; UTPGB.
DR   PIR; A48170; A48170.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33
FT   MOD_RES      21     21       BLOCKED.
FT   VARIANT      30     30       R -> Z.
FT   CONFLICT     40     40       N -> D (IN REF. 3).
FT   CONFLICT     62     62       V -> R (IN REF. 3).
FT   CONFLICT     83     83       S -> I (IN REF. 3).
FT   CONFLICT     87     87       I -> S (IN REF. 3).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
SQ   SEQUENCE   141 AA;  14889 MW;  DA2EF539 CRC32;

  Query Match           23.5%;  Score 598;  DB 1;  Length 141;
  Best Local Similarity  66.4%;  Pred. No. 8.48e-114;
  Matches    71;  Conservative   19;  Mismatches  17;  Indels   0;  Gaps   0;

Db     27 PLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELSFAS 86
          | |||||||||| |:|:|||||||  |:|||||||:| ||| : ||::|| || ||:: | |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 IRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDRP 133
          ||||||| ||:| ||::|||||:|: || |::|||||: :||:|| |
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 304


RESULT   14
ID   LSHB_RAT       STANDARD;      PRT;   141 AA.
AC   P01230;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE; 83273673.
RA   CHIN W.W., GODINE J.E., KLEIN D.R., CHANG A.S., TAN L.K.,
RA   HABENER J.F.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 80:4649-4653(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85080043.
RA   JAMESON L., CHIN W.W., HOLLENBERG A.N., CHANG A.S., HABENER J.F.;
RL   J. BIOL. CHEM. 259:15474-15480(1984).
RN   [3]
RP   SEQUENCE OF 4-141 FROM N.A.
RC   STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   ZOOL. SCI. 7:877-885(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01542; G758262; -.
DR   EMBL; J00749; G205176; -.
DR   EMBL; D00576; G220808; -.
DR   PIR; A01498; UTRTB.
DR   PIR; S42527; S42527.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       PROBABLE.
SQ   SEQUENCE   141 AA;  15177 MW;  6E0C19BA CRC32;

  Query Match           23.5%;  Score 597;  DB 1;  Length 141;
  Best Local Similarity  64.2%;  Pred. No. 1.49e-113;
  Matches    70;  Conservative   23;  Mismatches  16;  Indels   0;  Gaps   0;

Db     27 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELRFAS 86
          | |||:||||| |:| ||||||  |:||||||:| ||| : ||::|| || ||::|| |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLPHL 135
          :|||||| ||:|:||::|||||:|: || |::|||||: :|:||| |::
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 306


RESULT   15
ID   LSHB_BALAC     STANDARD;      PRT;   118 AA.
AC   P33088;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
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DE   LUTROPIN BETA CHAIN (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.
RA   KARASEV V.S., PANKOV Y.A.;
RL   BIOKHIMIIA 50:1972-1986(1985).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; PN0139; PN0139.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; FALSE_NEG.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID      9     57       BY SIMILARITY.
FT   DISULFID     23     72       BY SIMILARITY.
FT   DISULFID     26    110       BY SIMILARITY.
FT   DISULFID     34     88       BY SIMILARITY.
FT   DISULFID     38     90       BY SIMILARITY.
FT   DISULFID     93    100       BY SIMILARITY.
FT   CARBOHYD     13     13
SQ   SEQUENCE   118 AA;  12414 MW;  DE251ECF CRC32;

  Query Match           23.4%;  Score 595;  DB 1;  Length 118;
  Best Local Similarity  60.6%;  Pred. No. 4.61e-113;
  Matches    66;  Conservative   25;  Mismatches  17;  Indels   1;  Gaps   1;

Db       7 PLCRPINATLAAZBZACPVCITFTTSICAGYCPSMVRVLPAALPPVPZPVCTYRZLRFAS 66
           | ||||||||| ::::|||||| |:|||||||:| ||| : ||::|: || ||::|| |
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      67 IRLPGCPPGVBPMVSFPVALSCHCGPCRLSSSBCGPGRAZPLACBRSPR 115
           ||||||| ||:|:||::|||||:|: || |:::||  : :||:|:  ||
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD-DPR 305


Search completed: Wed May  6 09:03:50 1998
Job time : 21 secs.
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:04:08 1998; MasPar time 17.16 Seconds
824.654 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-8
Description: (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.....PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 43.140; Variance 76.550; scale 0.564

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1024	40.3	145	2	Q13991	BETA-GONADOTROPIN.	1.18e-204
2	1024	40.3	165	2	Q14000	CHORIONIC GONADOTROPIN	1.18e-204
3	975	38.4	471	4	O19131	TUMOR NECROSIS FACTOR-	3.72e-193
4	945	37.2	180	4	Q95185	TUMOUR NECROSIS FACTOR	3.95e-186
5	596	23.5	135	4	O19102	LUTEINIZING HORMONE BE	2.28e-105
6	595	23.4	139	10	Q62778	TESTICULAR LUTEINIZING	3.86e-105
7	582	22.9	141	10	Q60844	LUTEINIZING HORMONE BE	3.51e-102
8	430	16.9	140	12	Q98849	GONADOTROPIN II BETA S	4.94e-68
9	391	15.4	80	10	Q63013	TESTICULAR LUTEINIZING	1.91e-59
10	361	14.2	147	12	Q91121	GONADOTROPIN II BETA S	6.60e-53
11	353	13.9	137	12	Q90225	GONADOTROPIN BETA-SUBU	3.56e-51
12	321	12.6	130	12	O13050	GONADOTROPIN I BETA SU	2.68e-44
13	312	12.3	130	12	Q98848	GONADOTROPIN I BETA SU	2.21e-42
14	306	12.0	138	4	P79357	THYROTROPIN BETA CHAIN	4.14e-41
15	304	12.0	138	4	Q28376	THYROTROPIN BETA CHAIN	1.10e-40
16	303	11.9	138	2	Q16163	THYROID-STIMULATING HO	1.79e-40
17	301	11.8	150	12	O13051	THYROTROPIN BETA SUBUN	4.73e-40
18	294	11.6	147	12	O13052	THYROTROPIN BETA SUBUN	1.42e-38
19	289	11.4	150	12	O13049	THYROTROPIN BETA SUBUN	1.60e-37
20	271	10.7	101	10	Q62590	BETA-THYROTROPIN (FRAG	9.17e-34
21	250	9.8	253	2	O00276	LYMPHOCYTE ASSOCIATED	1.96e-29
22	249	9.8	277	2	O14866	SOLUBLE DEATH RECEPTOR	3.14e-29
23	250	9.8	380	2	O00280	LYMPHOCYTE ASSOCIATED	1.96e-29
24	250	9.8	418	2	O00275	LYMPHOCYTE ASSOCIATED	1.96e-29
25	249	9.8	426	2	O14865	DEATH RECEPTOR 3 BETA.	3.14e-29
26	214	8.4	348	11	Q85407	HOMOLOG OF VACCINIA VI	3.49e-22
27	214	8.4	349	11	Q89098	GARCIA-1966 RIGHT NEAR	3.49e-22
28	214	8.4	349	11	Q89118	SOMALIA-1977 RIGHT NEA	3.49e-22
29	210	8.3	87	2	Q15962	THYROTROPIN BETA SUBUN	2.15e-21
30	210	8.3	355	11	Q85308	SECRETED RECEPTOR BIND	2.15e-21
31	205	8.1	61	10	Q63012	TESTICULAR LUTEINIZING	2.07e-20
32	206	8.1	459	10	Q62327	TUMOR NECROSIS FACTOR	1.32e-20
33	187	7.4	267	4	O02764	OX40 PRECURSOR (FRAGME	6.32e-17
34	182	7.2	259	2	O14755	TRAIL RECEPTOR 3.	5.67e-16
35	180	7.1	283	2	Q92956	HERPESVIRUS ENTRY MEDI	1.36e-15
36	180	7.1	299	2	O14798	CYTOTOXIC TRAIL RECEPT	1.36e-15
37	180	7.1	401	10	O08727	OSTEOPROTEGERIN.	1.36e-15
38	178	7.0	324	10	Q63199	FAS ANTIGEN PRECURSOR.	3.24e-15
39	179	7.0	401	2	O00300	OSTEOPROTEGERIN.	2.10e-15
40	178	7.0	411	2	O15517	CYTOTOXIC TRAIL RECEPT	3.24e-15
41	178	7.0	411	2	O15508	P53-REGULATED DNA DAMA	3.24e-15
42	178	7.0	411	2	O14720	DEATH RECEPTOR 5.	3.24e-15
43	179	7.0	425	2	Q16042	TUMOR NECROSIS FACTOR	2.10e-15
44	178	7.0	440	2	O14763	APOPTOSIS INDUCING REC	3.24e-15
45	178	7.0	440	2	O15531	APOPTOSIS INDUCING PRO	3.24e-15

ALIGNMENTS

RESULT 1
ID Q13991 PRELIMINARY; PRT; 145 AA.

AC Q13991;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE BETA-GONADOTROPIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84093590.
RA TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL NATURE 307:37-40(1984).
DR EMBL; X00266; E27486; -.
KW SIGNAL.
SQ SEQUENCE 145 AA; 15488 MW; AC321C60 CRC32;

Query Match 40.3%; Score 1024; DB 2; Length 145;
Best Local Similarity 99.3%; Pred. No. 1.18e-204;
Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP 126
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db    127 SLPSPSRLPGPSDTPILPQ 145
          ||||||||||||||||||
Qy    318 SLPSPSRLPGPSDTPILPQ 336
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RESULT 2
ID Q14000 PRELIMINARY; PRT; 165 AA.

AC Q14000;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

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DE   CHORIONIC GONADOTROPIN BETA SUBUNIT.
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
DR   EMBL; K03183; G180444; -.
DR   EMBL; K00092; G180444; JOINED.
DR   EMBL; K03182; G180444; JOINED.
SQ   SEQUENCE   165 AA;  17729 MW;  B1CAA0B1 CRC32;

  Query Match           40.3%;  Score 1024;  DB 2;  Length 165;
  Best Local Similarity  99.3%;  Pred. No. 1.18e-204;
  Matches   138;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      27 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPPP 146
           ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Db     147 SLPSPSRLPGPSDTPILPQ 165
           |||||||||||||||||||
Qy     318 SLPSPSRLPGPSDTPILPQ 336


RESULT    3
ID   O19131         PRELIMINARY;   PRT;   471 AA.

AC   O19131;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR-RECEPTOR I.
GN   TNF-RI.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AORTA;
RA   LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U90937; G2290398; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
SQ   SEQUENCE   471 AA;  51368 MW;  1D60FF4A CRC32;

  Query Match           38.4%;  Score 975;  DB 4;  Length 471;
  Best Local Similarity  67.8%;  Pred. No. 3.72e-193;
  Matches   116;  Conservative   27;  Mismatches  27;  Indels   1;  Gaps   1;

Db      41 ESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCL 100
           :| |||||| |||::|||||||||||||||||||||:|||| | :|:::|| |||||:||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160
           |||:|| || |||||:| ||||||||||||||| ||:|  |:|:||||| ||||:::|||
Qy      83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 RQDTICHCHMGFFLKGAKCISCHDCKNK-ECEKLCPTRPSTGKDSQDPGTT 210
           :|:|:| || ||||:   |:|| :||:  || |||  :    | ::|:|||
Qy     143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193


RESULT    4
ID   Q95185         PRELIMINARY;   PRT;   180 AA.

AC   Q95185;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN   TNFR-1.
OS   FELIS SILVESTRIS CATUS (CAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CARNIVORA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   DUTHIE S., NASIR L., ECKERSALL P.D.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72344; G1613880; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
FT   NON_TER       1      1
FT   NON_TER     180    180
SQ   SEQUENCE   180 AA;  20399 MW;  5452A6B2 CRC32;

  Query Match           37.2%;  Score 945;  DB 4;  Length 180;
  Best Local Similarity  86.0%;  Pred. No. 3.95e-186;
  Matches   117;  Conservative    9;  Mismatches  10;  Indels   0;  Gaps   0;

Db      45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
           ||||||||||:|||||||||||||||:||| |||||||:|:|||||| ||:|||||
Qy      26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db     105 KCRKEMYQVEISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQN 164
           |||||| |||||:||| |||||||||||||| ||||  |||:||||||||||::|| | ||
Qy      86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db     165 TVCTCHAGFFLRGNEC 180
           |||||||||||| |||
Qy     146 TVCTCHAGFFLRENEC 161


RESULT    5
ID   O19102         PRELIMINARY;   PRT;   135 AA.

AC   O19102;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LUTEINIZING HORMONE BETA SUBUNIT (FRAGMENT).
OS   CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED RHINOCEROS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 97449288.
RA   SHERMAN G.B., LUND L.A., BUNICK D., WINN R.J.;
RL   GENE 195:131-139(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   SHERMAN G.B., LUND L.A.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72659; G2462779; -.
FT   NON_TER       1      1
SQ   SEQUENCE   135 AA;  14212 MW;  F4F196D2 CRC32;

  Query Match           23.5%;  Score 596;  DB 4;  Length 135;
  Best Local Similarity  66.4%;  Pred. No. 2.28e-105;
  Matches    71;  Conservative   20;  Mismatches  16;  Indels   0;  Gaps   0;

Db      21 PLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPAPQPVCTYHELRFAS 80
           | ||||||||| |:|:|||||| |:||||||:| ||| : ||: || || |:::|| |
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      81 IRLPGCPPGVDPMVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDRP 127
           ||||||| ||:|:||::|||||:|: || |::|||||: :|||:|| |
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Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 304


RESULT    6
ID   Q62778         PRELIMINARY;   PRT;   139 AA.

AC   Q62778;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   TESTICULAR LUTEINIZING HORMONE BETA-SUBUNIT.
GN   TLHB1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAQUE DAWLEY;
RX   MEDLINE; 95283549.
RA   ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR   EMBL; U25653; G915217; -.
SQ   SEQUENCE   139 AA;  14880 MW;  5B2E7DBF CRC32;

  Query Match           23.4%;  Score 595;  DB 10;  Length 139;
  Best Local Similarity  63.3%;  Pred. No. 3.86e-105;
  Matches    69;  Conservative   24;  Mismatches  16;  Indels   0;  Gaps   0;

Db     25 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRILPAALPPVPQPVCTYRELRFAS 84
          | |||:||||| |:| |||||| |:|||||||:| |:| : ||::|| || ||::|| |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     85 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLPHL 133
          :|||||| ||:|:||::|||||:|: || |::|||||: :|:||| |::
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 306


RESULT    7
ID   Q60844         PRELIMINARY;   PRT;   141 AA.

AC   Q60844;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LUTEINIZING HORMONE BETA (LUTENIZING HORMONE BETA-SUBUNIT).
GN   LHB.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129 SVEV;
RA   KAPUR V., MATZUK M.M.;
RL   SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U25145; G930345; -.
DR   MGD; MGI:96782; LHB.
SQ   SEQUENCE   141 AA;  15028 MW;  BE50AB2B CRC32;

  Query Match           22.9%;  Score 582;  DB 10;  Length 141;
  Best Local Similarity  62.4%;  Pred. No. 3.51e-102;
  Matches    68;  Conservative   24;  Mismatches  17;  Indels   0;  Gaps   0;

Db     27 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELAFAS 86
          | |||:||||| |:| |||||| |:|||||||:| ||| : ||::|| || ||:: | |
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMACDLPHL 135
          :|||||| ||:|:||::|||||:|: || |::|||||: :|::|| |::
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 306


RESULT    8
ID   Q98849         PRELIMINARY;   PRT;   140 AA.

AC   Q98849;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D88024; G1644243; -.
KW   SIGNAL.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    140       GONADOTROPIN II BETA SUBUNIT.
SQ   SEQUENCE   140 AA;  15533 MW;  7205FD03 CRC32;

  Query Match           16.9%;  Score 430;  DB 12;  Length 140;
  Best Local Similarity  50.0%;  Pred. No. 4.94e-68;
  Matches    54;  Conservative   22;  Mismatches  32;  Indels   0;  Gaps   0;

Db     27 PPCEPVNETVAVEKEGCPKCLVLQTTICSGHCLTKEPVYKSPFSTVYQHVCTYRDVRYET 86
          | | |:| |:|||||||| |: : |||:| | |:  |  : :::: | || |||||:|:
Qy    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db     87 VRLPDCPPGVDPHITYPVALSCDCSLCTMDTSDCTIESLQPDFCMSQR 134
          :||| || ||:| ::|:|||||:|:||   |:||     :|  |   |
Qy    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 305


RESULT    9
ID   Q63013         PRELIMINARY;   PRT;    80 AA.

AC   Q63013;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   TESTICULAR LUTEINIZING HORMONE BETA SUBUNIT.
GN   TLHB3.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAQUE DAWLEY;
RX   MEDLINE; 95283549.
RA   ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR   EMBL; U25803; G904026; -.
SQ   SEQUENCE   80 AA;  8515 MW;  74FA772D CRC32;

  Query Match           15.4%;  Score 391;  DB 10;  Length 80;
  Best Local Similarity  60.0%;  Pred. No. 1.91e-59;
  Matches    45;  Conservative   18;  Mismatches  11;  Indels   1;  Gaps   1;

Db      1 MVRVLPAALPPVPQPVCTYRE-RFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDC 59
          | ||| : ||::|| || ||: || |:|||||| ||:|:||::|||||:|: || |::||
Qy    232 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291

Db     60 GGPRTQPMTCDLPHL 74
          |||: :|:||| |::
Qy    292 GGPKDHPLTCDDPRF 306


RESULT   10
ID   Q91121         PRELIMINARY;   PRT;   147 AA.

AC   Q91121;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
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DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS   MORONE SAXATILIS (STRIPED BASS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
DR   EMBL; L35096; G598255; -.
KW   SIGNAL.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33    147       GONADOTROPIN II BETA SUBUNIT.
SQ   SEQUENCE   147 AA;  16398 MW;  292F2F62 CRC32;

  Query Match           14.2%;  Score 361;  DB 12;  Length 147;
  Best Local Similarity  44.5%;  Pred. No. 6.60e-53;
  Matches    49;  Conservative   24;  Mismatches  36;  Indels   1;  Gaps   1;

Db      36 PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVIKIPFSNVYQHVCTYRDLHYKT 95
           | |: || |:::|||||| |  |:||||:| | |:  |:   :: : | || |||::: :
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      96 FELPDCPPGVDPTVTYPVAQSCHCGRCAMDTSDCTFESLQPNFCMNDIPF 145
           : || || ||:| |:|:|| ||:|: |   |:||     :|  | :|  |
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC-DDPRF 306


RESULT   11
ID   Q90225         PRELIMINARY;   PRT;   137 AA.

AC   Q90225;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN BETA-SUBUNIT.
OS   ACANTHOPAGRUS LATUS.
OC   EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES;
OC   ACTINOPTERYGII; PERCIFORMES; PERCOIDEI; SPARIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   TSAI H.J., YANG L.T.;
RL   SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; L11722; G437308; -.
SQ   SEQUENCE   137 AA;  15330 MW;  F87577B5 CRC32;

  Query Match           13.9%;  Score 353;  DB 12;  Length 137;
  Best Local Similarity  44.5%;  Pred. No. 3.56e-51;
  Matches    49;  Conservative   22;  Mismatches  36;  Indels   3;  Gaps   3;

Db      28 PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVMKTRY-VYQHV-CTYRDLHYKT 85
           | |: || |:::|||||| |  |:||||:| | |:  |:        :| | |||::: :
Qy     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db      86 FELPDCPLGVDPTVTYPVAVSCNCGLCAMDTSDCTFESLQPNFCMNDIPF 135
           : || || ||:| |:|:||:|| |:||   |:||     :|  | :|  |
Qy     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC-DDPRF 306


RESULT   12
ID   O13050         PRELIMINARY;   PRT;   130 AA.

AC   O13050;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CYPRINUS CARPIO (COMMON CARP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., IWASAKI M., KONDO H., YOSHIURA Y., WATABE S.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB003583; D1020895; -.
KW   SIGNAL.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    130       GONADOTROPIN I BETA SUBUNIT.
SQ   SEQUENCE   130 AA;  14393 MW;  3D37E6B1 CRC32;

  Query Match           12.6%;  Score 321;  DB 12;  Length 130;
  Best Local Similarity  41.3%;  Pred. No. 2.68e-44;
  Matches    43;  Conservative   24;  Mismatches  35;  Indels   2;  Gaps   2;

Db      26 CRLTNISITVESEECGSCITIDTTACAGLCKTQESVYRSPL-MLSYQNTCNFREWTYETY 84
           ||  | :::|| | |  |||::|| ||| | |   | :: |  |: |  ||:|:  :|:
Qy     200 CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI 258

Db      85 EFKGCPARADSVFTYPVALSCECSKCNSDITDCGALSQQTLSCN 128
           : |||   ::| :|:|||||:|: |    ||||:  :: |:|:
Qy     259 RLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 302


RESULT   13
ID   Q98848         PRELIMINARY;   PRT;   130 AA.

AC   Q98848;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D88023; G1644241; -.
KW   SIGNAL.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    130       GONADOTROPIN I BETA SUBUNIT.
SQ   SEQUENCE   130 AA;  14422 MW;  3C222BFD CRC32;

  Query Match           12.3%;  Score 312;  DB 12;  Length 130;
  Best Local Similarity  40.4%;  Pred. No. 2.21e-42;
  Matches    42;  Conservative   23;  Mismatches  37;  Indels   2;  Gaps   2;

Db      26 CRLTNISITVESEECGSCITIDTTACAGLCKTQESVYRSPL-MLSYQNTCNFREWTYETY 84
           ||  | :::|| | |  |||::|| ||| | |   | :: |  |: |  ||:|:  :|:
Qy     200 CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI 258

Db      85 EFKGCPARADSIFTYPVALSCECSKCNSDITDCGVLSQQTLGCN 128
           : |||   ::: :|:|||||:|: |    ||||   :: | |:
Qy     259 RLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 302


RESULT   14
ID   P79357         PRELIMINARY;   PRT;   138 AA.

AC   P79357;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE   THYROTROPIN BETA CHAIN.
OS   LAMA GLAMA (LLAMA).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RA   KANIA S.A., FRANK L.A., ODOM T.F.;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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DR   EMBL; U89294; G1872550; -.
SQ   SEQUENCE   138 AA;  15571 MW;  332E4E82 CRC32;

  Query Match           12.0%;  Score 306;  DB 4;  Length 138;
  Best Local Similarity  47.9%;  Pred. No. 4.14e-41;
  Matches    46;  Conservative   18;  Mismatches  26;  Indels   6;  Gaps   4;

Db      22 CIPTEYMMHVERKECAYCLTINTTICAGYC--MTRDFNGKLFLPKFALSQDVCTYRDFMY 79
           | | :  : ||:  |: |:|:|||||||||  ||| : | : ||  ||:| || |||  :
Qy     200 CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQG-V-LP--ALPQVVCNYRDVRF 255

Db      80 KTVEIPGCPHHVTPYFSYPVAVSCKCGKCDTDYSDC 115
             :: :||||: | |  ||:||:|| |: |    :||
Qy     256 ESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291


RESULT   15
ID   Q28376         PRELIMINARY;   PRT;   138 AA.

AC   Q28376;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   THYROTROPIN BETA CHAIN.
GN   TSH-BETA.
OS   EQUUS CABALLUS (HORSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RA   KANIA S.A., OLCHOWY T.W., FRANK L.A.;
RL   SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U51789; G1262916; -.
SQ   SEQUENCE   138 AA;  15663 MW;  2DA6B024 CRC32;

  Query Match           12.0%;  Score 304;  DB 4;  Length 138;
  Best Local Similarity  47.9%;  Pred. No. 1.10e-40;
  Matches    46;  Conservative   17;  Mismatches  27;  Indels   6;  Gaps   4;

Db      22 CIPTEYMMHVERKECAYCLTINTTICAGYC--MTRDINGKLFLPKYALSQDVCTYRDFMY 79
           | | :  : ||:  |: |:|:|||||||||  ||| : | : ||  ||:| || |||  :
Qy     200 CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQG-V-LP--ALPQVVCNYRDVRF 255

Db      80 KTVEIPGCPDHVTPYFSYPVAVSCKCGKCNTDYSDC 115
             :: :||||  | |  ||:||:|| |: |    :||
Qy     256 ESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291


Search completed: Wed May  6 09:05:27 1998
Job time : 79 secs.
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